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43804 SEARCH REQUEST FORM

Scientific and Technical Information Center

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Requester's Full Name: Natasha Davis Examiner #: 78462 Date: 6-4-01
 Art Unit: 1642 Phone Number 308-6410 Serial Number: 09/587574
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL
9E12 CM 9B09

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: 92-97

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search SEQ ID NO: 2, 3, 4, 5, 6, 7, 8, 9, 10

Also search conductive for diagnosis + treatment of tumors. see claims 1, 6, + 21

Search claim 15.

Point of Contact:
 Beverly Shears
 Technical Info. Specialist
 CM1 12C14 Tel: 308-4994

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	Type of Search	Vendors and cost where applicable
Searcher: <u>Beverly 24994</u>	NA Sequence (#) _____	STN <u>✓</u>
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Searcher Location: _____	Structure (#) <u>1</u>	Questel/Orbit _____
Date Searcher Picked Up: _____	Bibliographic _____	Dr.Link _____
Date Completed: <u>06-11-01</u>	Litigation <u>1</u>	Lexis/Nexis _____
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Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: _____	Other _____	Other (specify) <u>CGN</u>

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09/587574

FILE 'REGISTRY' ENTERED AT 11:09:26 ON 11 JUN 2001
E CONDUCTINE/CN

FILE 'CAPLUS' ENTERED AT 11:09:46 ON 11 JUN 2001

L1 0 S CONDUCTINE

FILE 'MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH,
JICST-EPLUS, JAPIO, CANCERLIT' ENTERED AT 11:10:14 ON 11 JUN 2001

L2 6 S L1

L3 6 DUP REM L2 (0 DUPLICATES REMOVED)

L3 ANSWER 1 OF 6 JAPIO COPYRIGHT 2001 JPO

ACCESSION NUMBER: 1996-024402 JAPIO
TITLE: GAME BALL PASSING SENSOR
INVENTOR: YOSHIKAWA TOSHISUKE
PATENT ASSIGNEE(S): KYOWA GIKEN KK, JP (CO)
PATENT INFORMATION:

PATENT NO	KIND	DATE	ERA	MAIN IPC
JP 08024402	A	19960130	Heisei	(6) A63F007-02

JP

APPLICATION INFORMATION

ST19N FORMAT: JP1994-169178 19940721

ORIGINAL: JP06169178 Heisei

SOURCE: PATENT ABSTRACTS OF JAPAN (CD-ROM), Unexamined
Applications, Vol. 96, No. 1

AN 1996-024402 JAPIO

AB PURPOSE: To prevent an erroneous operation by electromagnetic wave
or external light, and precisely detect the passing of game ball by
making an operating piece pushed into a switch housing part when the
ball passes the through-hole of a switch case, thereby a switch is
brought into non-conductive state and the passing of the
ball is detected.

CONSTITUTION: When no game ball passes a through-hole 30, one end of
an operating piece 70 supported in the inner part of a switch
housing part 40 is in the state capable of protruding into the
through-hole 30, and the energizing force of a torsion spring 60
acts on the free end part on the other end to energize the operating
piece 70 in the protruding direction. Both ends of the torsion
spring 60 come into contact with a fixed pin 54 and a contact pin 53
in this state to hold the conductive state between the connecting
terminals 51, 52 of a base 50. When a game ball passes the
through-hole 30, the operating piece 70 is pushed against the
energizing force of the torsion spring 60. Thus, one end of the
torsion spring 60 is pushed in and separated from the contact pin 53
to bring the connecting terminals 51, 52 into the non-conductive

Searcher : Shears 308-4994

state, thereby the passing of the game ball can be detected.

L3 ANSWER 2 OF 6 MEDLINE
 ACCESSION NUMBER: 90181913 MEDLINE
 DOCUMENT NUMBER: 90181913 PubMed ID: 2560672
 TITLE: [Sodium conductin of the human brain: purification and functional characterization].
 La conductine au sodium du cerveau humain: purification et caracterisation fonctionnelle.
 AUTHOR: Materne-De Rycker C
 SOURCE: BULLETIN ET MEMOIRES DE L ACADEMIE ROYALE DE MEDECINE DE BELGIQUE, (1989) 144 (8-9) 426-33.
 Journal code: BOX; 7608462. ISSN: 0377-8231.
 PUB. COUNTRY: Belgium
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: French
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199004
 ENTRY DATE: Entered STN: 19900601
 Last Updated on STN: 19900601
 Entered Medline: 19900426

AB A sodium channel enriched preparation was obtained from human brain. Human sodium channel appeared as a heterocomplex peptide alpha beta 1 beta 2. Functional properties of the protein were maintained since, after reconstitution into liposomes, ion fluxes were sensitive to sodium channel specific toxins and to membrane potential. Moreover, the reconstituted protein showed a well defined ionic selectivity.

L3 ANSWER 3 OF 6 WPIDS COPYRIGHT 2001 DERWENT INFORMATION LTD

ACCESSION NUMBER: 1988-347509 [49] WPIDS
 DOC. NO. NON-CPI: N1988-263366
 TITLE: Semiconductor shift register in memory output state
 - has two conductive type transistor connected in series between power supply terminal and node.
 DERWENT CLASS: U14
 INVENTOR(S): NAKAGAWA, K; TAKEUCHI, Y
 PATENT ASSIGNEE(S): (TOKE) TOSHIBA KK
 COUNTRY COUNT: 5
 PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
EP 293808	A	19881207	(198849)*	EN	15
R: DE FR GB					
JP 63304494	A	19881212	(198904)		
US 4856034	A	19890808	(198939)		14
EP 293808	B1	19930929	(199339)	EN	16

Searcher : Shears 308-4994

R: DE FR GB
DE 3884460 G 19931104 (199345)

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
EP 293808	A	EP 1988-108632	19880530
JP 63304494	A	JP 1987-139405	19870603
US 4856034	A	US 1988-199914	19880527
EP 293808	B1	EP 1988-108632	19880530
DE 3884460	G	DE 1988-3884460	19880530
		EP 1988-108632	19880530

FILING DETAILS:

PATENT NO	KIND	PATENT NO
DE 3884460	G Based on	EP 293808

PRIORITY APPLN. INFO: JP 1987-139405 19870603

AN 1988-347509 [49] WPIDS

AB EP 293808 A UPAB: 19930923

The circuit has a logic circuit (12) with two inputs connected to receive a control clock signal (Phi G) and an input signal (Vin) a two ~~conductine~~ type transistors (P11 P12) are connected in series between a power supply terminal and a node. The first transistor (P11) has a gate connected to receive an output signal of the logic circuit. The other transistor (P12) has a gate connected to receive the control clock signal.

A third transistor (N11) of a different conductive type connects the first node and the second power supply terminal together.

The transistor gate is connected to receive the output signal of the logic circuit.

USE/ADVANTAGE - Latch circuit or swift register in the output stage of the memory.

3

ABEQ US 4856034 A UPAB: 19930923

The semiconductor integrated circuit consists of a three-valued logic circuit connected to receive an output signal of a logic circuit to receive at one input a control clock signal and at the other input an input signal. A flip-flop circuit is composed of a clocked inverter to receive the output signal of the three-valued logic circuit, and another inverter.

ABEQ EP 293808 B UPAB: 19931123

A semiconductor integrated circuit, comprising: a logic circuit (12) consisting of a NOR gate (72) or a NAND gate (82) and having a first

and a second input connected to receive a control clock signal (G) and an input signal (Vin), respectively; first and second transistors (P11, P12) of a first conductivity type connected in series between a first power supply terminal (Vcc) and a first node (1), said first transistor (P11) having a gate connected to receive an output signal of said logic circuit, and said second transistor (P12) having a gate connected to receive the control clock signal; a third transistor (N11) of a second conductivity type connected between said first node and a second power supply terminal (Vss) and having a gate connected to receive the output signal of said logic circuit; fourth and fifth transistors (P13, P14) of the first conductivity type connected in series between said first power supply terminal and a second node (2) connected to said first node, said fourth transistor (P14) having a gate connected to receive the output signal of said logic circuit, and said fifth transistor (P13) having a gate connected to a third node (3); sixth and seventh transistors (N14, N13) of the second conductivity type connected in series between said second power supply terminal and said second node, said sixth transistor (N14) having a gate connected to receive the clock signal, and said seventh transistor (N13) having a gate connected to said third node; an eighth transistor (P15) of the first conductivity type connected between said third node and said first power supply terminal and having a gate connected to said second node; and a ninth transistor (N15) of the second conductivity type connected between said third node and said second power supply terminal, and having a gate connected to said second node; an output signal (Vout) of said semiconductor integrated circuit being taken from at least one of said second node and said third node.

Dwg.1/10

L3 ANSWER 4 OF 6 WPIDS COPYRIGHT 2001 DERWENT INFORMATION LTD
 ACCESSION NUMBER: 1978-A8315A [04] WPIDS
 TITLE: Insulated splice and terminal - is made from crimped composite strip of non-conductive and electrically conducting materials.
 DERWENT CLASS: V04
 INVENTOR(S): FISCHER, E M; MEISINGER, W R; ZAHN, I
 PATENT ASSIGNEE(S): (GEST-N) GEN STAPLE CO
 COUNTRY COUNT: 1
 PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
US 4067105	A	19780110	(197804)*		

PRIORITY APPLN. INFO: US 1973-335417 19730223; US 1974-537532

Searcher : Shears 308-4994

19741230; US 1976-711604 19760804

AN 1978-A8315A [04] WPIDS

AB US 4067105 A UPAB: 19930901

An elongated layer of non-conductive materials is adhered to an elongated layer of electrically conductive material so as to form a composite supply strip. A predetermined length is severed and crimped about the elements to be joined until the electrically conductive material is in electrical contact with the elements and so that the non-conductive material forms an outer insulated layer enclosing the splice or at least a portion of the terminal.

In a pref. method there is further step of causing the non-conductive material of the splice to "flow" whereby a resultant sealed splice is produced which is impervious to moisture and other contaminants. PRef. the non-conductive material is a thermoplastic resin and the conductive material is brass.

L3 ANSWER 5 OF 6 JAPIO COPYRIGHT 2001 JPO

ACCESSION NUMBER: 1977-115854 JAPIO

TITLE: ELECTRICALLY CONDUCTIVE RESIN AND
INTERMEDIATES AND ELECTRICALLY CONDUCTIVE COATED
PAPERS

INVENTOR: JIYOSEFU RII GAANAA

PATENT ASSIGNEE(S): DOW CHEM CO:THE, US (CO 000723)

PATENT INFORMATION:

PATENT NO	KIND	DATE	ERA	MAIN IPC
JP 52115854	A	19770928	Showa	(2) C08L025-06

JP

APPLICATION INFORMATION

ST19N FORMAT: JP1977-29130 19770316

ORIGINAL: JP52029130 Showa

PRIORITY APPLN. INFO.: US1976 668335 19760319

AN 1977-115854 JAPIO

L3 ANSWER 6 OF 6 JAPIO COPYRIGHT 2001 JPO

ACCESSION NUMBER: 1977-019984 JAPIO

TITLE: MANUFACTURE PROCESS FOR A ISOLATION LAYER USED
TO MAKE A SEMICONDUCTOR ELEMENT

INVENTOR: KOMATSU RYOSAKU; HARUHARA YOSHIO

PATENT ASSIGNEE(S): NIPPON TELEGR & TELEPH CORP <NTT>, JP (CO
000422)

PATENT INFORMATION:

PATENT NO	KIND	DATE	ERA	MAIN IPC

09/587574

JP 52019984 A 19770215 Showa (2) H01L021-76

JP

APPLICATION INFORMATION

ST19N FORMAT: JP1975-96053 19750807

ORIGINAL: JP50096053 Showa

SOURCE: PATENT ABSTRACTS OF JAPAN, Unexamined
Applications, Section: E, Sect. No. 34, Vol. 1,
No. 851, P. 1733 (19770809)

AN 1977-019984 JAPIO

AB PURPOSE: To pour p type ion to the N type semiconductor substrate an
order to make a p type **conductine** area as a isolation
layer. In this way, we make plural isolation layers at the same time
with a desired size and high precision, saving the manufacture work.

FILE 'REGISTRY' ENTERED AT 11:14:12 ON 11 JUN 2001
E CONDUCTIN/CN

L4 2 SEA ABB=ON PLU=ON ("CONDUCTIN (HUMAN FETAL BRAIN
REDUCED)"/CN OR "CONDUCTIN (HUMAN)"/CN)

FILE 'CAPLUS' ENTERED AT 11:14:41 ON 11 JUN 2001

L5 25 SEA ABB=ON PLU=ON L4 OR CONDUCTIN

L6 15 SEA ABB=ON PLU=ON L5 AND (TUMOUR OR TUMOR OR NEOPLAS?
OR CANCER? OR CARCIN?)

L6 ANSWER 1 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 2001:208094 CAPLUS

DOCUMENT NUMBER: 134:247261

TITLE: Agents for treating human diseases, especially
for treating **tumors** such as colon
cancers and melanomas or for
regenerating tissue and promoting hair growth
Birchmeier, Walter; Von Kries, Jens-peter
PATENT ASSIGNEE(S): Max-Delbruck-Centrum fur Molekulare Medizin,
Germany

SOURCE: PCT Int. Appl., 28 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: German

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001019353	A2	20010322	WO 2000-DE3104	20000907
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK,				

Searcher : Shears 308-4994

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LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ,
PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ,
UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU,
TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH,
CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE,
BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

DE 19944404 A1 20010322 DE 1999-19944404 19990916

PRIORITY APPLN. INFO.: DE 1999-19944404 A 19990916

AB The invention relates to agents for treating human diseases which are based on substances that specifically influence the binding of .beta.-catenin with LEF-1/TCF transcription factors, APC or conductin/axin. The invention particularly relates to the identification and use of hydrophobic pockets on the mol. surface in the proximity of the essential binding points for the binding partners of .beta.-catenin with the aim of optimizing these substances. The invention also relates to the use of the substances, preferably for treating tumors, e.g. colon cancers and melanomas, or for regenerating tissue and promoting hair growth.

L6 ANSWER 2 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 2000:735507 CAPLUS

DOCUMENT NUMBER: 134:28066

TITLE: Mutations in AXIN2 cause colorectal cancer with defective mismatch repair by activating .beta.-catenin/TCF signaling

AUTHOR(S): Liu, Wanguo; Dong, Xiangyang; Mai, Ming; Seelan, Ratnam S.; Taniguchi, Ken; Krishnadath, Kausilia K.; Halling, Kevin C.; Cunningham, Julie M.; Qian, Chiping; Christensen, Eric; Roche, Patrick C.; Smith, David I.; Thibodeau, Stephen N.

CORPORATE SOURCE: Div. of Experimental Pathol., Dep. of Lab. Med. and Pathol., Mayo Clinic and Mayo Med. Sch., Rochester, MN, USA

SOURCE: Nat. Genet. (2000), 26(2), 146-147
CODEN: NGENEC; ISSN: 1061-4036

PUBLISHER: Nature America Inc.

DOCUMENT TYPE: Journal; General Review

LANGUAGE: English

AB Colorectal cancer (CRC) with defective DNA mismatch repair (MMR) is assocd. with alterations in one of several DNA MMR genes. Here we show that AXIN2 encoding a Wnt signaling component, is mutated in 11 of 45 CRC with defective MMR. We tested the functional importance of AXIN2 mutations in the development of CRC with defective MMR in a TCF reporter assay. Our findings now provide a link between defective MMR and the activation of TCF-dependent transcription, as mutations in AXIN2 alter the APC

Searcher : Shears 308-4994

pathway.

REFERENCE COUNT: 14
 REFERENCE(S): (1) Behrens, J; Science 1998, V280, P596 CAPLUS
 (2) Boland, C; Cancer Res 1998, V58, P5248
 CAPLUS
 (3) Chan, E; Nature Genet 1999, V21, P410 CAPLUS
 (4) Ganguly, A; Proc Natl Acad Sci USA 1993,
 V90, P10325 CAPLUS
 (5) Ishitani, T; Nature 1999, V399, P798 CAPLUS
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 3 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 2000:651706 CAPLUS
 DOCUMENT NUMBER: 134:1816
 TITLE: Hot spots in .beta.-catenin for interactions
 with LEF-1, **conductin** and APC
 AUTHOR(S): Von Kries, Jens Peter; Winbeck, Georgia;
 Asbrand, Christian; Schwarz-Romond, Thomas;
 Sochnikova, Natalia; Dell'Oro, Andrea; Behrens,
 Jurgen; Birchmeier, Walter
 CORPORATE SOURCE: Max-Delbruck-Center for Molecular Medicine,
 Berlin, 13093, Germany
 SOURCE: Nat. Struct. Biol. (2000), 7(9), 800-807
 CODEN: NSBIEW; ISSN: 1072-8368
 PUBLISHER: Nature America Inc.
 DOCUMENT TYPE: Journal
 LANGUAGE: English

AB Interactions between .beta.-catenin and LEF-1/TCF, APC and
conductin/axin are essential for wnt-controlled
 stabilization of .beta.-catenin and transcriptional activation. The
 wnt signal transduction pathway is important in both embryonic
 development and tumor progression. We identify here amino
 acid residues in .beta.-catenin that distinctly affect its binding
 to LEF-1/TCF, APC and **conductin**. These residues form sep.
 surface clusters, termed hot spots, along the armadillo superhelix
 of .beta.-catenin. We also show that complementary charged and
 hydrophobic amino acids are required for formation of the bipartite
 .beta.-catenin-LEF-1 transcription factor. Moreover, we demonstrate
 that **conductin**/axin binding to .beta.-catenin is essential
 for .beta.-catenin degrdn., and that APC acts as a cofactor of
conductin/axin in this process. Binding of APC to
conductin/axin activates the latter and occurs between their
 SAMP and RGS domains, resp.

REFERENCE COUNT: 50
 REFERENCE(S): (1) Aberle, H; EMBO J 1997, V16, P3797 CAPLUS
 (2) Aberle, H; J Cell Sci 1994, V107, P3655
 CAPLUS
 (3) Behrens, J; Nature 1996, V382, P638 CAPLUS

Searcher : Shears 308-4994

(4) Behrens, J; Science 1998, V280, P596 CAPLUS
 (5) Brunner, E; Nature 1997, V385, P829 CAPLUS
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 4 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 2000:547045 CAPLUS

DOCUMENT NUMBER: 134:27977

TITLE: Control of .beta.-catenin signaling in
 tumor development

AUTHOR(S): Behrens, Jurgun

CORPORATE SOURCE: Max-Delbruck-Center for Molecular Medicine,
 Berlin, 13122, Germany

SOURCE: Ann. N. Y. Acad. Sci. (2000), 910(Colorectal
 Cancer), 21-35

CODEN: ANYAA9; ISSN: 0077-8923

PUBLISHER: New York Academy of Sciences

DOCUMENT TYPE: Journal; General Review

LANGUAGE: English

AB A review, with 72 refs. The wnt signal transduction pathway is involved in various differentiation events during embryonic development and leads to tumor formation when aberrantly activated. The wnt signal is transmitted to the nucleus by the cytoplasmic component .beta.-catenin: in the absence of wnts, .beta.-catenin is constitutively degraded in proteasomes, whereas in the presence of wnts .beta.-catenin is stabilized and can assoc. with HMG box transcription factors of the LEF/TCF family. The LEF/TCF/.beta.-catenin complexes activate specific wnt target genes. In tumors, .beta.-catenin degrading is blocked by mutations of .beta.-catenin or of the tumor suppressor gene product APC. As a consequence, .beta.-catenin is stabilized, constitutive complexes with LEF/TCF factors are formed, and oncogenic target genes, such as c-myc, cyclin D1, and c-jun, are activated. Thus, control of .beta.-catenin is a major regulatory event in normal wnt signaling and during tumor formation. It has been found that a multiprotein complex assembled by the cytoplasmic component conductin induces degrading of cytoplasmic .beta.-catenin. The complex includes APC, the serine/threonine kinase GSK3.beta., and .beta.-catenin, which bind to conductin at distinct domains. In colon carcinoma cells, forced expression of conductin down-regulates .beta.-catenin, whereas in normal cells mutants of conductin that are deficient in complex formation stabilize .beta.-catenin. Fragments of APC that contain a conductin-binding domain also block .beta.-catenin degrading. In Xenopus embryos, conductin inhibits the wnt pathway. In situ hybridization anal. shows that conductin is expressed in various embryonal tissues known to be regulated by wnts, such as the developing brain, mesenchyme below the epidermis, lung mesenchyme, and kidney. It is suggested that conductin

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controls wnt signaling by assembling the essential components of the .beta.-catenin degrdn. pathway. Alterations of conductin function may lead to tumor formation.

REFERENCE COUNT: 72

REFERENCE(S): (1) Aberle, H; EMBO J 1997, V16, P3797 CAPLUS
(2) Ahmed, Y; Cell 1998, V93, P1171 CAPLUS
(3) Aoki, M; Proc Natl Acad Sci 1999, V96, P139 CAPLUS
(4) Bauer, A; Proc Natl Acad Sci 1998, V95, P14787 CAPLUS
(5) Behrens, J; Cancer Metastasis Rev 1999, V18, P15 CAPLUS

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 5 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 2000:275313 CAPLUS

DOCUMENT NUMBER: 132:313670

TITLE: Coated substrates for blood, plasma, or tissue washing and columns equipped with these substrates

INVENTOR(S): Dunzendorfer, Udo; Will, Gottfried

PATENT ASSIGNEE(S): Germany

SOURCE: Ger. Offen., 30 pp.

CODEN: GWXXBX

DOCUMENT TYPE: Patent

LANGUAGE: German

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
DE 19845286	A1	20000427	DE 1998-19845286	19981001
EP 1004598	A2	20000531	EP 1999-118541	19990918
EP 1004598	A3	20000607		

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO

PRIORITY APPLN. INFO.: DE 1998-19845286 19981001

AB Columns, filters, cannulas, etc. contg. substrates coated with specific antibodies can be used during plasmapheresis to remove pathogenic cytokines such as tumor necrosis factor (TNF), anti-TNF, fragments of TNF or anti-TNF, or TNF transport proteins from blood, plasma, or tissues. The substrates may addnl. be coated with antibodies to microbial or viral pathogens or mixts. of pathogens as well as to polysaccharide antigens, viral capsids, microbial antigens, reverse transcriptase, endothelin, protein A, etc. Selective removal of these pathogens, antigens, proteins, etc. leaves all normal plasma components unchanged and obviates the need for supplementation of the plasma with these components. Suitable

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substrates include polymers, polymer-coated metals, cellulose derivs., starch, and Sepharose; these may be derivatized for covalent binding of the pathogens or pathogenic mols. Thus, Escherichia coli pyelonephritis was successfully treated by plasmapheresis coupled with columns loaded with anti-TNF-.alpha. for 14 days, 4 h/day, as detd. by decreases in plasma TNF-.alpha. levels and colony counts in urine cultures.

L6 ANSWER 6 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 2000:94336 CAPLUS
DOCUMENT NUMBER: 133:56735
TITLE: The regulation of .beta.-catenin degradation and cancer
AUTHOR(S): Kishida, Shosei; Kikuchi, Akira
CORPORATE SOURCE: Sch. Med., Hiroshima Univ., Hiroshima, 734-8551, Japan
SOURCE: Mol. Med. (Tokyo) (2000), 37(2), 166-175
CODEN: MOLMEL; ISSN: 0918-6557
PUBLISHER: Nakayama Shoten
DOCUMENT TYPE: Journal; General Review
LANGUAGE: Japanese

AB A review with 37 refs. The structure of .beta.-catenin is described. .beta.-Catenin accumulates in colon cancer and malignant melanoma. .beta.-Catenin is degraded by the ubiquitin/proteasome system. Axin (conductin) possesses regulators of G protein signaling (RGS) for binding APC at N-terminus, GSK-3.beta. and .beta.-catenin binding domains at central region, and DIX region at C-terminus. Wnt protein releases .beta.-catenin from the Axin complex.

L6 ANSWER 7 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 2000:53973 CAPLUS
DOCUMENT NUMBER: 132:303902
TITLE: The yin-yang of TCF/.beta.-catenin signaling
AUTHOR(S): Barker, Nick; Morin, Patrice J.; Clevers, Hans
CORPORATE SOURCE: Department of Immunology, University Hospital, Utrecht, 85500, Neth.
SOURCE: Adv. Cancer Res. (2000), 77, 1-24
CODEN: ACRSAJ; ISSN: 0065-230X
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English

AB A review with 90 refs. Wingless/Wnt signaling directs cell-fate choices during embryonic development. In Drosophila, Wingless signaling mediates endoderm induction and the establishment of segment polarity in the developing embryo. The fly Wingless cascade is strikingly similar to the vertebrate Wnt signaling pathway, which controls a no. of key developmental decisions such as dorsal-ventral

patterning in *Xenopus*. Factors of the TCF/LEF HMG domain family (Tcfs) have recently been established as the downstream effectors of the Wingless/Wnt signal transduction pathways. Upon Wingless/Wnt signaling, a cascade is initiated that results in the accumulation of cytoplasmic β -catenin (or its fly homolog, Armadillo). There is also a concomitant translocation of β -catenin/Armadillo to the nucleus, where it interacts with a specific sequence motif at the N terminus of Tcfs to generate a transcriptionally active complex. This bipartite transcription factor is targeted to the upstream regulatory regions of Tcf target genes including *Siamois* and *Nodal* related gene-3 in *Xenopus*, *engrailed* and *Ultrabithorax* in *Drosophila* via the sequence-specific HMG box, and mediates their transcriptional activation by virtue of transactivation domains contributed by β -catenin/Armadillo. In the absence of Wingless/Wnt signals, a key neg. regulator of the pathway, GSK3 β , is activated, which mediates the downregulation of cytoplasmic β -catenin/Armadillo via the ubiquitin-proteasome pathway. In the absence of nuclear β -catenin, the Tcfs recruit the corepressor protein Groucho to the target gene enhancers and actively repress their transcription. An addnl. corepressor protein, CREB-binding protein (CBP), may also be involved in this repression of Tcf target gene activity. Several other proteins, including adenomatous polyposis coli (APC), GSK3 β , and Axin/**Conductin**, are instrumental in the regulation of β -catenin/Armadillo. In APC-deficient colon carcinoma cell lines, β -catenin accumulates and is constitutively complexed with nuclear Tcf-4. A proportion of APC wild-type colon carcinomas and melanomas also contains constitutive nuclear Tcf-4/ β -catenin complexes as a result of dominant mutations in the N terminus of β -catenin that render it insensitive to downregulation by APC, GSK3 β , and Axin/**Conductin**. This results in the unregulated expression of Tcf-4 target genes such as c-myc. Based on the established role for Tcf-4 in maintaining intestinal stem cells it is likely that deregulation of c-myc expression as a result of constitutive Tcf-4/ β -catenin activity promotes uncontrolled intestinal cell proliferation. This would readily explain the formation of intestinal polyps during colon carcinogenesis. Similar mechanisms leading to deregulation of Tcf target gene activity are likely to be involved in melanoma and other forms of cancer. (c) 2000 Academic Press.

REFERENCE COUNT:

90

REFERENCE(S):

- (2) Barker, N; Am J Pathol 1999, V154, P29
CAPLUS
- (3) Behrens, J; Nature (London) 1996, V382, P638
CAPLUS
- (4) Behrens, J; Science 1998, V280, P596 CAPLUS
- (5) Bhanot, P; Nature (London) 1996, V382, P225

09/587574

CAPLUS

(6) Bienz, M; Trends Genet 1994, V10, P22 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 8 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 1999:737696 CAPLUS

DOCUMENT NUMBER: 132:90977

TITLE: Identification and characterization of E-APC, a
novel Drosophila homolog of the tumor
suppressor APC

AUTHOR(S): Hamada, Fumihiko; Murata, Yoji; Nishida, Ayumu;
Fujita, Fumitaka; Tomoyasu, Yoshinori; Nakamura,
Makoto; Toyoshima, Kumao; Tabata, Tetsuya; Ueno,
Naoto; Akiyama, Tetsu

CORPORATE SOURCE: Department of Oncogene Research, Research
Institute for Microbial Diseases, Osaka
University, Suita, 565-0871, Japan

SOURCE: Genes Cells (1999), 4(8), 465-474
CODEN: GECEFL; ISSN: 1356-9597

PUBLISHER: Blackwell Science Ltd.

DOCUMENT TYPE: Journal

LANGUAGE: English

AB We have identified a novel Drosophila homolog of APC, E-APC, which
is similar to but differs in several respects from D-APC. The E-APC
cDNA encodes a protein of predicted 1067 amino acids, with 7
armadillo repeats, 2 copies of the 15-amino acid repeat, 5 copies of
the 20-amino acid repeat, and 1 Axin/conductin binding
site. E-APC directly interacts with D-Axin and Armadillo (Arm, the
Drosophila homolog of .beta.-catenin) in vitro, destabilizes
intracellular .beta.-catenin, and suppresses .beta.-catenin/TCF-
regulated transcription in APC/- colon cancer cells. The
E-APC mRNA is ubiquitously expressed throughout all developmental
stages in Drosophila. Our findings suggest that E-APC may be
universally involved in the regulation of the Wingless signaling
pathway by down-regulating the level of Arm in Drosophila.

REFERENCE COUNT: 35

REFERENCE(S): (1) Ahmed, Y; Cell 1998, V93, P1171 CAPLUS
(2) Baeg, G; EMBO J 1995, V14, P5618 CAPLUS
(3) Behrens, J; Science 1998, V280, P596 CAPLUS
(4) Cadigan, K; Genes Dev 1997, V11, P3286
CAPLUS
(5) Hamada, F; Science 1999, V283, P1739 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 9 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 1999:733931 CAPLUS

DOCUMENT NUMBER: 131:333485

TITLE: Signaling through .beta.-catenin and Lef/Tcf

Searcher : Shears 308-4994

AUTHOR(S): Novak, A.; Dedhar, S.
 CORPORATE SOURCE: Sunnybrook Health Science Center, Toronto, ON,
 M4N 3M5, Can.
 SOURCE: Cell. Mol. Life Sci. (1999), 56(5/6), 523-537
 CODEN: CMLSFI; ISSN: 1420-682X
 PUBLISHER: Birkhaeuser Verlag
 DOCUMENT TYPE: Journal; General Review
 LANGUAGE: English

AB A review with 167 refs. is given. .beta.-Catenin plays a structural role in cell adhesion by binding to cadherins at the intracellular surface of the plasma membrane and a signaling role in the cytoplasm as the penultimate downstream mediator of the wnt signaling pathway. The ultimate mediator of this pathway is a nuclear complex of .beta.-catenin acting as a coactivator with lymphoid enhancer factor/T cell factor (Lef/Tcf) transcription factors to stimulate transcription of a variety of target genes. Signaling through .beta.-catenin is regulated by modulating its degrdn. and nuclear translocation. In the absence of an activating signal, phosphorylation of .beta.-catenin by glycogen synthase kinase 3 (GSK3) acting in conjunction with adenomatous polyposis coli and axin/ conductin causes .beta.-catenin to interact with the .beta.-transducin repeat-contg. protein which results in its ubiquitination and degrdn. Signaling from the wnt pathway activates dishevelled which, in an as yet undefined manner, inhibits the activity of GSK3 resulting in an increase in the cytoplasmic free pool of .beta.-catenin, and translocation into the nucleus. The integrin-linked kinase (ILK) pathway also activates .beta.-catenin-Lef/Tcf signaling. ILK phosphorylates CISK3 to inhibit its activity and translocates .beta.-catenin into the nucleus. In addn., ILK downregulates the expression of E-cadherin and upregulates Lef-1 expression. In the final step of the .beta.-catenin-Lef/Tcf signaling pathway, nuclear .beta.-catenin binds pontin52-TATA binding protein and displaces Groucho-related gene or CREB-binding protein corepressors from Lef/ Tcf resulting in stimulation of transcription. During development, .beta.-catenin-Lef/Tcf signaling is involved in the formation of dorsal mesoderm and dorsal axis. Furthermore, defects in the .beta.-catenin-Lef/Tcf pathway are involved in the development of several types of cancers.

REFERENCE COUNT: 167

REFERENCE(S): (1) Aberle, H; EMBO J 1997, V16, P3797 CAPLUS
 (2) Aberle, H; J Cell Biochem 1996, V61, P514 CAPLUS
 (4) Ahmed, Y; Cell 1998, V93, P1171 CAPLUS
 (5) Aoki, M; Proc Natl Acad Sci USA 1999, V96, P139 CAPLUS
 (7) Axelrod, J; Science 1996, V271, P1826 CAPLUS
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 10 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 1999:549289 CAPLUS

DOCUMENT NUMBER: 131:194280

TITLE: Agents for treating cancer and other human illnesses based on .beta.-catenin

INVENTOR(S): Birchmeier, Walter; Von Kries, Jens-Peter

PATENT ASSIGNEE(S): Max-Delbrueck-Centrum fuer Molekulare Medizin, Germany

SOURCE: PCT Int. Appl., 26 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: German

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9942481	A2	19990826	WO 1999-DE554	19990222
WO 9942481	A3	20000210		
W: CA, JP, US				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
DE 19909251	A1	19990826	DE 1999-19909251	19990222
EP 1054899	A2	20001129	EP 1999-913097	19990222
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, NL, SE, PT, IE, FI				

PRIORITY APPLN. INFO.: DE 1998-19807390 A 19980221
 WO 1999-DE554 W 19990222

AB C.beta.-catenin is a central mol. of the Wnt signal path. Increasing .beta.-catenin in the cell leads to its translocation into the cell nucleus and to its interaction with transcription factors of the LEF-1/TCF family. This can lead to colonic **cancers** and melanomas (oncogenic signal path). However, .beta.-catenin also interacts with the **tumor-suppressor** genes APC, **conductin**, and E-cadherin, which have a contrary effect on the cell (antioncogenic effect). Peptides derived from LEF-1-/TCF-4 transcription factors and analogous mols. can be used in the treatment of **tumors**, esp. colonic **cancers** and melanomas. These peptides and analogous mols. influence the interaction between .beta.-catenin and LEF-1/TCF. The peptides comprise parts of the LEF-1/TCF-4 transcription factors and variants and mutations thereof, preferably the 10-40 N-terminal amino acids of LEF-1 or TCF-4, as well as peptides derived from the armadillo region of .beta.-catenin which were identified as interaction domains with LEF-1/TCF, APC, **conductin**, and E-cadherin. The peptides constituting interaction domains with APC or **conductin** can increase the concn. of .beta.-catenin in

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the cell. These last mols. can be used to influence the formation of tissues and organs, e.g. to promote hair growth.

IT 221220-50-4, **Conductin** (human)

RL: BPR (Biological process); BIOL (Biological study); PROC (Process)

(interaction with .beta.-catenin, modulators of; agents for treating **cancer** and other human illnesses based on .beta.-catenin)

L6 ANSWER 11 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 1999:189197 CAPLUS

DOCUMENT NUMBER: 130:232471

TITLE: The protein **conductin** and its application for diagnosis and gene therapy of colon **cancer**

INVENTOR(S): Behrens, Jorgen; Birchmeier, Walter

PATENT ASSIGNEE(S): Max-Delbruck-Centrum fur Molekulare Medizin, Germany

SOURCE: PCT Int. Appl., 22 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: German

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9911780	A2	19990311	WO 1998-DE2621	19980901
WO 9911780	A3	19990527		
W: CA, JP, US				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
DE 19840875	A1	19990512	DE 1998-19840875	19980901
EP 1029047	A2	20000823	EP 1998-954120	19980901
R: AT, BE, CH, DE, DK, FR, GB, IT, LI, NL, SE, FI				

PRIORITY APPLN. INFO.: DE 1997-19738205 A 19970902
WO 1998-DE2621 W 19980901

AB The invention concerns the novel protein **conductin** that is able to regulate the .beta.-catenin function and interacts with the **tumor** suppressor adenomatous polyposis coli (APC); and its application in the gene therapy of colon **cancer**. The 840 amino acid contg. protein contains domains with various activities: 78-200 is the RGS (Regulator of G-Protein Signalling) binding sequence; 343-396 is the GSK 3.beta. (glycogen synthase kinase 3.beta.) binding sequence; 397-465 is the .beta.-catenin binding sequence; 783-833 is the Dishevelled homol. region. Mutations, variants and fragments of **conductin** with the corresponding coding genes and mRNA sequences are also included. Antibodies and

Searcher : Shears 308-4994

nucleic acid probes for the detection of *conductin* are part of the diagnosis tools. For therapeutic purposes a vector contg. the *conductin* gene is constructed; substances that activate and reactivate *conductin* in the body are co-administered, e.g. a substance that activates the *conductin* promoter or stabilizes mRNA. The effect of *conductin* was proved using SW480 cells with APC mutation and thus increased *.beta.-catenin* level. Introduction of *conductin* resulted in the decrease of *.beta.-catenin* to the same concn. as in non APC mutated SW480 cells. In an expt. with *Xenopus* embryos it was shown that *conductin* inhibits the Wnt/Wingless signaling pathway via its interaction with *.beta.-catenin*.

IT 221220-50-4, *Conductin* (human)

RL: BAC (Biological activity or effector, except adverse); PRP (Properties); BIOL (Biological study)

(amino acid sequence; protein *conductin* and application for diagnosis and gene therapy of colon cancer)

L6 ANSWER 12 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 1999:179719 CAPLUS

DOCUMENT NUMBER: 131:16667

TITLE: APC protein: protein interactions and cellular functions

AUTHOR(S): Jais, Philippe; Laurent-Puig, Pierre; Olschwang, Sylviane

CORPORATE SOURCE: Unite des Marqueurs Genetiques des Cancers (UMGC), Institut Gustave-Roussy, Villejuif, 94805, Fr.

SOURCE: Gastroenterol. Clin. Biol. (1998), 22(12), 1071-1080

CODEN: GCBIDC; ISSN: 0399-8320

PUBLISHER: Masson Editeur

DOCUMENT TYPE: Journal; General Review

LANGUAGE: French

AB A review with 112 refs., discussing structures of APC gene and protein; functions of APC protein in epithelial cell homeostasis and cell adhesion; assocn. of APC protein with *.beta.-catenin*, *conductin*, and GSK3.*beta.* in normal and transformed cells and other proteins-assocns.

REFERENCE COUNT: 112

REFERENCE(S): (1) Aberle, H; EMBO J 1997, V16, P3797 CAPLUS
(3) Behrens, J; Nature 1996, V382, P638 CAPLUS
(4) Behrens, J; Science 1998, V280, P596 CAPLUS
(5) Beinhauer, J; J Cell Biol 1997, V139, P717 CAPLUS
(6) Beroud, C; Nucleic Acids Res 1996, V24, P121 CAPLUS

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 13 OF 15 CAPLUS COPYRIGHT 2001 ACS
 ACCESSION NUMBER: 1999:134134 CAPLUS
 DOCUMENT NUMBER: 131:14675
 TITLE: Cloning of the Human Homolog of Conduction
 (AXIN2), a Gene Mapping to Chromosome 17q23-q24
 AUTHOR(S): Mai, Ming; Qian, Chiping; Yokomizo, Akira;
 Smith, David I.; Liu, Wanguo
 CORPORATE SOURCE: Division of Experimental Pathology, Mayo
 Clinic/Foundation, Rochester, MN, 55905, USA
 SOURCE: Genomics (1999), 55(3), 341-344
 CODEN: GNMCEP; ISSN: 0888-7543
 PUBLISHER: Academic Press
 DOCUMENT TYPE: Journal
 LANGUAGE: English

AB Conduction or Axil, an Axin homolog, plays an important role in the regulation of .beta.-catenin stability in the Wnt signaling pathway. To facilitate the mol. anal. of the human gene, we isolated the human homolog, AXIN2. The cDNA contains a 2529-bp open reading frame and encodes a putative protein of 843 amino acids. Compared with rat and mouse homologs, AXIN2 shows an overall 89% amino acid identity. Several functional domains in this protein are highly conserved including the GRS (95.9%), GSK-3.beta. (96.3%), Dsh (98%), and .beta.-catenin (89.9%) domains. Radiation hybrid mapping localized the AXIN2 gene to human chromosome 17q23-q24, a region that shows frequent loss of heterozygosity in breast cancer, neuroblastoma, and other tumors. Human AXIN2 is thus a very strong candidate involved in multiple tumor types.
 (c) 1999 Academic Press.

IT 226387-63-9, Conduction (human fetal brain reduced)
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
 (amino acid sequence; cloning of the human homolog of conductin (AXIN2), a gene mapping to chromosome 17q23-q24)

REFERENCE COUNT: 22
 REFERENCE(S): (1) Aberle, H; EMBO J 1997, V16, P3797 CAPLUS
 (2) Aberle, H; J Cell Sci 1994, V107, P3655 CAPLUS
 (3) Barlund, M; Genes Chromosomes Cancer 1997, V20, P372 CAPLUS
 (4) Behrens, J; Nature 1996, V382, P638 CAPLUS
 (5) Behrens, J; Science 1998, V280, P596 CAPLUS
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 14 OF 15 CAPLUS COPYRIGHT 2001 ACS
 ACCESSION NUMBER: 1999:106086 CAPLUS

Searcher : Shears 308-4994

09/587574

DOCUMENT NUMBER: 130:323365
TITLE: Identification of APC2, a homolog of the
adenomatous polyposis coli tum r
suppressor
AUTHOR(S): Van Es, J. H.; Kirkpatrick, C.; Van de Wetering,
M.; Molenaar, M.; Miles, A.; Kuipers, J.;
Destree, O.; Peifer, M.; Clevers, H.
CORPORATE SOURCE: Department of Immunology, University Hospital,
Utrecht, 3508 GA, Neth.
SOURCE: Curr. Biol. (1999), 9(2), 105-108
CODEN: CUBLE2; ISSN: 0960-9822
PUBLISHER: Current Biology Publications
DOCUMENT TYPE: Journal
LANGUAGE: English

AB We report the identification and genomic structure of APC homologs.
Mammalian APC2, which closely resembles APC in overall domain
structure, was functionally analyzed and shown to contain 2 SAMP
domains, both of which are required for binding to **conductin**
. Like APC, APC2 regulates the formation of active
.beta.-catenin-Tcf complexes, as demonstrated using transient
transcriptional activation assays in APC-/- colon carcinoma
cells. Human APC2 maps to chromosome 19p13.3. APC and APC2 may
therefore have comparable functions in development and
cancer.

REFERENCE COUNT: 23
REFERENCE(S): (1) Aberle, H; EMBO J 1997, V16, P3797 CAPLUS
(2) Behrens, J; Nature 1996, V382, P638 CAPLUS
(3) Behrens, J; Science 1998, V280, P596 CAPLUS
(4) Brunner, E; Nature 1997, V385, P829 CAPLUS
(5) Cadigan, K; Genes Dev 1997, V11, P3286
CAPLUS

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 15 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 1998:302214 CAPLUS
TITLE: Functional interaction of an axin homolog,
conductin, with .beta.-catenin, APC and
GSK3.beta.
AUTHOR(S): Behrens, Jurgens; Jerchow, Boris-Alexander;
Wurtele, Martin; Grimm, Jan; Asbrand, Christian;
Wirtz, Ralph; Kuhl, Michael; Wedlich, Doris;
Birchmeier, Walter
CORPORATE SOURCE: Max Delbrück Cent. Molecular Med., Berlin,
13122, Germany
SOURCE: Science (Washington, D. C.) (1998), 280(5363),
596-599
CODEN: SCIEAS; ISSN: 0036-8075
PUBLISHER: American Association for the Advancement of

Searcher : Shears 308-4994

09/587574

DOCUMENT TYPE: Science
Journal
LANGUAGE: English

AB Control of stability of .beta.-catenin is central in the wnt signaling pathway. Here, the protein **conductin** was found to form a complex with both .beta.-catenin and the tumor suppressor gene product adenomatous polyposis coli (APC). **Conductin** induced .beta.-catenin degrdn., whereas mutants of **conductin** that were deficient in complex formation stabilized .beta.-catenin. Fragments of APC that contained a **conductin**-binding domain also blocked .beta.-catenin degrdn. Thus, **conductin** is a component of the multiprotein complex that directs .beta.-catenin to degrdn. and is located downstream of APC. In *Xenopus* embryos, **conductin** interfered with wnt-induced axis formation.

(FILE 'MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH, JICST-EPLUS, JAPIO, CANCERLIT' ENTERED AT 11:17:14 ON 11 JUN 2001)

L7 57 S L6

L8 22 DUP REM L7 (35 DUPLICATES REMOVED)

L8 ANSWER 1 OF 22 WPIDS COPYRIGHT 2001 DERWENT INFORMATION LTD

ACCESSION NUMBER: 2001-246094 [26] WPIDS

DOC. NO. CPI: C2001-074206

TITLE: Agent for tumor therapy, tissue regeneration or stimulation of hair growth, comprising inhibitor of binding of beta-catenin to LEF-1/TCF-transcription factors, APC or **conductin**, obtained by specific screening method.

DERWENT CLASS: B04 D16

INVENTOR(S): BIRCHMEIER, W; VON KRIES, J

PATENT ASSIGNEE(S): (DELB-N) DELBRUECK CENT MOLEKULARE MEDIZIN MAX

COUNTRY COUNT: 94

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
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DE 19944404	A1	20010322	(200126)*		14
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WO 2001019353	A2	20010322	(200126)	GE	
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RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC
MW MZ NL OA PT SD SE SL SZ TZ UG ZW

W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE
DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG
KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ
PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN
YU ZA ZW

Searcher : Shears 308-4994

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
DE 19944404	A1	DE 1999-19944404	19990916
WO 2001019353	A2	WO 2000-DE3104	20000907

PRIORITY APPLN. INFO: DE 1999-19944404 19990916

AN 2001-246094 [26] WPIDS

AB DE 19944404 A UPAB: 20010515

NOVELTY - An agent (I) for therapy of human disorders, comprising an inhibitor of the binding of beta -catenin to LEF-1/TCF-transcription factors, APC (undefined) or **conductin**, is new.

DETAILED DESCRIPTION - An INDEPENDENT CLAIM is included for identifying agents (I), comprising identifying hydrophobic pockets in the vicinity of essential binding sites in the beta -catenin molecule, and synthesizing compounds which fit in these pockets.

ACTIVITY - Cytostatic.

No biological data is given.

MECHANISM OF ACTION - Inhibition of binding of beta -catenin to LEF-1/TCF-transcription factors, APC or **conductin**.

USE - For therapy of tumors (e.g. colon **carcinoma** or melanoma), for tissue regeneration or for stimulation of hair growth (claimed).

Dwg.0/3

L8 ANSWER 2 OF 22 EMBASE COPYRIGHT 2001 ELSEVIER SCI. B.V.

ACCESSION NUMBER: 2001083138 EMBASE

TITLE: Oncogenic targets of .beta.-catenin-mediated transcription in molecular pathogenesis of intestinal polyposis.

AUTHOR: Watson S.A.

CORPORATE SOURCE: S.A. Watson, Academic Unit of Cancer Studies, University of Nottingham, Nottingham NG7 2UH, United Kingdom. sue.watson@nottingham.ac.uk

SOURCE: Lancet, (24 Feb 2001) 357/9256 (572-573).

Refs: 14

ISSN: 0140-6736 CODEN: LANCAO

COUNTRY: United Kingdom

DOCUMENT TYPE: Journal; Note

FILE SEGMENT: 016 Cancer
022 Human Genetics
029 Clinical Biochemistry
048 Gastroenterology

LANGUAGE: English

L8 ANSWER 3 OF 22 WPIDS COPYRIGHT 2001 DERWENT INFORMATION LTD

09/587574

ACCESSION NUMBER: 2000-293152 [25] WPIDS
DOC. NO. NON-CPI: N2000-219772
DOC. NO. CPI: C2000-088675
TITLE: Novel human tumor suppressor gene,
adenomatous polyposis coli (APC)-2, used in the
diagnosis, prevention, and treatment of
cancer.
DERWENT CLASS: B04 C06 D16 P14 S03
INVENTOR(S): CLEVERS, J C; PELFER, M A; VAN ES, J H
PATENT ASSIGNEE(S): (UYUT-N) RIJKSUNIV UTRECHT
COUNTRY COUNT: 89
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2000018913	A1	20000406	(200025)*	EN	42
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC					
MW NL OA PT SD SE SL SZ TZ UG ZW					
W: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE DK DM					
EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ					
LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD					
SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW					
AU 9960106	A	20000417	(200035)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2000018913	A1	WO 1999-NL595	19990924
AU 9960106	A	AU 1999-60106	19990924

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 9960106	A Based on	WO 200018913

PRIORITY APPLN. INFO: EP 1998-203237 19980925

AN 2000-293152 [25] WPIDS

AB WO 200018913 A UPAB: 20000524

NOVELTY - Isolated and/or recombinant nucleic acid (NA) or a specific fragment, homolog or derivative thereof (I), corresponding to a gene located at position 19p13.3 in humans and comprising the 2397 base pair (bp) sequence given in the specification (adenomatous polyposis coli (APC)-2), is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) an expression vector comprising (I);

Searcher : Shears 308-4994

- (2) a cell comprising (I) or the expression vector of (1);
- (3) an animal comprising the cell of (2);
- (4) a protein, derivative, or fragment encoded by (I) or produced by the cell of (2);
- (5) an antibody directed against the protein of (4);
- (6) identifying a candidate drug (especially a drug for use in a cancer patient), by using of the cell of (2), animal of (3), protein of (4), or antibody of (5); and
- (7) diagnosing cancer by using (I), the cell of (2), animal of (3), protein of (4), or antibody of (5).

ACTIVITY - Cytostatic.

MECHANISM OF ACTION - The adenomatous polyposis coli (APC)-2 tumor suppressor gene controls the Wnt pathway by the formation of a complex with GSK-3b, axin/conductin and beta -catenin, inducing the rapid degradation of the latter.

USE - The adenomatous polyposis coli (APC)-2 polynucleotides are used for the diagnosis (claimed), prevention and treatment of cancer. They are also used for the recombinant production of APC-2 proteins. The methods are used to identify candidate drugs (claimed), especially for use in the treatment of cancers, preferably a fetal cancer, cancers with a stem cell phenotype, brain, lung, kidney or intestinal cancer (all claimed).

ADVANTAGE - None given.

DESCRIPTION OF DRAWING(S) - The figure shows the comparison of adenomatous polyposis coli (APC) and APC-2. Domain structures conserved between these APC relatives are indicated in various boxes.

Dwg.1A/4

L8 ANSWER 4 OF 22 SCISEARCH COPYRIGHT 2001 ISI (R)
 ACCESSION NUMBER: 2000:808103 SCISEARCH
 THE GENUINE ARTICLE: 366KD
 TITLE: Differential regulation of glycogen synthase kinase 3 beta by insulin and Wnt signaling
 AUTHOR: Ding V W; Chen R H; McCormick F (Reprint)
 CORPORATE SOURCE: UNIV CALIF SAN FRANCISCO, CANC RES INST, 2340 SUTTER ST, BOX 0128, SAN FRANCISCO, CA 94115 (Reprint); UNIV CALIF SAN FRANCISCO, CANC RES INST, SAN FRANCISCO, CA 94143
 COUNTRY OF AUTHOR: USA
 SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (20 OCT 2000) Vol. 275, No. 42, pp. 32475-32481.
 Publisher: AMER SOC BIOCHEMISTRY MOLECULAR BIOLOGY INC, 9650 ROCKVILLE PIKE, BETHESDA, MD 20814.
 ISSN: 0021-9258.
 DOCUMENT TYPE: Article; Journal
 FILE SEGMENT: LIFE

09/587574

LANGUAGE: English
REFERENCE COUNT: 53

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Glycogen synthase kinase 3 beta (GSK3 beta) is a key component in many biological processes including insulin and Wnt signaling. Since the activation of each signaling pathway results in a decrease in GSK3 beta activity, we examined the specificity of their downstream effects in the same cell type. Insulin induces an increased activity of glycogen synthase but has no influence on the protein level of beta-catenin. In contrast, Wnt increases the cytosolic pool of beta-catenin but not glycogen synthase activity. We found that, unlike insulin, neither the phosphorylation status of the serine9 residue of GSK3 beta nor the activity of protein kinase B is regulated by Wnt. Although the decrease in GSK3 beta activity is required, GSK3 beta may not be the limiting component for Wnt signaling in the cells that we examined. Our results suggest that the axin-conductin complexed GSK3 beta may be dedicated to Wnt rather than insulin signaling. Insulin and Wnt pathways regulate GSK3 beta through different mechanisms, and therefore lead to distinct downstream events.

L8 ANSWER 5 OF 22 MEDLINE DUPLICATE 1
ACCESSION NUMBER: 2000455676 MEDLINE
DOCUMENT NUMBER: 20423090 PubMed ID: 10966653
TITLE: Hot spots in beta-catenin for interactions with LEF-1, conductin and APC.
AUTHOR: von Kries J P; Winbeck G; Asbrand C; Schwarz-Romond T; Sochnikova N; Dell'Oro A; Behrens J; Birchmeier W
CORPORATE SOURCE: Max-Delbruck-Center for Molecular Medicine, Robert-Rossle-Strasse 10, 13093 Berlin, Germany.
SOURCE: NATURE STRUCTURAL BIOLOGY, (2000 Sep) 7 (9) 800-7. Journal code: B98; 9421566. ISSN: 1072-8368.
PUB. COUNTRY: United States
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200009
ENTRY DATE: Entered STN: 20001005
Last Updated on STN: 20001005
Entered Medline: 20000928

AB Interactions between beta-catenin and LEF-1/TCF, APC and conductin/axin are essential for wnt-controlled stabilization of beta-catenin and transcriptional activation. The wnt signal transduction pathway is important in both embryonic development and tumor progression. We identify here amino acid residues in beta-catenin that distinctly affect its binding to LEF-1/TCF, APC and conductin. These residues form separate surface clusters, termed hot spots, along the armadillo superhelix

Searcher : Shears 308-4994

of beta-catenin. We also show that complementary charged and hydrophobic amino acids are required for formation of the bipartite beta-catenin-LEF-1 transcription factor. Moreover, we demonstrate that conductin/axin binding to beta-catenin is essential for beta-catenin degradation, and that APC acts as a cofactor of conductin/axin in this process. Binding of APC to conductin/axin activates the latter and occurs between their SAMP and RGS domains, respectively.

L8 ANSWER 6 OF 22 BIOSIS COPYRIGHT 2001 BIOSIS
 ACCESSION NUMBER: 2000:275471 BIOSIS
 DOCUMENT NUMBER: PREV200000275471
 TITLE: Human conductin (Axin2), like its mouse counterpart, binds to APC, GSK3beta and beta-catenin.
 AUTHOR(S): Dong, Xiangyang (1); Mai, Ming (1); Seelan, Ratnam (1); Qian, Chiping (1); Smith, David I. (1); Liu, Wanguo (1)
 CORPORATE SOURCE: (1) Mayo Clin, Rochester, MN USA
 SOURCE: Proceedings of the American Association for Cancer Research Annual Meeting, (March, 2000) No. 41, pp. 745. print..
 Meeting Info.: 91st Annual Meeting of the American Association for Cancer Research. San Francisco, California, USA April 01-05, 2000
 ISSN: 0197-016X.
 DOCUMENT TYPE: Conference
 LANGUAGE: English
 SUMMARY LANGUAGE: English

L8 ANSWER 7 OF 22 MEDLINE DUPLICATE 2
 ACCESSION NUMBER: 2000123741 MEDLINE
 DOCUMENT NUMBER: 20123741 PubMed ID: 10656974
 TITLE: Biochemical interactions in the wnt pathway.
 AUTHOR: Seidensticker M J; Behrens J
 CORPORATE SOURCE: Max-Delbruck-Center for Molecular Medicine, Robert-Rossle-Strasse 10, 13122, Berlin, Germany.
 SOURCE: BIOCHIMICA ET BIOPHYSICA ACTA, (2000 Feb 2) 1495 (2) 168-82. Ref: 143
 Journal code: AOW; 0217513. ISSN: 0006-3002.
 PUB. COUNTRY: Netherlands
 Journal; Article; (JOURNAL ARTICLE)
 General Review; (REVIEW)
 (REVIEW, TUTORIAL)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200005
 ENTRY DATE: Entered STN: 20000512
 Last Updated on STN: 20000512

09/587574

Entered Medline: 20000502

AB The wnt signal transduction pathway is involved in many differentiation events during embryonic development and can lead to tumor formation after aberrant activation of its components. The cytoplasmic component beta-catenin is central to the transmission of wnt signals to the nucleus: in the absence of wnts beta-catenin is constitutively degraded in proteasomes, whereas in the presence of wnts beta-catenin is stabilized and associates with HMG box transcription factors of the LEF/TCF family. In tumors, beta-catenin degradation is blocked by mutations of the tumor suppressor gene APC (adenomatous polyposis coli), or of beta-catenin itself. As a consequence, constitutive TCF/beta-catenin complexes are formed and activate oncogenic target genes. This review discusses the mechanisms that silence the pathway in cells that do not receive a wnt signal and goes on to describe the regulatory steps involved in the activation of the pathway.

L8 ANSWER 8 OF 22 MEDLINE

DUPLICATE 3

ACCESSION NUMBER: 2001019501 MEDLINE
DOCUMENT NUMBER: 20472311 PubMed ID: 11017067
TITLE: Mutations in AXIN2 cause colorectal cancer with defective mismatch repair by activating beta-catenin/TCF signalling.
AUTHOR: Liu W; Dong X; Mai M; Seelan R S; Taniguchi K; Krishnadath K K; Halling K C; Cunningham J M; Qian C; Christensen E; Roche P C; Smith D I; Thibodeau S N
CORPORATE SOURCE: Division of Experimental Pathology, Department of Laboratory Medicine and Pathology, Mayo Clinic and Mayo Medical School, Rochester, Minnesota, USA..
liu.wanguo@mayo.edu
CONTRACT NUMBER: CA 48031 (NCI)
CA 60117 (NCI)
SOURCE: NATURE GENETICS, (2000 Oct) 26 (2) 146-7.
Journal code: BRO. ISSN: 1061-4036.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200011
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20001108

L8 ANSWER 9 OF 22 MEDLINE

DUPLICATE 4

ACCESSION NUMBER: 2000400028 MEDLINE
DOCUMENT NUMBER: 20369556 PubMed ID: 10911903
TITLE: Control of beta-catenin signaling in tumor development.

Searcher : Shears 308-4994

AUTHOR: Behrens J
 CORPORATE SOURCE: Max-Delbrück-Center for Molecular Medicine, Berlin, Germany.. jbehren@mdc-berlin.de
 SOURCE: ANNALS OF THE NEW YORK ACADEMY OF SCIENCES, (2000 Jun) 910 21-33; discussion 33-5. Ref: 72
 Journal code: 5NM; 7506858. ISSN: 0077-8923.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 General Review; (REVIEW)
 (REVIEW, TUTORIAL)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200008
 ENTRY DATE: Entered STN: 20000824
 Last Updated on STN: 20000824
 Entered Medline: 20000817

AB The wnt signal transduction pathway is involved in various differentiation events during embryonic development and leads to tumor formation when aberrantly activated. The wnt signal is transmitted to the nucleus by the cytoplasmic component beta-catenin: in the absence of wnts, beta-catenin is constitutively degraded in proteasomes, whereas in the presence of wnts beta-catenin is stabilized and can associate with HMG box transcription factors of the LEF/TCF family. The LEF/TCF/beta-catenin complexes activate specific wnt target genes. In tumors, beta-catenin degradation is blocked by mutations of beta-catenin or of the tumor suppressor gene product APC. As a consequence, beta-catenin is stabilized, constitutive complexes with LEF/TCF factors are formed, and oncogenic target genes, such as c-myc, cyclin D1, and c-jun, are activated. Thus, control of beta-catenin is a major regulatory event in normal wnt signaling and during tumor formation. It has been found that a multiprotein complex assembled by the cytoplasmic component conductin induces degradation of cytoplasmic beta-catenin. The complex includes APC, the serine/threonine kinase GSK3 beta, and beta-catenin, which bind to conductin at distinct domains. In colon carcinoma cells, forced expression of conductin downregulates beta-catenin, whereas in normal cells mutants of conductin that are deficient in complex formation stabilize beta-catenin. Fragments of APC that contain a conductin-binding domain also block beta-catenin degradation. In Xenopus embryos, conductin inhibits the wnt pathway. In situ hybridization analysis shows that conductin is expressed in various embryonal tissues known to be regulated by wnts, such as the developing brain, mesenchyme below the epidermis, lung mesenchyme, and kidney. It is suggested that conductin controls wnt signaling by assembling the essential components of the beta-catenin degradation pathway. Alterations of

conductin function may lead to tumor formation.

L8 ANSWER 10 OF 22 MEDLINE DUPLICATE 5
 ACCESSION NUMBER: 2000017120 MEDLINE
 DOCUMENT NUMBER: 20017120 PubMed ID: 10549354
 TITLE: The Yin-Yang of TCF/beta-catenin signaling.
 AUTHOR: Barker N; Morin P J; Clevers H
 CORPORATE SOURCE: Department of Immunology, University Hospital,
 Utrecht, The Netherlands.
 SOURCE: ADVANCES IN CANCER RESEARCH, (2000) 77 1-24. Ref:
 100
 Journal code: 2J6; 0370416. ISSN: 0065-230X.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 General Review; (REVIEW)
 (REVIEW, ACADEMIC)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199911
 ENTRY DATE: Entered STN: 20000111
 Last Updated on STN: 20000111
 Entered Medline: 19991123

AB Wingless/Wnt signaling directs cell-fate choices during embryonic development. In Drosophila, Wingless signaling mediates endoderm induction and the establishment of segment polarity in the developing embryo. The fly Wingless cascade is strikingly similar to the vertebrate Wnt signaling pathway, which controls a number of key developmental decisions such as dorsal-ventral patterning in Xenopus. Factors of the TCF/LEF HMG domain family (Tcfs) have recently been established as the downstream effectors of the Wingless/Wnt signal transduction pathways. Upon Wingless/Wnt signaling, a cascade is initiated that results in the accumulation of cytoplasmic beta-catenin (or its fly homolog, Armadillo). There is also a concomitant translocation of beta-catenin/Armadillo to the nucleus, where it interacts with a specific sequence motif at the N terminus of Tcfs to generate a transcriptionally active complex. This bipartite transcription factor is targeted to the upstream regulatory regions of Tcf target genes including Siamois and Nodal related gene-3 in Xenopus, engrailed and Ultrabithorax in Drosophila via the sequence-specific HMG box, and mediates their transcriptional activation by virtue of transactivation domains contributed by beta-catenin/Armadillo. In the absence of Wingless/Wnt signals, a key negative regulator of the pathway, GSK3 beta, is activated, which mediates the downregulation of cytoplasmic beta-catenin/Armadillo via the ubiquitin-proteasome pathway. In the absence of nuclear beta-catenin, the Tcfs recruit the corepressor protein Groucho to the target gene enhancers and actively repress their transcription. An additional corepressor protein, CREB-binding

protein (CBP), may also be involved in this repression of Tcf target gene activity. Several other proteins, including adenomatous polyposis coli (APC), GSK3 beta, and Axin/Conductin, are instrumental in the regulation of beta-catenin/Armadillo. In APC-deficient colon carcinoma cell lines, beta-catenin accumulates and is constitutively complexed with nuclear Tcf-4. A proportion of APC wild-type colon carcinomas and melanomas also contains constitutive nuclear Tcf-4/beta-catenin complexes as a result of dominant mutations in the N terminus of beta-catenin that render it insensitive to downregulation by APC, GSK3 beta, and Axin/Conductin. This results in the unregulated expression of Tcf-4 target genes such as c-myc. Based on the established role for Tcf-4 in maintaining intestinal stem cells it is likely that deregulation of c-myc expression as a result of constitutive Tcf-4/beta-catenin activity promotes uncontrolled intestinal cell proliferation. This would readily explain the formation of intestinal polyps during colon carcinogenesis. Similar mechanisms leading to deregulation of Tcf target gene activity are likely to be involved in melanoma and other forms of cancer

L8 ANSWER 11 OF 22 WPIDS COPYRIGHT 2001 DERWENT INFORMATION LTD
 ACCESSION NUMBER: 1999-214706 [18] WPIDS
 DOC. NO. NON-CPI: N1999-158020
 DOC. NO. CPI: C1999-063258
 TITLE: Tumor-suppressing protein
 conductin - used for treatment and
 diagnosis of tumors.
 DERWENT CLASS: B04 D16 S03
 INVENTOR(S): BEHRENS, J; BIRCHMEIER, W
 PATENT ASSIGNEE(S): (DELB-N) DELBRUECK CENT MOLEKULARE MEDIZIN MAX
 COUNTRY COUNT: 22
 PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 9911780	A2	19990311	(199918)*	GE	21
RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE					
W: CA JP US					
DE 19840875	A1	19990512	(199925)		
EP 1029047	A2	20000823	(200041)	GE	
R: AT BE CH DE DK FI FR GB IT LI NL SE					

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 9911780	A2	WO 1998-DE2621	19980901

Searcher : Shears 308-4994

09/587574

DE 19840875 A1
EP 1029047 A2

DE 1998-19840875 19980901
EP 1998-954120 19980901
WO 1998-DE2621 19980901

FILING DETAILS:

PATENT NO	KIND	PATENT NO
EP 1029047	A2 Based on	WO 9911780

PRIORITY APPLN. INFO: DE 1997-19738205 19970902

AN 1999-214706 [18] WPIDS

AB WO 9911780 A UPAB: 19990511

NOVELTY - The protein **conductin** (I) and its variants, mutants and fragments are new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following: (1) composition for diagnosing **tumors** comprising an agent that detects (I), the (I)-encoding gene (II) or derived mRNA; (2) composition for treating **tumors** containing an agent that activates or reactivates (I) in vivo; (3) cDNA (III) that encodes (I), its variants, mutants or fragments; (4) use of (II) for gene therapy of **tumors**; and (5) partial sequences of the adenomatosis polyposis coli (APC) protein comprising amino acids (aa) 1464-1604, 1516-1595, 1690-1778 or 1995-2083 as RGS-domain interaction sites (RGS = regulator of G-protein signaling).

USE - Detecting presence or amount of (I), at protein or nucleic acid levels, is used to diagnose **tumors**, while agents that (re)activate (I) are used for **tumor** therapy. Antitumor. (I) binds to beta -catenin and induces its cytoplasmic degradation, resulting in blockade of the Wnt/Wingless signaling pathway in vertebrates. (I) also binds to APC fragments and, in conjunction with APC, acts as a **tumor** suppressor. In SW840 cells APC is mutated, leading to increased levels of beta -catenin in cytoplasm and the nucleus. When (I) was introduced into these cells, beta -catenin was depleted in both cell compartments, with the effect being as strong as that for wild-type APC.
Dwg.0/4

L8 ANSWER 12 OF 22 WPIDS COPYRIGHT 2001 DERWENT INFORMATION LTD

ACCESSION NUMBER: 1999-470389 [40] WPIDS

DOC. NO. CPI: C1999-138212

TITLE: Agents for treating human diseases, particularly **cancer**, modulate interaction of beta-catenin with transcription factors or **tumor** suppressor gene products.

DERWENT CLASS: B04 D16

INVENTOR(S): BIRCHMEIER, W; VON KRIES, J

Searcher : Shears 308-4994

09/587574

PATENT ASSIGNEE(S): (DELB-N) DELBRUECK CENT MOLEKULARE MEDIZIN MAX
COUNTRY COUNT: 22
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
DE 19909251	A1	19990826	(199940)*		15
WO 9942481	A2	19990826	(199942)	GE	
RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE					
W: CA JP US					
EP 1054899	A2	20001129	(200063)	GE	
R: AT BE CH DE DK ES FI FR GB GR IE IT LI NL PT SE					

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
DE 19909251	A1	DE 1999-19909251	19990222
WO 9942481	A2	WO 1999-DE554	19990222
EP 1054899	A2	EP 1999-913097	19990222
		WO 1999-DE554	19990222

FILING DETAILS:

PATENT NO	KIND	PATENT NO
EP 1054899	A2 Based on	WO 9942481

PRIORITY APPLN. INFO: DE 1998-19807390 19980221

AN 1999-470389 [40] WPIDS

AB DE 19909251 A UPAB: 19991004

NOVELTY - Agent (A) for treating human disease is based on substances (I) that modulate (inhibit or promote) the interaction of beta -catenin (bC) with transcription factors or products of tumor suppressor genes.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following: (a) peptide (II) comprising part of the LEF-1/TCF-4 transcription factors, or their variants and mutants; (b) peptide and related molecules (III) from the armadillo domain (arm units 3-8) of bC, and mutants of the complete bC molecule, that include at least one of the specific interaction domains for LEF-1, TCF-4, APC, conductin or E-cadherin; and (c) enzyme-linked immunosorbent assay (ELISA) for screening substance libraries for compounds that modulate interaction of bC with LEF-1/TCF, APC, conductin or E-cadherin.

ACTIVITY - Antitumor.

MECHANISM OF ACTION - bC is a key compound in the Wnt signaling pathway and is involved in development of tumors.

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Generally its interaction with LEF-1 or TCF-4 is oncogenic but interaction with APC, **conductin** or E-cadherin is anti-oncogenic.

USE - (A) which inhibit interaction are particularly used to treat **tumors**, especially **carcinoma** of the colon and melanoma, but also, where they promote interaction, to stimulate regeneration of organs and tissues, specifically hair growth.
Dwg.0/6

L8 ANSWER 13 OF 22 MEDLINE

DUPLICATE 6

ACCESSION NUMBER: 2000047719 MEDLINE

DOCUMENT NUMBER: 20047719 PubMed ID: 10580987

TITLE: beta-catenin signaling and **cancer**.

AUTHOR: Morin P J

CORPORATE SOURCE: Laboratory of Biological Chemistry, Gerontology
Research Center, National Institute on Aging, 5600
Nathan Shock Drive, Baltimore, MD 21224, USA..
MorinP@grc.nia.nih.gov

SOURCE: BIOESSAYS, (1999 Dec) 21 (12) 1021-30. Ref: 88
Journal code: 9YY; 8510851. ISSN: 0265-9247.

PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200002

ENTRY DATE: Entered STN: 20000209

Last Updated on STN: 20000209

Entered Medline: 20000203

AB Since its discovery as a protein associated with the cytoplasmic region of E-cadherin, beta-catenin has been shown to perform two apparently unrelated functions: it has a crucial role in cell-cell adhesion in addition to a signaling role as a component of the Wnt/wg pathway. Wnt/wg signaling results in beta-catenin accumulation and transcriptional activation of specific target genes during development. It is now apparent that deregulation of beta-catenin signaling is an important event in the genesis of a number of malignancies, such as colon **cancer**, melanoma, hepatocellular **carcinoma**, ovarian **cancer**, endometrial **cancer**, medulloblastoma pilomatricomas, and prostate **cancer**. beta-catenin mutations appear to be a crucial step in the progression of a subset of these **cancers**, suggesting an important role in the control of cellular proliferation or cell death. The APC/beta-catenin pathway is highly regulated and includes players such as GSK3-beta, CBP, Groucho, Axin, **Conductin**, and TCF. c-MYC and cyclin D1 were recently identified as a key transcriptional targets of this pathway.

Searcher : Shears 308-4994

and additional targets are likely to emerge. Published 1999 John Wiley & Sons, Inc.

L8 ANSWER 14 OF 22 MEDLINE DUPLICATE 7
 ACCESSION NUMBER: 2001120045 MEDLINE
 DOCUMENT NUMBER: 21079826 PubMed ID: 11212302
 TITLE: Signaling through beta-catenin and Lef/Tcf.
 AUTHOR: Novak A; Dedhar S
 CORPORATE SOURCE: Cancer Research, S-218, Sunnybrook Health Science Centre, Toronto, Ontario, Canada.
 SOURCE: CELLULAR AND MOLECULAR LIFE SCIENCES, (1999 Oct 30) 56 (5-6) 523-37. Ref: 167

 Journal code: CLE. ISSN: 1420-682X.
 PUB. COUNTRY: Switzerland
 Journal; Article; (JOURNAL ARTICLE)
 General Review; (REVIEW)
 (REVIEW, ACADEMIC)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200102
 ENTRY DATE: Entered STN: 20010322
 Last Updated on STN: 20010322
 Entered PubMed: 20010209
 Entered Medline: 20010215

AB Beta-catenin plays a structural role in cell adhesion by binding to cadherins at the intracellular surface of the plasma membrane and a signaling role in the cytoplasm as the penultimate downstream mediator of the wnt signaling pathway. The ultimate mediator of this pathway is a nuclear complex of beta-catenin acting as a coactivator with lymphoid enhancer factor/T cell factor (Lef/Tcf) transcription factors to stimulate transcription of a variety of target genes. Signaling through beta-catenin is regulated by modulating its degradation and nuclear translocation. In the absence of an activating signal, phosphorylation of beta-catenin by glycogen synthase kinase 3 (GSK3) acting in conjunction with adenomatous polyposis coli and axin/conductin causes beta-catenin to interact with the beta-transducin repeat-containing protein which results in its ubiquitination and degradation. Signaling from the wnt pathway activates dishevelled which, in an as yet undefined manner, inhibits the activity of GSK3 resulting in an increase in the cytoplasmic free pool of beta-catenin, and translocation into the nucleus. The integrin-linked kinase (ILK) pathway also activates beta-catenin-Lef/Tcf signaling. ILK phosphorylates GSK3 to inhibit its activity and translocates beta-catenin into the nucleus. In addition, ILK downregulates the expression of E-cadherin and upregulates Lef-1 expression. In the final step of the beta-catenin-Lef/Tcf signaling pathway, nuclear beta-catenin binds pontin52-TATA binding protein and displaces Groucho-related gene or

CREB-binding protein corepressors from Lef/Tcf resulting in stimulation of transcription. During development, beta-catenin-Lef/Tcf signaling is involved in the formation of dorsal mesoderm and dorsal axis. Furthermore, defects in the beta-catenin-Lef/Tcf pathway are involved in the development of several types of cancers.

L8 ANSWER 15 OF 22 MEDLINE

DUPLICATE 8

ACCESSION NUMBER: 1999457298

MEDLINE

DOCUMENT NUMBER: 99457298 PubMed ID: 10526234

TITLE: Identification and characterization of E-APC, a novel *Drosophila* homologue of the tumour suppressor APC.

AUTHOR: Hamada F; Murata Y; Nishida A; Fujita F; Tomoyasu Y; Nakamura M; Toyoshima K; Tabata T; Ueno N; Akiyama T

CORPORATE SOURCE: Department of Oncogene Research, Research Institute for Microbial Diseases, Osaka University, 3-1 Yamadaoka, Suita 565-0871, Japan. and.

SOURCE: GENES TO CELLS, (1999 Aug) 4 (8) 465-74.
Journal code: CUF; 9607379. ISSN: 1356-9597.

PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199912

ENTRY DATE: Entered STN: 20000113

Last Updated on STN: 20000915

Entered Medline: 19991223

AB BACKGROUND: Mutations in the adenomatous polyposis coli (APC) tumour suppressor gene are implicated in the genesis of colorectal cancers. The product of the APC gene forms a complex with beta-catenin, glycogen synthase kinase 3beta (GSK-3beta) and Axin/conductin, and induces the degradation of beta-catenin. RESULTS: We have identified a novel *Drosophila* homologue of APC, E-APC, which is similar to but differs in several respects from D-APC. The E-APC cDNA encodes a protein of predicted 1067 amino acids, with seven armadillo repeats, two copies of the 15-amino acid repeat, five copies of the 20-amino acid repeat, and one Axin/conductin binding site. E-APC directly interacts with D-Axin and Armadillo (Arm, the *Drosophila* homologue of beta-catenin) in vitro, destabilizes intracellular beta-catenin, and suppresses beta-catenin/TCF-regulated transcription in APC-/- colon cancer cells. The E-APC mRNA is ubiquitously expressed throughout all developmental stages in *Drosophila*. CONCLUSION: Our findings suggest that E-APC may be universally involved in the regulation of the Wingless signalling pathway by down-regulating the level of Arm in *Drosophila*.

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L8 ANSWER 16 OF 22 MEDLINE

DUPLICATE 9

ACCESSION NUMBER: 1999168905 MEDLINE
DOCUMENT NUMBER: 99168905 PubMed ID: 10049590
TITLE: Cloning of the human homolog of **conductin**
(AXIN2), a gene mapping to chromosome 17q23-q24.
AUTHOR: Mai M; Qian C; Yokomizo A; Smith D I; Liu W
CORPORATE SOURCE: Department of Laboratory Medicine and Pathology, Mayo
Clinic/Foundation, Rochester, Minnesota 55905, USA.
CONTRACT NUMBER: CA48031 (NCI)
SOURCE: GENOMICS, (1999 Feb 1) 55 (3) 341-4.
Journal code: GEN; 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States

LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF078165
ENTRY MONTH: 199905
ENTRY DATE: Entered STN: 19990607
Last Updated on STN: 19990607
Entered Medline: 19990524

AB **Conductin** or Axil, an Axin homolog, plays an important role in the regulation of beta-catenin stability in the Wnt signaling pathway. To facilitate the molecular analysis of the human gene, we isolated the human homolog, AXIN2. The cDNA contains a 2529-bp open reading frame and encodes a putative protein of 843 amino acids. Compared with rat and mouse homologs, AXIN2 shows an overall 89% amino acid identity. Several functional domains in this protein are highly conserved including the GRS (95.9%), GSK-3beta (96.3%), Dsh (98%), and beta-catenin (89.9%) domains. Radiation hybrid mapping localized the AXIN2 gene to human chromosome 17q23-q24, a region that shows frequent loss of heterozygosity in breast **cancer**, neuroblastoma, and other **tumors**. Human AXIN2 is thus a very strong candidate involved in multiple tumor types.

L8 ANSWER 17 OF 22 SCISEARCH COPYRIGHT 2001 ISI (R)

ACCESSION NUMBER: 2000:63768 SCISEARCH
THE GENUINE ARTICLE: 274MZ
TITLE: Modulation of Wnt signaling by Axin and Axil
AUTHOR: Kikuchi A (Reprint)
CORPORATE SOURCE: HIROSHIMA UNIV, SCH MED, DEPT BIOCHEM, MINAMI KU,
1-2-3 KASUMI, HIROSHIMA 7348551, JAPAN (Reprint)
COUNTRY OF AUTHOR: JAPAN
SOURCE: CYTOKINE & GROWTH FACTOR REVIEWS, (SEP-DEC 1999)
Vol. 10, No. 3-4, pp. 255-265.
Publisher: ELSEVIER SCI LTD, THE BOULEVARD, LANGFORD
LANE, KIDLINGTON, OXFORD OX5 1GB, OXON, ENGLAND.
ISSN: 1359-6101.

Searcher : Shears 308-4994

09/587574

DOCUMENT TYPE: Article; Journal
LANGUAGE: English
REFERENCE COUNT: 97

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The Wnt signaling pathway is conserved in various species from worms to mammals, and, plays important roles in development, cellular proliferation, and differentiation. The molecular mechanisms by which the Wnt signal regulates cellular functions are becoming increasingly well understood. Wnt stabilizes cytoplasmic beta-catenin, which stimulates the expression of genes including c-myc, c-jun, fra-1, and cyclin D1. Axin and its homolog Axil, newly recognized as components of the Wnt signaling pathway, negatively regulate this pathway. Other components of the Wnt signaling pathway, including Dvl, glycogen synthase kinase-3 beta (GSK-3 beta), beta-catenin, and adenomatous polyposis coli (APC), interact with Axin, and the phosphorylation and stability of beta-catenin are regulated in the Axin complex. Axil has similar functions to Axin. Thus, Axin and Axil act as scaffold proteins in the Wnt signaling pathway, thereby modulating the Wnt-dependent cellular functions.
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L8 ANSWER 18 OF 22 MEDLINE DUPLICATE 10
ACCESSION NUMBER: 1999147086 MEDLINE
DOCUMENT NUMBER: 99147086 PubMed ID: 10021369
TITLE: Identification of APC2, a homologue of the adenomatous polyposis coli tumour suppressor.
AUTHOR: van Es J H; Kirkpatrick C; van de Wetering M; Molenaar M; Miles A; Kuipers J; Destree O; Peifer M; Clevers H
CORPORATE SOURCE: Department of Immunology, University Hospital, P.O. Box 85500, 3508 GA, Utrecht, The Netherlands.
SOURCE: CURRENT BIOLOGY, (1999 Jan 28) 9 (2) 105-8.
JOURNAL CODE: B44; 9107782. ISSN: 0960-9822.
PUB. COUNTRY: ENGLAND: United Kingdom
JOURNAL: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF091430; GENBANK-AJ012652; GENBANK-AJ130783; GENBANK-AJ130784; GENBANK-AJ130785; GENBANK-AJ130786; GENBANK-AJ130787; GENBANK-AJ130788; GENBANK-AJ130789; GENBANK-AJ130790; GENBANK-AJ130791; GENBANK-AJ130792; GENBANK-AJ130793; GENBANK-AJ130794; GENBANK-AJ130795; GENBANK-AJ130796; GENBANK-AJ131187
ENTRY MONTH: 199903
ENTRY DATE: Entered STN: 19990402
Last Updated on STN: 20000303
Entered Medline: 19990323

Searcher : Shears 308-4994

AB The adenomatous polyposis coli (APC) tumour-suppressor protein controls the Wnt signalling pathway by forming a complex with glycogen synthase kinase 3beta (GSK-3beta), axin/ conductin and betacatenin. Complex formation induces the rapid degradation of betacatenin. In colon carcinoma cells, loss of APC leads to the accumulation of betacatenin in the nucleus, where it binds to and activates the Tcf-4 transcription factor (reviewed in [1] [2]). Here, we report the identification and genomic structure of APC homologues. Mammalian APC2, which closely resembles APC in overall domain structure, was functionally analyzed and shown to contain two SAMP domains, both of which are required for binding to conductin. Like APC, APC2 regulates the formation of active betacatenin-Tcf complexes, as demonstrated using transient transcriptional activation assays in APC -/- colon carcinoma cells. Human APC2 maps to chromosome 19p13.3. APC and APC2 may therefore have comparable functions in development and cancer.

L8 ANSWER 19 OF 22 JICST-EPlus COPYRIGHT 2001 JST

ACCESSION NUMBER: 990756513 JICST-EPlus

TITLE: Arthroscopic treatment for dorsal wrist ganglion.

AUTHOR: NISHIKAWA SHINJI; ARAI KOICHI; TAKEUCHI KAZUNARI;
FUKUDA AKIRA; WADA KAN'ICHIRO

CORPORATE SOURCE: Mutsu Gen. Hosp.

SOURCE: Kansetsukyo (Arthroscopy), (1999) vol. 24, no. 1, pp. 85-90. Journal Code: L0107A (Fig. 7, Ref. 9)
ISSN: 0910-223X

PUB. COUNTRY: Japan

DOCUMENT TYPE: Conference; Article

LANGUAGE: Japanese

STATUS: New

AB In excising a ganglion located at the dorsum of the wrist joint, one may lose sight of the base of the ganglion, which may result in a recurrence of the condition; or the surgical procedure may leave a large, unsightly surgical cicatrix on the dorsum of the hand due to the size of the lesion. To eliminate these problems, we have been conductin surgery on ganglions of the dorsal wrist joint under arthroscopy. The details are reported below. A total of 16 joints(10 right and 6 left) in 16 patients(7 males and 9 females, ages ranging from 12 to 83 years, with a mean of 42 years) have undergone the arthroscopic procedure. A nodule was palpated at the center of the dorsum of the wrist in each patients and all reported pain that was associated with movement. Six had experienced repeated recurrences for six months or more; the condition had developed for the first time in eight(among whom, two had been subjected to repeated aspiration therapy); and the condition had returned in one following surgical therapy. MRI was conducted prior to surgery to confirm that there was communication between the ganglion and the

scapholunate joint (SL joint). Arthroscopy was conducted at portals I-II and a probe and a shaver were inserted through portals IV-V. The position of the base of the ganglion that was palpated at the dorsum of the scapholunate ligament (SL ligament) was confirmed under arthroscopy and excised with the shaver. No recurrence was noted and the postoperative course was satisfactory for a follow-up period that lasted from 2 to 15 months (mean, 6.4). The method introduced above applies to all ganglions that originate at the SL joint: but it is particularly suitable for large growths that are likely to leave prominent surgical scars or for radical treatment of those that return repeatedly after aspiration and cause pain associated with wrist movement. (author abst.)

L8 ANSWER 20 OF 22 BIOSIS COPYRIGHT 2001 BIOSIS
 ACCESSION NUMBER: 1999:174930 BIOSIS
 DOCUMENT NUMBER: PREV199900174930
 TITLE: Cloning of the human homolog of conduction (AXIN2), a gene mapping to chromosome 17q23-24.
 AUTHOR(S): Mai, M. (1); Qian, C.; Yokomizo, A.; Smith, D. I.; Liu, W.
 CORPORATE SOURCE: (1) Div. Exp. Pathol., Dep. Lab. Med. Pathol., Rochester, MN 55905 USA
 SOURCE: Proceedings of the American Association for Cancer Research Annual Meeting, (March, 1999) Vol. 40, pp. 34.
 Meeting Info.: 90th Annual Meeting of the American Association for Cancer Research Philadelphia, Pennsylvania, USA April 10-14, 1999 American Association for Cancer Research
 . ISSN: 0197-016X.
 DOCUMENT TYPE: Conference
 LANGUAGE: English

L8 ANSWER 21 OF 22 BIOSIS COPYRIGHT 2001 BIOSIS DUPLICATE 11
 ACCESSION NUMBER: 1999:165640 BIOSIS
 DOCUMENT NUMBER: PREV199900165640
 TITLE: APC protein: Protein interactions and cellular functions.
 AUTHOR(S): Jais, Philippe (1); Laurent-Puig, Pierre; Olschwang, Sylviane
 CORPORATE SOURCE: (1) Unite Marqueurs Genet. Cancers, Inst. Gustave-Roussy, 39 rue Camille-Desmoulins, 94805 Villejuif Cedex France
 SOURCE: Gastroenterologie Clinique et Biologique, (Dec., 1998) Vol. 22, No. 12, pp. 1071-1080.
 ISSN: 0399-8320.
 DOCUMENT TYPE: General Review
 LANGUAGE: French

L8 ANSWER 22 OF 22 MEDLINE

DUPLICATE 12

ACCESSION NUMBER: 1998221239 MEDLINE

DOCUMENT NUMBER: 98221239 PubMed ID: 9554852

TITLE: Functional interaction of an axin homolog,
conductin, with beta-catenin, APC, and
GSK3beta.AUTHOR: Behrens J; Jerchow B A; Wurtele M; Grimm J; Asbrand
C; Wirtz R; Kuhl M; Wedlich D; Birchmeier WCORPORATE SOURCE: Max Delbruck Center for Molecular Medicine,
Robert-Rossle-Strasse 10, 13122 Berlin, Germany.

SOURCE: SCIENCE, (1998 Apr 24) 280 (5363) 596-9.

Journal code: UJ7; 0404511. ISSN: 0036-8075.

PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-AF073788

ENTRY MONTH: 199805

ENTRY DATE: Entered STN: 19980514

Last Updated on STN: 20000303

Entered Medline: 19980507

AB Control of stability of beta-catenin is central in the wnt signaling pathway. Here, the protein **conductin** was found to form a complex with both beta-catenin and the tumor suppressor gene product adenomatous polyposis coli (APC). **Conductin** induced beta-catenin degradation, whereas mutants of **conductin** that were deficient in complex formation stabilized beta-catenin. Fragments of APC that contained a **conductin**-binding domain also blocked beta-catenin degradation. Thus, **conductin** is a component of the multiprotein complex that directs beta-catenin to degradation and is located downstream of APC. In *Xenopus* embryos, **conductin** interfered with wnt-induced axis formation.

(FILE 'CAPLUS' ENTERED AT 11:20:11 ON 11 JUN 2001)

L9 150 SEA FILE=CAPLUS ABB=ON PLU=ON CONDUCTING(3A) (PROTEIN
OR PEPTIDE)L10 3 SEA FILE=CAPLUS ABB=ON PLU=ON L9 AND (TUMOUR OR TUMOR
OR NEOPLAS? OR CANCER? OR CARCIN?)

L11 3 S L10 NOT L6

L11 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 1996:427508 CAPLUS

DOCUMENT NUMBER: 125:135608

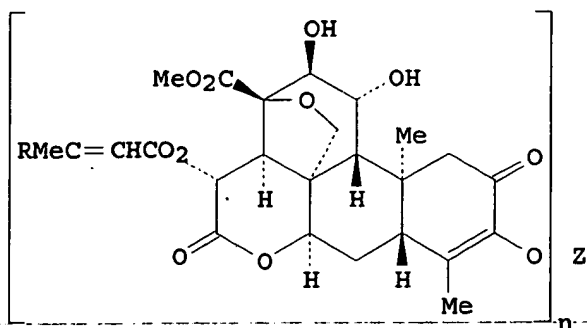
TITLE: Co-translational effects of temperature on

membrane insertion and orientation of
P-glycoprotein sequences
AUTHOR(S): Zhang, Jian-Ting; Chong, Crispina H.
CORPORATE SOURCE: Dep. Physiol. Biophys., Univ. Texas Med. Branch,
Galveston, TX, 77555-0641, USA
SOURCE: Mol. Cell. Biochem. (1996), 159(1), 25-31
CODEN: MCBIB8; ISSN: 0300-8177
DOCUMENT TYPE: Journal
LANGUAGE: English

AB P-glycoprotein (pgp) is a membrane transport protein that causes multidrug resistance (MDR) by actively extruding a wide variety of cytotoxic agents out of cells. In may also function as a peptide transporter, a vol.-regulated chloride channel, and an ATP channel. Previously, it has been shown that hamster pgp1 Pgp is expressed in more than one topos. form and that the generation of these structures is modulated by charged amino acids flanking the predicted transmembrane (TM) segments 3 and 4 and by sol. cytoplasmic factors. Different topos. structures of Pgp may be related to its different functions. This study examd. the effects of translation temp. on the membrane insertion process and the topologies of Pgp. The rabbit reticulocyte lysate expression system was used to show that translation at different temps. affects the membrane insertion and orientation of the putative TM3 and TM4 of hamster pgp1 Pgp in a co-translational manner. This observation suggests that the membrane insertion process of TM3 and TM4 of Pgp mols. may involve a protein conducting channel and/or the interaction between TM3 and TM4, which act in a temp. sensitive manner. Manipulating temp. may provide a way to understand the structure-function relationship of Pgp and help overcome Pgp-related multidrug resistance of cancer cells.

L11 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 1982:400304 CAPLUS
DOCUMENT NUMBER: 97:304
TITLE: Antitumor agents. XLVIII: structure-activity relationships of quassinoids as in vitro protein synthesis inhibitors of P-388 lymphocytic leukemia tumor cell metabolism
AUTHOR(S): Liou, Y. F.; Hall, I. H.; Okano, M.; Lee, K. H.; Chaney, S. G.
CORPORATE SOURCE: Sch. Med., Univ. North Carolina, Chapel Hill, NC, 27514, USA
SOURCE: J. Pharm. Sci. (1982), 71(4), 430-5
CODEN: JPMSAE; ISSN: 0022-3549
DOCUMENT TYPE: Journal
LANGUAGE: English
GI



- I, R=CHMe₂, Z=H, n=1
 II, R=Me, Z=H, n=1
 III, R=Me, Z=COCH₂CO, n=2

AB A series of brusatol, bisbrusatol, and bruceantin esters were examd. for their ability to inhibit protein synthesis in P-388 lymphocytic leukemia cells. Compds. which produced high antileukemic activities resulted in ID50 of 5.4-15.5 .mu.M for inhibition of whole cell protein synthesis, ID50 of 1.3-13 .mu.M for inhibition of endogenous protein synthesis in cell homogenates, and ID50 of 1.9-6 .mu.M for inhibition of polyuridine directed polyphenylalanine synthesis using runoff ribosomes and a pH 5 enzyme prepn. The polyuridine directed polyphenylalanine synthesis requires neither initiation nor termination factors, suggesting that quassinoids are exclusively elongation inhibitors. bruceantin (I) [41451-75-6], brusatol (II) [14907-98-3], and bisbrusatolyl malonate (III) [80096-78-2] allowed a runoff of the polyribosomes to 80-S free ribosomes. However, formation of the ternary complex and 80-S initiation complex were not inhibited by the quassinoids. Thus, these agents do not affect the individual steps leading to the formation of a stable 80-S initiation complex in P-388 cells. Brusatol, bruceantin, and bisbrusatolyl malonate inhibited the formation of the first peptide bond between puromycin and [3H]methionyl-transfer RNA bound to the initiation complex, indicating peptidyl transferase activity is inhibited by the quassinoids in P-388 cells. Apparently, the free 80-S ribosome is the site of binding by the quassinoid. Ribosomes actively conducting protein synthesis will continue protein synthesis and terminate before the quassinoids bind. Thus, quassinoids are elongation inhibitors of tumor cells. A strong correlation was obsd. between potent antileukemic activity and the ability to inhibit protein synthesis in P-388 lymphocytic leukemia cells.

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L11 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 1960:24381 CAPLUS

DOCUMENT NUMBER: 54:24381

ORIGINAL REFERENCE NO.: 54:4860c-d

TITLE: The nature of the interaction of biologically active agents with tissue constituents

AUTHOR(S): Mason, R.

CORPORATE SOURCE: Univ. Coll., London

SOURCE: Acta Unio Intern. contra Cancrum (1959), 15, 650-1

DOCUMENT TYPE: Journal

LANGUAGE: Unavailable

AB The electronic structure of carcinogen-protein mol. complexes was examd. theoretically and the possibility of charge transfer in the complex discussed. A banded-electronic model of a protein suggests that electron transfer within such a mol. complex will take place only when the energy levels of the mols. of the complex are closely matched. Aromatic carcinogens satisfy a precise criterion for such matching of levels, and carcinogenesis is to be assocd. with the induction of conducting properties in the protein.

(FILE 'MEDLINE', BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH, JICST-EPLUS, JAPIO, CANCERLIT' ENTERED AT 11:22:50 ON 11 JUN 2001)

L12 18 S L10

L13 18 S L12 NOT (L2 OR L7)

L14 9 DUP REM L13 (9 DUPLICATES REMOVED)

L14 ANSWER 1 OF 9 WPIDS COPYRIGHT 2001 DERWENT INFORMATION LTD

ACCESSION NUMBER: 2001-266373 [27] WPIDS

DOC. NO. NON-CPI: N2001-190479

DOC. NO. CPI: C2001-080736

TITLE: Detection of proteins by using a protein fingerprinting system which comprises linearizing the protein, labeling a first amino acid residue type and detecting first and second residue types, useful in the diagnosis of cancer.

DERWENT CLASS: B04 D16 S03

INVENTOR(S): BRENT, R; BURBULIS, I E; CARLSON, R H

PATENT ASSIGNEE(S): (MOLE-N) MOLECULAR SCI INST INC

COUNTRY COUNT: 93

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
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WO 2001025794	A2	20010412	(200127)*	EN	55
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RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC
MW MZ NL OA PT SD SE SL SZ TZ UG ZW

Searcher : Shears 308-4994

W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE
 DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG
 KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ
 PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG UZ VN YU
 ZA ZW

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2001025794	A2	WO 2000-US26958	20000929

PRIORITY APPLN. INFO: US 1999-412732 19991005

AN 2001-266373 [27] WPIDS

AB WO 200125794 A UPAB: 20010518

NOVELTY - A new method (M1) for detecting proteins having at least two different types of residues comprises giving a detectable set of distinguishing ancillary properties (a 'fingerprint') to the proteins and then detecting the fingerprint by linearizing the protein, labeling the first type of residue and detecting first and second amino acid residues.

DETAILED DESCRIPTION - A new method (M1) for detecting proteins having at least two different types of residues comprises giving a detectable set of distinguishing ancillary properties (a 'fingerprint') to the proteins and then detecting the fingerprint by linearizing the protein, labeling the first type of residue and detecting first and second amino acid residues.

In detail, M1 comprises:

- (a) linearizing the protein molecule with a denaturation means;
- (b) labeling each of the first type of amino acid residue with a tag;
- (c) detecting the fingerprint of the protein with a detection means, by detecting a first fingerprint constituent imparted by the tag and a second fingerprint constituent imparted by the second type of amino acid residue.

INDEPENDENT CLAIMS are also included for the following:

(1) identifying a protein molecule having at least two different amino acid residue types in a sample containing several proteins, by linearizing each protein as in M1 step (a), isolating the protein, conducting steps (b) and (c) of M1, and comparing the fingerprint obtained (optionally using a computer receiving signals from the detection means) to a library of fingerprints of known protein molecules;

(2) a library of fingerprint values of known proteins, listing the identity of the proteins and first and second (and optionally third) fingerprint constituents of each protein, being representative of the number and sequence of the first and second

(and optionally third) types of amino acid residues respectively;

(3) characterizing protein molecules, by isolating the protein and using M1 which is modified such that first and second types of amino acid types are both labeled with different tags;

(4) protein molecules having an identifiable fingerprint, comprising two amino acid residue types each separately tagged, or three amino acid types (optionally including tryptophan), imparting up to six fingerprint constituents by using combinations of excitation and emitted radiations; and

(5) identifying a protein in a sample containing several proteins, following the method of (1) which is modified such that first and second residue types are both labeled with different tags.

USE - The method is useful to enable rapid identification of protein molecules, especially in biological samples e.g. plant, microorganism or animal (especially human) tissues or cells e.g. in clinical or research applications to identify aberrant or mutant forms of proteins involved in diseases such as cancers or inherited disorders such as cystic fibrosis and hemophilia. It also enables the production of a library of known proteins and their corresponding fingerprints, useful to identify unknown proteins in a sample.

Dwg.0/33

L14 ANSWER 2 OF 9 WPIDS COPYRIGHT 2001 DERWENT INFORMATION LTD
 ACCESSION NUMBER: 2001-050022 [06] WPIDS
 DOC. NO. NON-CPI: N2001-038339
 DOC. NO. CPI: C2001-013790
 TITLE: Assessing translocation of proteins such as glucose transporter GLUT4, cystic fibrosis transmembrane conductance regulator by using modified protein of interest comprising the protein and detectable tags.
 DERWENT CLASS: B04 D16 S03
 INVENTOR(S): BOGAN, J S; LODISH, H
 PATENT ASSIGNEE(S): (GEHO) GEN HOSPITAL CORP; (WHED) WHITEHEAD INST BIOMEDICAL RES
 COUNTRY COUNT: 93
 PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
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WO 2000075188	A1	20001214	(200106)*	EN	75
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RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC
 MW MZ NL OA PT SD SE SL SZ TZ UG ZW

W: AE AG AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE DK
 DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP
 KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL
 PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU

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ZA ZW

AU 2000054775 A 20001228 (200119)

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2000075188	A1	WO 2000-US15904	20000609
AU 2000054775	A	AU 2000-54775	20000609

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 2000054775	A Based on	WO 200075188

PRIORITY APPLN. INFO: US 1999-154078 19990915; US 1999-138237
19990609

AN 2001-050022 [06] WPIDS

AB WO 200075188 A UPAB: 20010126

NOVELTY - Translocation of a protein of interest from an intracellular location to the plasma membrane in mammalian cells, when the cells are exposed to a condition or a stimulus, is assessed by using a modified protein of interest (MP) comprising the protein of interest and an epitope tag in an extracellular domain and a fluorescent tag in an intracellular domain.

DETAILED DESCRIPTION - Translocation of a protein of interest from an intracellular location to the plasma membrane in mammalian cells, when the cells are exposed to a condition or a stimulus, is assessed by using a modified protein of interest (MP) comprising the protein of interest and an epitope tag in an extracellular domain and a fluorescent tag in an intracellular domain.

The method (I) comprises:

(a) culturing mammalian cells (test cells) expressing MP, under a condition or a stimulus to be assessed for its effects on translocation of the protein of interest;

(b) determining a value corresponding to proportion of MP at the cell membrane to total MP in the test cells that produces a test value; and

(c) comparing the test value with a control value, where the control value corresponds to the proportion of MP at the cell membrane to MP in control cells, where the control cells are the same cells as are cultured in (a), except that the control cells are not cultured under the condition or stimulus to be assessed, where the test value greater than the control value indicates that translocation of MP has occurred.

INDEPENDENT CLAIMS are also included for the following:

(1) determining (II) whether a protein of interest undergoes

Searcher : Shears 308-4994

translocation from an intracellular location to the plasma membrane in mammalian cells in the presence of a condition or stimulator, comprising:

- (a) culturing cells that express MP in the absence of the stimulator producing cultured cells;
 - (b) determining the relative proportion of MP at the plasma membrane of cultured cells to total MP in the cultured cells, by producing a control value;
 - (c) culturing cells that express MP under the same conditions as in (a) and in the presence of the stimulator, by producing test cells;
 - (d) determining the relative proportion of MP at the plasma membrane of test cells to total MP in the test cells, by producing a test value; and
 - (e) comparing the control value and the test value, where a test value that is greater than the control value indicates that protein of interest undergoes translocation following stimulation of the cells by the stimulator;
- (2) identifying (III) a drug which enhances translocation of a protein of interest from an intracellular location to the plasma membrane in mammalian cells by:
- (a) culturing cells which express RT in the presence of a candidate drug;
 - (b) determining the relative proportion of MP at the plasma membrane of cultured cells to total MP in the cultured cells, producing a test value; and
 - (c) comparing the test value with the control value, which is the relative proportion of the protein of interest at the plasma membrane to MP in cells cultured under same conditions in the absence of drug, where the test value greater than the control value indicates that the candidate drug enhances translocation of the protein of interest; and
- (3) eukaryotic cells (IV) expressing MP comprising a protein of interest and a detectable tag in an extracellular domain and at least 1 detectable tag in an intracellular domain, where the tags are different from each other and the protein of interest undergoes translocation in the eukaryotic cells upon contact with or exposure to a condition.

USE - The method is useful for determining translocation of a protein of interest such as aquaporin-2, cystic fibrosis transmembrane conductance regulator, gastric H⁺/K⁺ATPase, in particular GLUT4 from an intracellular location to the plasma membrane in mammalian cells in the presence of a condition or a stimulator. (III) is useful for assessing the effect of a drug on translocation of a protein such as GLUT4. Such drugs are useful in treating insulin resistance such as in adult-onset diabetes, obesity and polycystic ovary syndrome.

ADVANTAGE - Translocation of the protein of interest can be

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easily assessed using the tags. The tags can be detected individually, quantified and the addition of tags does not alter trafficking of the protein of interest.

Dwg.0/7

L14 ANSWER 3 OF 9 WPIDS COPYRIGHT 2001 DERWENT INFORMATION LTD
ACCESSION NUMBER: 1999-571821 [48] WPIDS
DOC. NO. CPI: C1999-166854
TITLE: New isolated RGS-GEF polypeptides, used to develop products for modulating, e.g. cell proliferation and integrin-mediated interactions.
DERWENT CLASS: B04 D16
INVENTOR(S): BOLLAG, G; HART, M J; JIANG, X; KOZASA, T; POLAKIS, P; ROSCOE, W; STERNWEIS, P
PATENT ASSIGNEE(S): (ONYX-N) ONYX PHARM INC; (TEXA) UNIV TEXAS SYSTEM
COUNTRY COUNT: 82
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 9947557	A2	19990923	(199948)*	EN	75
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ UG ZW					
W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GE GH GM HR HU ID IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG UZ VN YU ZW					
AU 9931038	A	19991011	(200008)		
EP 1064373	A2	20010103	(200102)	EN	
R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE					

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 9947557	A2	WO 1999-US6051	19990318
AU 9931038	A	AU 1999-31038	19990318
EP 1064373	A2	EP 1999-912727	19990318
		WO 1999-US6051	19990318

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 9931038	A Based on	WO 9947557
EP 1064373	A2 Based on	WO 9947557

PRIORITY APPLN. INFO: US 1998-78634 19980318

Searcher : Shears 308-4994

AN 1999-571821 [48] WPIDS

AB WO 9947557 A UPAB: 19991122

NOVELTY - Isolated RGS-guanine nucleotide exchange factor (GEF) polypeptides are new.

DETAILED DESCRIPTION - A novel isolated RGS-GEF polypeptide or a biologically active fragment consists of an RGS domain of a GEF protein.

INDEPENDENT CLAIMS are also included for the following:

(1) an isolated RGS-GEF polypeptide or a biologically active fragment comprising an RGS domain of a GEF protein, with the proviso that the polypeptide does not comprise a dbl homology (DH) domain or a pleckstrin homology (PH) domain;

(2) an isolated RGS-GEF polypeptide, or a biologically active fragment, where the polypeptide is selected from p115 Rho-GEF, Lsc, KIAA380, and where the polypeptide is mutated in the RGS domain, and where the polypeptide has a specific binding affinity for a G protein alpha subunit (GAS), or a GTPase activating activity for a GAS;

(3) an isolated RGS-GEF nucleic acid consisting of a nucleotide sequence (NS) encoding a polypeptide comprising an RGS domain of a GEF protein;

(4) a nucleic acid as in (3) but, where the polypeptide does not include a DH domain or a PH domain;

(5) a transformed cell containing a nucleic acid as in (4);

(6) a vector comprising a nucleic acid as in (4), and

(7) identifying or assaying a molecule that:

(a) inhibits or enhances binding of a monomeric G protein guanine nucleotide exchange factor to a GAS comprising:

(i) incubating the GAS, or fragments with the monomeric G protein nucleotide exchange factor, or fragments, in the presence and absence of a test molecule, and

(ii) determining whether the presence of the test molecule inhibits or enhances binding between the monomeric G-protein guanine nucleotide exchange factor and the GAS;

(b) inhibits or enhances a stimulatory effect of a GEF on a GAS GTPase activity comprising:

(i) as in (ai), and

(ii) determining whether the presence of the test molecule inhibits or enhances the stimulatory effect of the GEF protein on GAS GTPase activity;

(c) specifically inhibits the stimulatory effect of an activated GAS on GEF mediated nucleotide exchange of a monomeric G protein, comprising conducting a first assay by:

(i) incubating an activated GAS, or its fragments, with a GEF protein, or fragments, and a monomeric G protein, or its fragments, in the presence and absence of a test inhibitor;

(ii) conducting a second assay by incubating a GEF protein, or fragments, and a monomeric G protein. or fragments in the presence

and absence of the test inhibitor, and

(iii) determining whether any inhibitory effect of the test inhibitor in the first assay is greater than any inhibitory effect of the test inhibitor in the second assay;

(d) specifically enhances the stimulatory effect of an activated GAS on GEF mediated nucleotide exchange of a monomeric G protein, comprising:

(i) conducting a first assay by incubating an activated GAS, or fragments with a GEF protein, and fragments, and a monomeric G protein, or fragments in the presence and absence of a test enhancer;

(ii) as in (cii), but in the presence/absence of the test enhancer, and

(iii) determining whether any enhancing effect of the test enhancer in the first assay is greater than any enhancing effect of the test enhancer in the second assay;

(e) mimics the stimulatory effect of an activated GAS on GEF mediated nucleotide exchange of a monomeric G protein comprising:

(i) identifying a test compound that exhibits a binding affinity for the RGS domain of GEF proteins, or fragments, incubating a GEF protein or fragments, and monomeric G protein, or fragments in the presence or absence of the test compound, and

(ii) determining whether the test compound exhibits a stimulatory effect on GEF mediated nucleotide exchange of a monomeric G protein, and

(f) mimics the stimulatory effect of an RGS domain of a GEF protein on GTPase activity of a GAS comprising:

(i) identifying a test compound that exhibits a binding affinity for a GAS, and

(ii) incubating a GTP loaded GAS in the presence or absence of the test compound to determine whether the test compound has a stimulatory effect on GAS GTPase activity.

USE - The RGS-GEF polypeptides can be used for modulating an activity of a GAS (claimed). The products can be used for the regulation of biological pathways in which a RGS-GEF polypeptide is involved, particularly pathological conditions, e.g. cell proliferation (e.g. cancer), growth control, morphogenesis, stress fiber formation, and integrin-mediated interactions, such as embryonic development, tumor cell growth and metastasis, programmed cell death, hemostasis, leukocyte homing and activation, bone resorption, clot retraction, and the response of cells to mechanical stress. The products can also be used for detection, diagnosis and production of transgenic animals.

ADVANTAGE - None given.

Dwg.0/18

L14 ANSWER 4 OF 9 MEDLINE

DUPLICATE 1

ACCESSION NUMBER: 1999439712 MEDLINE

Searcher : Shears 308-4994

09/587574

DOCUMENT NUMBER: 99439712 PubMed ID: 10508919
TITLE: A novel ADP-ribosylation like factor (ARL-6),
interacts with the **protein-**
conducting channel SEC61beta subunit.
AUTHOR: Ingley E; Williams J H; Walker C E; Tsai S; Colley S;
Sayer M S; Tilbrook P A; Sarna M; Beaumont J G;
Klinken S P
CORPORATE SOURCE: Laboratory for Cancer Medicine, Department of
Biochemistry, The University of Western Australia and
Royal Perth Hospital, Perth, W.A., Australia.
SOURCE: FEBS LETTERS, (1999 Oct 1) 459 (1) 69-74.
Journal code: EUH; 0155157. ISSN: 0014-5793.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF031903; GENBANK-AF133669; GENBANK-AF133670;
GENBANK-AF133910; GENBANK-AF133911; GENBANK-AF133912;
GENBANK-AF133913
ENTRY MONTH: 199911
ENTRY DATE: Entered STN: 20000111
Last Updated on STN: 20000111
Entered Medline: 19991101

AB We report here the isolation of a new member of the ADP-ribosylation factor (ARF)-like family (ARL-6) present in the J2E erythroleukemic cell line, but not its myeloid variants. Consistent with this lineage-restricted expression, ARL-6 mRNA increased with erythropoietin-induced maturation of J2E cells, and decreased with interleukin 6-induced differentiation of M1 monoblastoid cells. In tissues, ARL-6 mRNA was most abundant in brain and kidney. While ARL-6 protein was predominantly cytosolic, its membrane association increased following exposure to GTP-gammaS, like many members of the ARF/ARL family. Using the yeast two-hybrid system, six molecules which interact with ARL-6 were identified including SEC61beta, a subunit of the heterotrimeric **protein conducting** channel SEC61p. Co-immunoprecipitation of ARL-6 confirmed a stable association between ARL-6 and SEC61beta in COS cells. These results demonstrate that ARL-6, a novel member of the ADP-ribosylation factor-like family, interacts with the SEC61beta subunit.

L14 ANSWER 5 OF 9 JAPIO COPYRIGHT 2001 JPO

ACCESSION NUMBER: 1997-183797 JAPIO
TITLE: PHYSIOLOGICALLY ACTIVE PROTEIN RHOTEKIN
INVENTOR: NARUMIYA SHU
PATENT ASSIGNEE(S): KIRIN BREWERY CO LTD, JP (CO 330755)
PATENT INFORMATION:

PATENT NO	KIND	DATE	ERA	MAIN IPC
-----------	------	------	-----	----------

Searcher : Shears 308-4994

JP 09183797 A 19970715 Heisei (6) C07K014-47

JP

APPLICATION INFORMATION

ST19N FORMAT: JP1995-354328 19951228

ORIGINAL: JP07354328 Heisei

SOURCE: PATENT ABSTRACTS OF JAPAN (CD-ROM), Unexamined
Applications, Vol. 97, No. 7

AN 1997-183797 JAPIO

AB PURPOSE: TO BE SOLVED: To obtain a new protein having activated
Rho-protein binding ability, inhibiting Rho-protein GTPase activity,
thus capable of inhibiting tumor development and
metastasis through neutralizing Rho-protein involving tumor
development and metastasis.CONSTITUTION: protein is a new physiologically active protein
Rhotekin (or its modified product), which has activated Rho-protein
binding ability and inhibits Rho-protein GTPase activity, containing
part or the whole of an amino acid sequence of the formula, or an
equivalent sequence thereto. This protein is capable of neutralizing
the Rho protein closely involving tumor development and
metastasis, thus of inhibiting tumor development and
metastasis. This new protein is obtained by
conducting a library screening by yeast-two-hybrid system
using mouse fetal cDNA library to isolate the gene of mouse's
activated Rho- protein-binding protein followed by integrating a
vector with the gene which is then manifested in host cells.

L14 ANSWER 6 OF 9 MEDLINE DUPLICATE 2

ACCESSION NUMBER: 96408699 MEDLINE

DOCUMENT NUMBER: 96408699 PubMed ID: 8813706

TITLE: Co-translational effects of temperature on membrane
insertion and orientation of P-glycoprotein
sequences.

AUTHOR: Zhang J T; Chong C H

CORPORATE SOURCE: Department of Physiology and Biophysics, University
of Texas Medical Branch, Galveston 77555-0641, USA.

CONTRACT NUMBER: CA-64539 (NCI)

SOURCE: MOLECULAR AND CELLULAR BIOCHEMISTRY, (1996 Jun 7) 159
(1) 25-31.

Journal code: NGU; 0364456. ISSN: 0300-8177.

PUB. COUNTRY: Netherlands

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199612

ENTRY DATE: Entered STN: 19970128

Last Updated on STN: 19970128

Entered Medline: 19961210

AB P-glycoprotein (pgp) is a membrane transport protein that causes multidrug resistance (MDR) by actively extruding a wide variety of cytotoxic agents out of cells. It may also function as a peptide transporter, a volume-regulated chloride channel, and an ATP channel. Previously, it has been shown that hamster pgp 1 Pgp is expressed in more than one topological form and that the generation of these structures is modulated by charged amino acids flanking the predicted transmembrane (TM) segments 3 and 4 and by soluble cytoplasmic factors. Different topological structures of Pgp may be related to its different functions. In this study, we examined the effects of translation temperature on the membrane insertion process and the topologies of Pgp. Using the rabbit reticulocyte lysate expression system, we showed that translation at different temperatures affects the membrane insertion and orientation of the putative TM3 and TM4 of hamster pgp 1 Pgp in a co-translational manner. This observation suggests that the membrane insertion process of TM3 and TM4 of Pgp molecules may involve a protein conducting channel and/or the interaction between TM3 and TM4, which act in a temperature sensitive manner. We speculate that manipulating temperature may provide a way to understand the structure-function relationship of Pgp and help overcome Pgp-related multidrug resistance of cancer cells.

L14 ANSWER 7 OF 9 MEDLINE DUPLICATE 3
 ACCESSION NUMBER: 96381595 MEDLINE
 DOCUMENT NUMBER: 96381595 PubMed ID: 8789608
 TITLE: Expression of mRNAs of multiple growth factors and receptors by neuronal cell lines: detection with RT-PCR.
 AUTHOR: Zaheer A; Zhong W; Lim R.
 CORPORATE SOURCE: Department of Neurology, University of Iowa College of Medicine and Veterans Affairs Medical Center, Iowa City 52242, USA.
 SOURCE: NEUROCHEMICAL RESEARCH, (1995 Dec) 20 (12) 1457-63. Journal code: NX9; 7613461. ISSN: 0364-3190.
 PUB. COUNTRY: United States
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199610
 ENTRY DATE: Entered STN: 19961106
 Last Updated on STN: 20000303
 Entered Medline: 19961018

AB Neurons and glia are capable of both secreting and responding to a large variety of growth factors. However, information on multiple expression of growth factors and their receptors was usually obtained from uncorrelated observations, using cells from various

animals of origin, developmental stages, growth phases, culture ages and culture conditions. Because of its specificity and extreme sensitivity, reverse transcription-polymerase chain reaction (RT-PCR) is uniquely suitable to study a large panel of growth factors and their receptors from a limited cell sample, free of these intervening variables. In this paper we evaluate the expression of mRNA of a total of 35 growth factor-related proteins by conducting RT-PCR on three neuronal cell lines: the PC12 rat pheochromocytoma line, the MAH rat sympathoadrenal progenitor line, and the N18 mouse neuroblastoma line. Three types of results are presented. The first confirms the existing knowledge such as the presence of Trk-A (NFG receptor) in PC12. The second consists of new information that expands and extends earlier observations, such as the presence of CNTF receptor complex in PC12, which explains our previous report that CNTF enhances the biological effects of NGF on these cells. The third consists of novel information that leads the way to further experimentation by the more conventional methods. These include the strong expression of Trk-B by MAH, predicting the biological responsiveness of MAH to BDNF and NT-4, and the expression of CNTF receptor in N18. Our results also suggest that CNTF is an autocrine factor for PC12 and MAH, since both lines express the growth factor as well as the receptor. Thus, RT-PCR is a valuable tool in growth factor research that can be used in complement to, and interactively with, other approaches such as bioassay, receptor binding, and immunochemical determination. It will be particularly useful for screening a large number of growth factors in minute areas of the brain in patients suffering from neurodegenerative diseases such as Parkinson's and Alzheimer's.

L14 ANSWER 8 OF 9 BIOSIS COPYRIGHT 2001 BIOSIS
 ACCESSION NUMBER: 1991:333595 BIOSIS
 DOCUMENT NUMBER: BR41:30145
 TITLE: REGULATION OF SQUAMOUS CELL MARKER SMALL PROLINE-RICH
 PROTEIN IN CONDUCTING AIRWAY
 EPITHELIUM.
 AUTHOR(S): AN G; ROBINSON C B; TESFAIZZI J; CARLSON D M; WU R
 CORPORATE SOURCE: CALIF. PRIMATE RES. CENT., UNIV. CALIF., DAVIS,
 CALIF. 95616.
 SOURCE: INTERNATIONAL CONFERENCE OF THE AMERICAN LUNG
 ASSOCIATION AND THE AMERICAN THORACIC SOCIETY,
 ANAHEIM, CALIFORNIA, USA, MAY 12-15, 1991. AM REV
 RESPIR DIS, (1991) 143 (4 PART 2), A515.
 CODEN: ARDSBL. ISSN: 0003-0805.
 DOCUMENT TYPE: Conference
 FILE SEGMENT: BR; OLD
 LANGUAGE: English

L14 ANSWER 9 OF 9 MEDLINE DUPLICATE 4
 ACCESSION NUMBER: 82216354 MEDLINE
 DOCUMENT NUMBER: 82216354 PubMed ID: 7086652
 TITLE: Antitumor agents XLVIII: Structure-activity relationships of quassinoids as in vitro protein synthesis inhibitors of P-388 lymphocytic leukemia tumor cell metabolism.
 AUTHOR: Liou Y F; Hall I H; Okano M; Lee K H; Chaney S G
 CONTRACT NUMBER: CA 17625 (NCI)
 CA 22929 (NCI)
 CA 26466 (NCI)
 SOURCE: JOURNAL OF PHARMACEUTICAL SCIENCES, (1982 Apr) 71 (4) 430-5.
 Journal code: JO7; 2985195R. ISSN: 0022-3549.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 198208
 ENTRY DATE: Entered STN: 19900317
 Last Updated on STN: 19980206
 Entered Medline: 19820826

AB A series of brusatol, bisbrusatol, and bruceantin esters were examined for their ability to inhibit protein synthesis in P-388 lymphocytic leukemia cells. Compounds which produced high T/C % values (170-272) resulted in ID50 of 5.4-15.5 microM for inhibition of whole cell protein synthesis, ID50 of 1.3-13 microM for inhibition of endogenous protein synthesis in cell homogenates, and ID50 of 1.9-6 microM for inhibition of polyuridine directed polyphenylalanine synthesis using "runoff" ribosomes and a "pH 5" enzyme preparation. The polyuridine directed polyphenylalanine synthesis requires neither initiation nor termination factors, suggesting that quassinoids are exclusively elongation inhibitors. Bruceantin, brusatol, and bisbrusatolyl malonate allowed a runoff of the polyribosomes to 80S free ribosomes. However, formation of the ternary complex and 80S initiation complex were not inhibited by the quassinoids. Thus, these agents do not affect the individual steps leading to the formation of a stable 80S initiation complex in P-388 cells. Brusatol, bruceantin, and bisbrusatolyl malonate inhibited the formation of the first peptide bond between puromycin and [3H]methionyl-transfer RNA bound to the initiation complex, indicating peptidyl transferase activity is inhibited by the quassinoids in P-388 cells. These studies also suggest that the free 80S ribosome is the site of binding by the quassinoid. Ribosomes actively conducting protein synthesis will continue protein synthesis and terminate before the quassinoids bind. This proves quassinoids are elongation inhibitors of tumor cells. A strong correlation was observed between

09/587574

potent antileukemic activity and the ability to inhibit protein
synthesis in P-388 lymphocytic leukemia cells.

FILE 'HOME' ENTERED AT 11:25:17 ON 11 JUN 2001

Searcher : Shears 308-4994

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: June 7, 2001, 00:26:58 ; Search time 80.96 Seconds
(without alignments)
86.846 Million cell updates/sec

Title: US-09-587-574-2

Perfect score: 639

Sequence: 1 WTKSLHSLGQDQAYLFRT.....VMEENAVQFLTSDILEYV 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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18: /SID2/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SID2/gcgdata/geneseq/geneseq/AA1998.DAT.*
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22: /SID2/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	639	100.0	840	20	W93570 Human conductin pr
2	639	100.0	840	20	W93569 Human conductin pr
3	407	63.7	992	20	W96265 Murine axlin. Mus
4	401	62.8	900	20	W96264 Human axlin. Homo
5	186.5	29.2	235	21	Y97153 Human regulator of
6	177.5	27.8	235	21	Y97154 Murine regulator o
7	167.5	26.2	116	20	Y41020 RGS2 protein RGS r
8	167.5	26.2	220	21	B56929 Human prostate can
9	165	25.8	217	21	B43847 Human cancer assoc
10	164.5	25.7	116	20	Y41021 RGS3 protein RGS r
11	161	25.2	115	20	Y41019 RGS1 protein RGS r

12	160	25.0	181	19	W44834 Human p26 protein.
13	160	25.0	207	21	B54360 Human pancreatic c
14	160	25.0	243	19	W30561 Human regulator of
15	156.5	24.5	118	20	Y41001 Mouse RGS2 protein
16	156	24.4	181	19	W44833 Rat p26 protein se
17	155	24.3	181	19	W44835 Mouse p26 protein.
18	154.5	24.2	181	19	W62075 Human regulator of
19	154.5	24.2	181	21	Y53931 A human regulator
20	153	23.9	115	20	Y41024 RGS10 protein RGS
21	152.5	23.9	118	20	Y41000 Rat RGS4 protein R
22	146.5	22.9	116	20	Y41022 RGS4 protein RGS r
23	140.5	22.0	201	19	W59293 Mouse RAR1.1 prot
24	139.5	21.8	116	20	Y41028 Human GAIP protein
25	136.5	21.4	116	20	Y41026 RGS14 protein RGS
26	136.5	21.4	202	17	R88995 p53 response prote
27	136.5	21.4	202	18	W08133 Human cytokine res
28	136.5	21.4	202	21	W59294 Human RAR1.1 prot
29	136.5	21.4	202	21	Y87952 Human CRI protein.
30	135.5	21.2	159	19	W30560 Human regulator of
31	128	20.0	119	20	Y41004 Rat RGS14 protein
32	127.5	20.0	210	21	B41985 Human OREX ORF179
33	127	19.9	117	20	Y41027 rap1/2B.P. protein
34	125.5	19.6	118	20	Y41002 Human GAIP protein
35	123.5	19.3	217	21	B44826 Gene 48 human secr
36	123.5	19.3	217	21	B44827 Human secreted pro
37	123.5	19.3	555	18	W10167 Nematode regulator
38	116.5	18.2	116	20	Y41018 RET-RGS1 protein R
39	115	18.0	445	21	Y96955 Human GTPase assoc
40	114	17.8	123	18	W10178 Regulator of G-pro
41	113	17.7	119	20	Y41003 Rat RGS12 protein
42	110	17.2	117	20	Y41025 RGS12 protein RGS
43	101	15.8	420	18	W10168 Human regulator of
44	98	15.3	115	20	Y41023 RGS7* protein RGS
45	78	12.2	772	18	W34567 Thermotoga maritima

ALIGNMENTS

RESULT	ID	1	ALIGNMENTS
W93570	W93570	standard; Protein; 840 AA.	
XX	W93570;		
XX	17-JUN-1999	(first entry)	
DT	17-JUN-1999	(first entry)	
XX	Human conductin protein.		
DE	Human conductin protein.		
XX	Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour;		
KW	therapy; cytoplasmic degradation; blockade; Wnt signalling pathway;		
KW	Wingless signalling pathway; Adenomatous Polyposis Coll.; APC;		
KW	tumour suppressor.		
XX			
OS	Homo sapiens.		
XX			
PN	W09911780-A2.		
XX			
PD	11-MAR-1999.		
XX			
PF	01-SEP-1998; 98WO-DE02621.		
XX			
PR	02-SEP-1997; 97DE-1038205.		
XX			
PA	(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.		
XX			
PI	Behrens J, Birchmeier W;		
XX			
DR	WPI; 1999-214706/18.		
DR	N-PSDB; X23370.		
XX			
PT	Tumor-suppressing protein conductin - used for treatment and		
PT	diagnosis of tumors		

XX Claim 11; Fig 3; 22pp; German.
 CC This invention describes a novel human conductin protein which has
 CC anti-tumour activity. Detecting the presence or amount of conductin,
 CC at protein or nucleic acid levels, is used to diagnose tumours, while
 CC agents that (re)activate conductin are used for tumour therapy, while
 CC conductin binds to beta-catenin and induces its cytoplasmic degradation,
 CC resulting in blockade of the Wnt/Wingless signalling pathway in
 CC vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC)
 CC fragments and, in conjunction with APC, acts as a tumour suppressor.
 CC
 CC Sequence 840 AA:

Query Match 100.0%; Score 639; DB 20; Length 840;
 Best Local Similarity 100.0%; Pred. No. 2,7e-66;
 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WTKSLHSLLGDDGAYLFRFLERKCVDTLDFWACNGFRONMLKDTLTVAKAIYKR 60
 Db 78 WTKSLHSLLGDDGAYLFRFLERKCVDTLDFWACNGFRONMLKDTLTVAKAIYKR 137
 QY 61 YIENNSVSKQLKPAKTYIRDPGIRKQOIGSVMPDOATEIOAVMEENAYQVFLTSDIYL 120
 Db 138 YIENNSVSKQLKPAKTYIRDPGIRKQOIGSVMPDOATEIOAVMEENAYQVFLTSDIYL 197
 QY 121 EYV 123
 Db 198 EYV 200

RESULT 2
 ID W93569 standard; Protein; 840 AA.
 AC W93569;
 DT 17-JUN-1999 (first entry)

DE Human conductin protein.
 XX
 KW Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour;
 KW therapy; cytoplasmic degradation; blockade; Wnt signalling pathway;
 KW tumour suppressor.
 KW
 OS Homo sapiens.

Key Location/Qualifiers
 FT 78..200
 FT /note="Regulator of G protein signalling domain as
 FT Binding-site 343..396 described in claim 12"
 FT /note="GSK-3-beta binding region as described in
 FT Binding-site 397..465 claim 13"
 FT /note="Beta-catenin binding domain as described in
 FT Region 783..833 claim 14"
 FT /note="Dishevelled homology region as described in
 FT claim 15"

MO9911780-A2.
 PD 11-MAR-1999.
 PD 01-SEP-1998; 98WO-DE02621.
 PR 02-SEP-1997; 97DE-1038205.
 PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
 XX

PI Behrens J, Birchmeier W;
 DR WPI; 1999-214706/18.
 DR N-PSDB; X233369.
 PT Tumor-suppressing protein conductin - used for treatment and
 PT diagnosis of tumors
 PS Claim 11; Fig 1; 22pp; German.
 CC
 CC This invention describes a novel human conductin protein which has
 CC anti-tumour activity. Detecting the presence or amount of conductin,
 CC at protein or nucleic acid levels, is used to diagnose tumours, while
 CC agents that (re)activate conductin are used for tumour therapy.
 CC conductin binds to beta-catenin and induces its cytoplasmic degradation,
 CC resulting in blockade of the Wnt/Wingless signalling pathway in
 CC vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC)
 CC fragments and, in conjunction with APC, acts as a tumour suppressor.
 CC
 CC Sequence 840 AA:

Query Match 100.0%; Score 639; DB 20; Length 840;
 Best Local Similarity 100.0%; Pred. No. 2,7e-66;
 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WTKSLHSLLGDDGAYLFRFLERKCVDTLDFWACNGFRONMLKDTLTVAKAIYKR 60
 Db 78 WTKSLHSLLGDDGAYLFRFLERKCVDTLDFWACNGFRONMLKDTLTVAKAIYKR 137
 QY 61 YIENNSVSKQLKPAKTYIRDPGIRKQOIGSVMPDOATEIOAVMEENAYQVFLTSDIYL 120
 Db 138 YIENNSVSKQLKPAKTYIRDPGIRKQOIGSVMPDOATEIOAVMEENAYQVFLTSDIYL 197
 QY 121 EYV 123
 Db 198 EYV 200

RESULT 3
 ID W96265 standard; Protein; 992 AA.
 AC W96265;
 DT 14-JUN-1999 (first entry)

DE Murine axin.
 XX
 KW Axin; cancer; breast cancer; colorectal cancer;
 KW gastrointestinal cancer; esophageal cancer; carcinoma; melanoma;
 KW diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;
 KW beta-catenin.
 KW
 OS Mus musculus.

MO9902179-A1.
 PD 21-JAN-1999.
 PD 09-JUL-1998; 98WO-US14414.
 PR 10-JUL-1997; 97US-0890865.
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 PD
 PI Constantini F, Zeng L;
 DR WPI; 1999-120510/10.
 DR N-PSDB; X09013.

Newly isolated nucleic acid encoding "axis inhibition" protein
 (Axin) - useful for detecting, diagnosing and treating cancer

XX Claim 8; Figure 8; 95pp; English.
XQ
XS Nucleic acids encoding mutant and wild type Axin and
XC oligonucleotides derived from them are useful for detecting
CC mutations in the Axin gene and for determining whether a subject is
CC likely to develop cancer (including breast, colorectal, esophageal,
CC gastrointestinal, esophageal, carcinomas or melanomas). The wild
CC type Axin and homologues of Axin are useful for treating subjects
CC who are likely to develop cancer (thyroid carcinomas). The nucleic
CC acids are also useful for diagnosing cancer and for detecting
CC mutations in cancerous cells. Wild type Axin, its antisense
CC molecule and identified compounds form pharmaceutical compositions
CC in the treatment of cancer. The compositions are also useful for
CC treating cancer by inhibiting tumorigenesis (by inducing degradation
CC of beta-catenin). The nucleic acid encoding Axin acts through
CC negative regulation of the Wnt pathway in the Newhook Center.
CC
XX Sequence 992 AA;
XQ

Query Match	63.7%	Score 407	DB 20	Length 992
Best Local Similarity	61.9%	Pred. No. 5.3e-39		
Matches 78; Conservative	21	Mismatches 23	Indels 4	Gaps 2

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Db     214 waeelhldlqdgdsifrtllkkgcgadlldfwaesgfrkllepdcneekrlklral    273  
  
OY      58 YKRRI-ENNSVSKQLKPATRTTYTRDGIKKQAOIGSVFPDOAQETIQAVMBNAYOVLTG   116  
       | : |||||:::||:|||||:~::~|||:|||||:|||||:~::~|||:|||||:|||||:  
Db     274 yrkyllslnglvsvrqtcpaktsfkidcvmxqgdipamfidgaqlstgwteentypsfiks  333  
  
QY      117 DYLEXY    122          |||||  
Db     334 dylexy    339
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XX	ID	W96264 standard; Protein: 900 AA.
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XX	W96264;	
DT	14-JUN-1999	(first entry)
XX	XX	
DE	Human axin.	
XX	XX	
XX	Axin; cancer; breast cancer; colorectal cancer;	
KM	gastrointestinal cancer; esophageal cancer; melanoma;	
XX	diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;	
KM	beta-catenin.	
XX	XX	
OS	Homo sapiens.	
XX	XX	
PN	W09902179-A1.	
XX	XX	
PD	21-JAN-1999.	
XX	XX	
PE	09-JUL-1998; 98MO-US14414.	
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PR	10-JUL-1997; 97US-0890865.	
XX	XX	
XX	(UYCO) UNIV COLUMBIA NEW YORK.	
XX	XX	
PI	Constantini F, Zeng L;	
XX	XX	
DR	WPI: 1999-120510/10.	
XX	XX	
XX	N-PSDB; X09012.	
XX	XX	
PT	Newly isolated nucleic acid encoding "axis inhibition" protein	
XX	(Axin) - useful for detecting, diagnosing and treating cancer	

PS Disclosure: Figure 11, 95pp; English.
 CC Nucleic acids encoding mutant and wild type Axin and
 CC oligonucleotides derived from them are useful for detecting
 CC mutations in the Axin gene and for determining whether a subject is
 CC likely to develop cancer (including breast, colorectal,
 CC gastrointestinal, esophageal, carcinomas or melanomas). The wild
 CC type Axin and homologues of Axin are useful for treating subjects
 CC who are likely to develop cancer (thyroid carcinomas). The nucleic
 CC acids are also useful for diagnosing cancer and for detecting
 CC mutations in cancerous cells. Wild type Axin, its antisense
 CC molecule and identified compounds form pharmaceutical compositions
 CC in the treatment of cancer. The compositions are also useful for
 CC treating cancer by inhibiting tumorigenesis (by inducing degradation
 CC of beta-catenin). The nucleic acid encoding Axin acts through
 CC negative regulation of the Wnt pathway in The Nieuwkoop Center.
 XX
 SQ Sequence 900 AA:

Query Match	62.8%	Score 401	DB 20	Length 900
Best Local Similarity	62.7%	Pred. No. 2.3e-38		
Matches 79, Conservative	17	Mismatches 26	Indels 4	Gaps 2

```

QY 1 MTKSHLSLIGODDAVYLRFTLEBEKCVDTDFMFACNGFOMNLKOT---KTRVAKI 57
Db 122 waeshsllddgdqslsrltlkqegcadldlrfactqgflklopccsneekrlkral 101
QY 58 YKRYI-ENNSVSVSKOLKATRTYIRDGJIKKOOISSVAFDQOTETLOAVMEENAYQVRLTS 116
Db 102 yrkyllldngvsvrqlpkpaskslkgclmkqjldpamidqqatqteigatmeentyplsls 241
QY 117 DYLEY 122
Db 242 dyley 247

```

RESULT	5	
ID	Y97153	Y97153 standard; Protein; 235 AA.
XX		
AC	Y97153;	
XX		
DT	04-DEC-2000	(first entry)
XX		
DE	Human regulator of G-protein signaling protein.	
XX		
RGS:	regulators of G-protein signaling; GTPase activating protein; GAP;	
KW	G-alpha protein; cell adhesion; chemotaxis; vulneraray; immunosuppressor	
KW	anti-rheumatic; anti-arthritis; anti-diabetic; anti-inflammatory;	
KW	cytostatic; hepatotropic; anti-anaemic; modulator; gene therapy.	
XX		
OS	Homo sapiens.	
XX		
Key	Location/Qualifiers	
FH	82..201	
FT	Domain	
FT	/label= RGS_domain	
FT	Misc-difference 83	/note= "forms part of hydrophobic core"
FT	Misc-difference 90	/note= "forms part of hydrophobic core"
FT	Misc-difference 100	/note= "forms part of hydrophobic core"
FT	Misc-difference 103	/note= "forms part of hydrophobic core"
FT	Misc-difference 104	/note= "forms part of hydrophobic core"
FT	Misc-difference 107	/note= "forms part of hydrophobic core"
FT	Misc-difference 109	/note= "Makes direct contact with G-alpha-1"
FT	Misc-difference 111	/note= "Makes direct contact with G-alpha-1"
FT	Misc-difference 111	/note= "Makes direct contact with G-alpha-1"

Query Match	29.2%	Score 186.5	DB 21	Length 235
Best Local Similarity	34.6%	Pred. No. 5.9e-14		
Matches 44	Conservative 25	Mismatches 43	Indels 15	Gaps 3
QY	1	WTSLSHLDDQDQAVLFTFLERKCVDTLDWFAKNGFR-----QMLKDTKTLRYA	54	
Db	83	wgesfdkllshrdglaeftrflfkfeseeniefwiccedtkkxpgqqlh-----a	135	
QY	55	KAIKRYIENNSVSKOLKPKATKTYIRDKKQOIGSWFDAQOTELQAVMEENAYQVL	114	
Db	136	kaiyekitqcdapkevnldfthckveitnsltpqlns--fdaags-vvygimeqdsytrfl	193	
QY	115	TSDIYLE 121		
Db	194	ksdiylid 200		
RESULT	6			
Y97154	ID	Y97154 standard; Protein; 235 AA.		
XX	XX	Y97154;		
AC	XX			
DT	XX	04-DEC-2000 (first entry)		
DE	XX	Murine regulator of G-protein signaling protein.		
XX	XX	RGS; regulators of G-protein signaling; GTPase activating protein; GAP;		
KW	XX	G-alpha protein; cell adhesion; chemotaxis; vulnerability; immunosuppressor;		
KW	XX	anti-rheumatic; anti-arthritis; anti-diabetic; anti-inflammatory;		
XX	XX	cytostatic; hepatotropic; anti-anaemic; modulator; gene therapy.		
OS	XX	Mus sp.		
EH	XX			
FT	XX	Key	Location/Qualifiers	
FT	FT	Domain	82..201	
FT	FT	Misc-difference	83	
FT	FT	Misc-difference	90	
FT	FT	Misc-difference	100	
FT	FT	Misc-difference	103	
FT	FT	Misc-difference	104	
FT	FT	Misc-difference	107	
FT	FT	Misc-difference	109	
FT	FT	Misc-difference	111	
FT	FT	Misc-difference	112	
FT	FT	Misc-difference	115	
FT	FT	Misc-difference	116	
FT	FT	Misc-difference	138	
FT	FT	Misc-difference	139	
FT	FT	Misc-difference	142	
FT	FT	Misc-difference	143	
FT	FT	Misc-difference	151	
FT	FT	Misc-difference	152	
FT	FT	Misc-difference	154	
FT	FT	Misc-difference	154	

FT MISC-difference 183 /note= "Makes direct contact with G-alpha-1"
FT MISC-difference 184 /note= "Makes direct contact with G-alpha-1"
FT MISC-difference 187 /note= "forms part of hydrophobic core"
FT MISC-difference 188 /note= "Makes direct contact with G-alpha-1"
FT MISC-difference 189 /note= "Makes direct contact with G-alpha-1"
FT MISC-difference 191 /note= "forms part of hydrophobic core"
FT MISC-difference 192 /note= "Makes direct contact with G-alpha-1"
FT MISC-difference 193 /note= "forms part of hydrophobic core"
FT MISC-difference 198 /note= "forms part of hydrophobic core"
FT MISC-difference 198 /note= "forms part of hydrophobic core"
PN W0200046236-A2.
PD 10-AUG-2000.
PF 04-FEB-2000; 2000MO-US02977.
PR 04-FEB-1999; 99US-0244314.
PA (MILL-) MILLENNIUM PHARM INC.
PI Hodge MR, Yowe D;
DR WPI; 2000-532893/48.
DR N-PSDB; A52090.
XX Novel regulator of G-protein signaling nucleic acids and polypeptides,
XX useful as diagnostic and investigative tools and to treat G-protein
XX signaling disorders
XX
XX Claim 8; Page 104; 105pp; English.
XX
XX The RGS (regulators of G-protein signaling) protein genes, clones h16395
XX and m1975, were identified in human and murine spleen cDNA libraries. The
XX respectively. Both proteins have unique N- and C-terminal sequences. The
XX C-terminal location of the RGS domain is consistent with RGSs known to
XX act as GTPase activating proteins (GAPs) for G-alpha proteins. G-alpha-1
XX linked receptors support rapid adhesion and directed migration of
XX leukocytes and other cell types. The novel RGS proteins may be used to
XX modulate cell adhesion and chemotaxis, e.g. for aiding wound repair.
XX The RGS proteins, related cDNAs and anti-RGS antibodies are useful for
XX modulation, diagnosis and treatment of immune and respiratory disorders.
SQ Sequence 235 AA:

Query Match 27.8%; Score 177.5; DB 21; Length 235;
Best Local Similarity 31.7%; Pred. No. 6.7e-13;
Matches 39; Conservative 28; Mismatches 53; Indels 3; Gaps 2;

OY 1 WTRSLSLGDDGAVLFRFLERKCVDTLDFWFCNGFRONMLKDTKTLRVAKAIYKR 60
DB 83 wseafdklshrgvdaftfkfseenelefwacedfkck-epqqllyakalylek 141
OY 61 YIENNSVSKQLKATPTTYIRDGIRKQOIGSVMPDQOTEIGQVMEENAYOVFLTSIDYL 120
DB 142 flqndpkevnldfhtkvevlakslagptlins--fdtaqsrvyqmevnsykrflksetyl 199
OY 121 EYV 123
DB 200 h11 202

RESULT 7

Y41020
ID Y41020 standard; protein; 116 AA.
XX
AC Y41020;
DT 06-DEC-1999 (first entry)
XX
DE RGS2 protein RGS region.
XX
XX RGS; guanine nucleotide exchange factor; GEF; RGS domain; GAS; cancer;
XX G protein alpha subunit; cell proliferation; growth control; hemostasis;
XX morphogenesis; stress fiber formation; integrin-mediated interaction;
XX embryonic development; tumor cell growth; cell death; leukocyte homing;
XX bone resorption; clot retraction; db1 homology domain; mechanical stress;
XX pleckstrin homology domain.
OS Unidentified.
XX
XX W09947557-A2.
XX
XX 23-SEP-1999.
XX
XX 18-MAR-1999; 99MO-US06051.
XX
XX 18-MAR-1998; 98US-0078634.
XX
XX (ONYX-) ONYX PHARM INC.
XX
XX Bollag G, Hart MJ, Roscoe W, Polakis P, Sternweis P, Kozasa T;
XX Jiang X;
XX
XX WPI; 1999-571821/48.
XX
XX New isolated RGS-GEF polypeptides, used to develop products for
XX modulating, e.g. cell proliferation and integrin-mediated interactions
XX
XX
PS Disclosure; Fig 18; 75pp; English.
XX
XX The invention relates to isolated RGS-guanine nucleotide exchange factor
XX (GEF) polypeptides. The novel isolated RGS-GEF polypeptide consists of an
XX RGS domain of a GEF protein and does not comprise a db1 homology (DH)
XX domain or a pleckstrin homology (PH) domain. The RGS-GEF polypeptides can
XX be used for modulating an activity of a G protein alpha subunit (GAS).
XX The products can be used for the regulation of biological pathways in
XX which a RGS-GEF polypeptide is involved, particularly pathological
XX conditions, e.g. cell proliferation (e.g. cancer), morphogenesis, growth
XX control, stress fiber formation, and integrin-mediated interactions, such
XX as embryonic development, tumor cell growth and metastasis, programmed
XX cell death, hemostasis, leukocyte homing and activation, bone resorption,
XX clot retraction, and the response of cells to mechanical stress. The
XX products can also be used for detection, diagnosis and production of
XX transgenic animals. Sequences Y41014-028 represent RGS regions of several
XX proteins.
SQ Sequence 116 AA:

Query Match 26.2%; Score 167.5; DB 20; Length 116;
Best Local Similarity 32.8%; Pred. No. 4e-12;
Matches 39; Conservative 20; Mismatches 57; Indels 3; Gaps 2;

OY 1 WTRSLSLGDDGAVLFRFLERKCVDTLDFWFCNGFRONMLKDTKTLRVAKAIYKR 60
DB 1 wseafdklshrgvdaftfkfseenelefwacedfkck-spgklssarkklytd 59
OY 61 YIENNSVSKQLKATPTTYIRDGIRKQOIGSVMPDQOTEIGQVMEENAYOVFLTSIDYL 119
DB 60 flekapkevnldfhtkvevlakslagptlins--fdtaqsrvyqmevnsykrflksetyl 116

RESULT 8
B56929

ID	B56929	standard; Protein; 220 AA.
AC	B56929;	
XX		
DT	13-MAR-2001	(first entry)
DE		
KM	Human prostate cancer antigen protein sequence SEQ ID NO:1507.	
XX		
KW	Human; prostate cancer; prostate cancer antigen; detection; diagnosis;	
KW	neuroprotective; cytosolic; cardioactive; immunomodulatory; muscular;	
KW	vulnerary; gastrointestinal; nephrotoxic; antiinfective; gynaecological;	
KW	antibacterial; gene therapy; neutral; immune; reproductive; renal;	
KW	gastrointestinal; pulmonary; cardiovascular; proliferative disorder;	
KW	wound; infectious disease.	
XX		
OS	Homo sapiens.	
XX		
PN	WO20005174-A1.	
XX		
PD	21-SEP-2000.	
XX		
PF	08-MAR-2000; 2000MO-US05988.	
XX		
PR	12-MAR-1999; 99US-0124270.	
XX		
PA	(HUMA-) HDMAN GENOME SCI INC.	
XX		
PI	(ROSE/) ROSEN C A.	
XX		
PI	Rosen CA, Ruben SM;	
XX		
DR	WPI: 2000-587513/55.	
XX		
DR	N-PSDB: F16132.	
XX		
PT	Prostate cancer associated gene sequences, referred to as prostate	
XX	cancer antigens, useful for treatment, prevention, and diagnosis of	
XX	disorders such as prostate cancer	
PS	Claim 11; Page 1946-1947; 2338pp; English.	
XX		
CC	F15566 to F16505 encode the human prostate cancer associated proteins,	
XX	called prostate cancer antigens, given in B56363 to B57302. The prostate	
CC	cancer antigens can have neuroprotective, cytosolic, cardioactive,	
CC	immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotoxic,	
CC	antiinfective, gynaecological and antibacterial activities, and can be	
CC	used in gene therapy. The prostate cancer antigen polynucleotides may be	
CC	used for detection of prostate cancer, chromosome identification, as	
CC	chromosome markers, and for numerous other diagnostic or research	
CC	purposes. The prostate cancer antigens may be used to treat disorders	
CC	such as neural, immune, muscular, reproductive, gastrointestinal,	
CC	pulmonary, cardiovascular, renal, and proliferative disorders, wounds,	
CC	and infectious diseases. F16506 to B57303 represent sequences	
CC	used in the exemplification of the present invention.	
XX		
SQ	Sequence 220 AA;	
Query Match	26.2%; Score 167.5; DB 21; Length 220;	
Best Local Similarity	32.8%, Pred. No. 9,le-12;	
Matches 39; Conservative	20; Mismatches 57; Indels 3; Gaps 2;	
OY	1 WTKSHSLDGDGDAVLTFRTELEKRCVDTLDFMPACNGFROMLNKDKRTLRVAKAIYKR 60	
Dd	89 wseardelaaeylaaftraifksecfeenlefwaacidefkktk-spqklaskarkiyld 147	
OY	61 YIENNSVYSKOLPKATKYIIRDGIRKKOIGSVMEQADOTEIQAVMENAYOVETLSDIY 119	
Dd	148 ftekeapkeinhdfgtklliaqnl--gaatsgcfttaqrlysvlmeansypflesefy 204	
RESULT	9	
ID	B43847	
ID	B43847	standard; Protein; 217 AA.

[illegible]

[illegible]

Db 1 wsqslxkllanqlgnvlgsrlkseeenlelwlacedykkresulipck---deely 30

OY 59 KRIENNSVSKOLKPAKTYIRDIKQIGSMEDQOTETIQAVMEENAVQVLTSDI 118
 Db 57 kafyhsda--akqindfretrestakkikaprcctcdeqkvilylmekdsyrfiksd 114
 OY 119 Y 119
 Db 115 Y 115

RESULT 12
 W44834
 ID W44834 standard; peptide: 181 AA.
 AC W44834;
 AC W44834;
 DT 21-JUL-1998 (first entry)
 DE Human p26 protein.
 DE Human p26 protein.
 DE Human p26; brain; hybridisation; dephosphorylase inhibitory activity;
 KW probe; rat; haematogenesis.
 KW Homo sapiens.
 OS JP09299092-A.
 PN 25-NOV-1997.
 PD 26-DEC-1996; 96JP-0347877.
 PF 12-MAR-1996; 96JP-0055196.
 PR (TAKE) TAKEDA CHEM IND LTD.
 XX WPI: 1998-056555/06.
 DR N-PSDB: V19304.
 XX Mammalian p26 proteins and their related DNA - useful for screening
 PT for de-phosphorylase inhibitory compounds
 PS Claim 1; Fig 2; 40pp; Japanese.
 XX This amino acid sequence represents the human p26 protein. The encoding
 CC gene sequence was isolated from a human thymus cDNA library by phage
 CC plaque hybridisation using the rat p26 cDNA sequence (V19303) as a probe.
 CC The screening isolated the corresponding 889 bp sequence. p26 protein is
 CC useful as a reagent for screening for compounds having dephosphorylase
 CC inhibitory activity. It is also useful as a treating and preventive
 CC agent for diseases related to the haematogenic system.
 CC
 SO Sequence 181 AA;

Query Match 25.0%; Score 160; DB 19; Length 181;
 Best Local Similarity 32.0%; Pred No. 5.4e-11;
 Matches 39; Conservative 30; Mismatches 49; Indels 4; Gaps 3;

OY 1 WTKSLHSLLGDGDGAVLEFTEFLEREKCVDTLDFWACNGFRQNMKDKTKLRVAKAIYKR 60
 Db 38 waaslenlledepegvkrtreflkefseenvlflwaccedfkmgdk-tgmqekakeiynt 96
 OY 61 YIENNSVSVSKOLKPAKTYIRDIKQIGSMEDQOTETIQAVMEENAVQVLTSDIYL 120
 Db 97 fl--ssksssgvnnveggsrlneklliep-hplmtgkldqgflnltmkysyrfiksdfl 153
 OY 121 EX 122
 Db 154 Kh 155

RESULT 13
 B54360

ID B54360 standard; Protein: 207 AA.
 AC B54360;
 AC B54360;
 DT 09-MAR-2001 (first entry)
 DE Human pancreatic cancer antigen protein sequence SEQ ID NO:812.
 DE Human pancreatic cancer antigen protein sequence SEQ ID NO:812.
 DE Human; pancreas; pancreatic cancer; pancreatic cancer antigen;
 KW detection; diagnosis; identification; cytostatic; neuroprotective;
 KW neurotropic; immunomodulatory; relaxant; contraceptive; gynaecological;
 KW antinflammatory; cardiant; gene therapy; chromosome mapping;
 KW linkage analysis; tissue identification; tissue typing; forensic;
 KW neutral; immune system; muscular; reproductive; gastrointestinal;
 KW pulmonary; cardiovascular; renal; proliferative.
 KW Homo sapiens.
 OS WO200055320-A1.
 PN 21-SEP-2000.
 PD 08-MAR-2000; 2000WO-US05989.
 PF 12-MAR-1999; 99US-0124270.
 PR (HUMA-) HUMAN GENOME SCI INC.
 PA Rosen CA, Ruben SM;
 PI WPI: 2000-579444/54.
 DR N-PSDB: C99125.
 XX New nucleic acid that is a pancreatic cancer antigen for preventing,
 PT treating, or ameliorating a medical condition, particular pancreatic
 PT cancer, or for use in assays for diagnosing a pathological condition -
 XX
 XX Claim 11; Page 1267-1268; 1379pp; English.
 XX C98773 to C99231 encode the human pancreatic cancer associated proteins,
 CC called pancreatic cancer antigens, given in B54008 to B54466. The human
 CC pancreatic cancer antigens have cytostatic, neuroprotective, neurotropic,
 CC immunomodulatory, relaxant, contraceptive, gynaecological, cardiant and
 CC antinflammatory activities, and can be used in gene therapy. The
 CC polynucleotide and proteins can be used for preventing, treating, or
 CC ameliorating a medical condition or in assays for diagnosing a
 CC pathological condition or a susceptibility to one in a subject. Binding
 CC partners to the proteins and the activity of the proteins can be
 CC identified. The pancreatic cancer antigens can be used to detect, treat
 CC or prevent pancreatic disorders, especially cancer. Agonists and
 CC antagonists to the antigens can be screened for. The pancreatic cancer
 CC antigen polynucleotides can be used to design nucleic acid hybridisation
 CC probes that can be used in chromosome mapping, linkage analysis, tissue
 CC identification and/or typing and a variety of forensic and diagnostic
 CC methods. The proteins can be used to generate antibodies which are used
 CC to purify, detect and target the polypeptides, including both in vivo
 CC and in vitro diagnostic and therapeutic methods. The proteins can be
 CC used to treat or prevent neural, immune system, muscular, reproductive,
 CC gastrointestinal, pulmonary, cardiovascular, renal or proliferative
 CC disorders. C99232 to C99240 and B54467 represent sequences used in the
 CC exemplification of the present invention.
 CC
 SO Sequence 207 AA;

Query Match 25.0%; Score 160; DB 21; Length 207;
 Best Local Similarity 32.0%; Pred. No. 6.4e-11;
 Matches 39; Conservative 30; Mismatches 49; Indels 4; Gaps 3;

OY 1 WTKSLHSLLGDGDGAVLEFTEFLEREKCVDTLDFWACNGFRQNMKDKTKLRVAKAIYKR 60
 Db 64 waaslenlledepegvkrtreflkefseenvlflwaccedfkmgdk-tgmqekakeiynt 122

Qy	61	YIENNSVYSKOLKATKATKIVYIDGJJKKOISGVMPDQATELOAWEENAQVFLTSIDYL	12
Db	123	fl--sksssgvnevggrileep-hplmtqklqddqlfmkyosyrlksdfl	179
Qy	121	EV 122	
Db	180	kh 161	
RESULT	14		
ID	W30561	standerd; Protein; 243 AA.	
XX	W30561;		
AC	W30561;		
XX	18-JAN-1999	(first entry)	
XX	Human regulator of G-protein signalling 2 (RGPS-2).		
XX	Regulator of G-protein signalling 2; RGPS-2; human;		
XX	G protein coupled receptor; signal transduction; inflammation;		
XX	cell proliferation; cancer; diagnosis; therapy.		
OS	Homo sapiens.		
XX	Key	Location/Qualifiers	
FT	Region	126..142	
FT	/note-	"potential G-protein coupled receptor signature"	
FT	Region	58..177	
FT	/note-	"RGF motif"	
FT	Modified-site	8..11	
FT	/note-	"Asn may be N-glycosylated"	
FT	Modified-site	235..238	
FT	/note-	"potential cAMP- and cGMP-dependent protein kinase phosphorylation site"	
FT	Modified-site	11..14	
FT	/note-	"potential casein kinase II phosphorylation site"	
FT	Modified-site	66..69	
FT	/note-	"potential casein kinase II phosphorylation site"	
FT	Modified-site	220..223	
FT	/note-	"potential casein kinase II phosphorylation site"	
FT	Modified-site	93..95	
FT	/note-	"potential protein kinase C phosphorylation site"	
FT	Modified-site	97..99	
FT	/note-	"potential protein kinase C phosphorylation site"	
FT	Modified-site	161..164	
FT	/note-	"potential protein kinase C phosphorylation site"	
XX	W09844115-A2.		
XX	08-OCT-1998.		
XX	31-MAR-1998;	98WO-USO6336.	
XX	31-MAR-1997;	97US-0829110.	
XX	(INCY-)	INCYTE PHARM INC.	
XX	G011 SK,	Hillman JL;	
XX	WPI: 1998-557112/47.		
XX	N-PSDB; V45442.		
XX	New regulators of G-protein signalling - useful for, e.g. diagnosis, prevention and treatment of cancer and inflammation		

	PS	Claim 19, Page 45; 65pp; English.
xx	CC	This is the amino acid sequence of a novel human regulator of G-protein signaling, termed RGPS-2. It was deduced from a consensus nucleic acid sequence (see V45442) derived from thymus and other cDNA clones. RGPS-2 shares 46% and 37% identity with human B14 and RGS4, respectively. It shows significant expression in inflamed, immortalised or cancerous cells and tissues. The invention provides 2 regulators of G-protein signalling, i.e., RGPS-2 and RGS-1 (see W30560). The invention also features nucleic acids encoding RGPS polypeptides, oligonucleotides, peptide nucleic acids, fragments, portions or antisense molecules, and expression vectors and host cells. It also features antibodies specific for RGPS, and pharmaceutical compositions comprising purified RGPS. It also provides methods for stimulating cell proliferation using an RGPS or an agonist of RGPS and for treating or preventing disorders (e.g. cancer) associated with cell proliferation and inflammation using an antagonist of RGPS.
cc	XX	Sequence 243 AA;
SQ	XX	
	Query Match	25.0%; Score 160; DB 19; Length 243:
	Best Local Similarity	32.0%; Pred. No. 7.8e+11;
Matches	39; Conservative	30; Mismatches 49; Indels 4; Gaps 3
OY	D	WTKSHSLGDDGDVAFRTFLEREKCVDTLDFWACNGFRONMLKDRTLVARAKAYKR 60 :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: Db 100 waastlenlbedpeyvkrfreflikfeseenvilwladcedfkkmqdk-tqmgekaelymt 158
OY	G	6I YIENNVSYSKOLKPATRYTRDGICKQQIGSVNFDOAQETIOAVMEENAYOVFTLSDIYL 120 :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: DB 159 fl--sskassqvnevggsrlneklleep-hplmfqklqdqlfnlmkydysrlfsksdlfl 215
OY	E	121 EY 122
OY	:: ::	
Db	216 Kh 217	
	RESULT 15	
ID	V41001 standard; protein; 118 AA.	
XX AC	V41001;	
XX DT	06-DEC-1999 (first entry)	
DE	Mouse RGS2 protein RGS domain fragment.	
XX RG	RGS; guanine nucleotide exchange factor; GEF; RGS domain; GAS; cancer; G protein alpha subunit; cell proliferation; growth control; homeostasis; morphogenesis; stress fiber formation; integrin-mediated interaction; embryonic development; tumor cell growth; cell death; leukocyte homing; bone resorption; clot retraction; db1 homology domain; mechanical stress; pleckstrin homology domain.	
OS	Mus sp.	
PX PN	WO9947557-A2.	
PD	23-SEP-1999.	
PE	18-MAR-1999; 99MO-USO6051.	
PR	18-MAR-1998; 98US-0078634.	
PA	(ONYX-) ONYX PHARM INC.	
PI	Bollag G, Hart MJ, Roscoe W, Polakis P, Sternweis P, Kozasa T; Jiang X;	
DR	WP1; 1999-571821/48.	

XX New isolated RGS-GEF polypeptides, used to develop products for
 PT modulating, e.g. cell proliferation and integrin-mediated interactions
 PT
 XX

Example 1; Fig 1; 75pp; English.

CC The invention relates to isolated RGS-guanine nucleotide exchange factor
 CC (GEF) polypeptides. The novel isolated RGS-GEF polypeptide consists of an
 CC RGS domain of a GEF protein and does not comprise a dbl homology (DH)
 CC domain or a pleckstrin homology (PH) domain. The RGS-GEF polypeptides can
 CC be used for modulating an activity of a G protein alpha subunit (GAS).
 CC The products can be used for the regulation of biological pathways in
 CC which a RGS-GEF polypeptide is involved, particularly pathological
 CC conditions, e.g. cell proliferation (e.g. cancer), morphogenesis, growth
 CC control, stress fiber formation, tumor cell growth and metastasis, such
 CC as embryonic development, leukocyte homing and activation, bone resorption,
 CC cell death, hemostasis, and the response of cells to mechanical stress. The
 CC products can also be used for detection, diagnosis and production of
 CC transgenic animals. Sequences Y4100-008 represent conserved domain
 CC fragments from different RGS proteins.
 CC
 XX

SQ Sequence 118 AA;

Query Match 24.58; Score 156.5; DB 20; Length 118;
 Best Local Similarity 31.14; Pred. No. 8e-11;

Matches 37; Conservative 20; Mismatches 59; Indels 3; Gaps 2;

OY 1 WTKSLHSILGDOGAVLFRFTLEERKCVDTLDWFACNGFRQNLKDTTLRVAKAIYKR 60
 Db 1 waefdelaskyglaaafalksetceenlefwlacedfkklk-spqklskarkiyld 59
 OY 61 YIENNSVVSQQLKPATKTYIRDSIGIKQOIGSVAFDOQTEICAVMEENAYQVFLTSDIY 119
 Db 60 ftekeapkeinfdfqtkslagql--qeatsgcfttaqkrvyslmenmsyprflesefy 116

Search completed: June 7, 2001, 02:01:15
 Job time: 5657 sec

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OM protein - protein search, using sw model

Run on: June 7, 2001, 00:32:07 ; Search time 40.76 Seconds
(without alignments)
57.972 Million cell updates/sec

Title: US-09-587-574-2

Perfect score: 639
Sequence: 1 WTKSLHSLGDDGAYLFR.....YMEENAYQVLTSDIYLEYV 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database:

Issued Patents, AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCITUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	167.5	26.2	211	2	US-08-748-483-4
2	165	25.8	119	2	US-08-588-258B-31
3	165	25.8	119	3	US-08-460-505-31
4	165	25.8	119	5	PCT-US96-08295-31
5	165	25.8	196	2	US-08-829-110-5
6	165	25.8	196	2	US-08-748-483-3
7	160	25.0	243	2	US-08-829-110-3
8	158	24.7	121	2	US-08-588-258B-32
9	158	24.7	121	3	US-08-460-505-37
10	158	24.7	121	5	PCT-US96-08295-32
11	155.5	24.3	205	2	US-08-829-110-6
12	155.5	24.3	205	2	US-08-748-483-5
13	154.5	24.2	181	2	US-08-748-483-1
14	140.5	22.0	201	2	US-08-726-228-2
15	140.5	22.0	201	3	US-08-870-815-2
16	140.5	22.0	201	4	US-08-949-004-2
17	136.5	21.4	202	1	US-08-274-318-2
18	136.5	21.4	202	2	US-08-463-081B-2
19	136.5	21.4	202	2	US-08-461-379A-2
20	136.5	21.4	202	2	US-08-462-390B-2
21	136.5	21.4	202	2	US-08-754-108-2
22	136.5	21.4	202	3	US-08-870-815-4
23	136.5	21.4	202	3	US-08-463-074B-2
24	136.5	21.4	202	3	US-08-465-585C-2
25	136.5	21.4	202	3	US-08-652-446-2
26	136.5	21.4	202	4	US-08-949-004-4
27	135.5	21.2	159	2	US-08-829-110-1

28	133	20.8	123	2	US-08-588-258B-39	Sequence 39, Appl
29	133	20.8	123	5	PCT-US96-08295-39	Sequence 39, Appl
30	124.5	19.5	555	2	US-08-588-258B-24	Sequence 24, Appl
31	124.5	19.5	555	3	US-08-460-505-24	Sequence 24, Appl
32	124.5	19.5	555	5	PCT-US96-08295-24	Sequence 24, Appl
33	116	18.2	118	2	US-08-588-258B-38	Sequence 38, Appl
34	116	18.2	118	5	PCT-US96-08295-38	Sequence 38, Appl
35	114	17.8	123	2	US-08-588-258B-1	Sequence 1, Appl
36	114	17.8	123	3	US-08-460-505-1	Sequence 1, Appl
37	114	17.8	123	5	PCT-US96-08295-1	Sequence 1, Appl
38	113	17.7	119	2	US-08-588-258B-30	Sequence 30, Appl
39	113	17.7	119	3	US-08-460-505-30	Sequence 30, Appl
40	113	17.7	119	5	PCT-US96-08295-30	Sequence 30, Appl
41	101	15.8	420	2	US-08-588-258B-40	Sequence 40, Appl
42	101	15.8	420	5	PCT-US96-08295-40	Sequence 40, Appl
43	101	15.8	420	5	PCT-US96-08295-40	Sequence 40, Appl
44	64	10.0	764	1	US-08-375-300-4	Sequence 4, Appl
45	64	10.0	764	3	US-09-177-431-4	Sequence 4, Appl
				5	PCT-US95-16930-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-748-483-4
Sequence 4, Application US/08748483
Patent No. 595314
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: A NOVEL REGULATOR OF CELL SIGNALING
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESS: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,483
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0157 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 211 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 292037
US-08-748-483-4
Query Match 26.2%; Score 167.5; DB 2; Length 211;
Best Local Similarity 32.8%; Pred. No. 2.3e-13;

	Matches	39;	Conservative	20;	Mismatches	57;	Indels	3;	Gaps	2																																										
QY	1	W	K	S	L	S	L	I	D	D	G	A	L	L	P	F	T	E	R	K	C	V	D	T	L	E	M	F	A	N	C	N	G	E	R	O	M	L	N	K	D	T	L	A	K	A	I	A	I	R	60	
Db	80	W	S	E	A	D	E	L	L	A	S	K	A	L	L	P	F	T	E	R	K	C	V	D	T	L	E	M	F	A	N	C	N	G	E	R	O	M	L	N	K	D	T	L	A	K	A	I	A	I	R	138
QY	61	Y	I	E	N	N	S	V	A	S	K	O	L	M	P	A	T	K	I	R	I	N	G	I	K	Q	D	I	G	S	M	F	O	A	O	E	I	D	A	V	H	E	N	A	Q	V	L	T	S	D	I	119
Db	139	F	I	E	K	A	P	R	E	I	N	I	D	P	O	T	K	L	L	I	A	N	T	--	Q	E	T	S	C	F	T	A	A	C	R	A	S	T	L	E	N	N	S	I	P	F	L	S	E	I	195	

RESULT 2
US-08-588-258B-31

```

GENERAL INFORMATION:
APPLICANT: H. Robert Horvitz et al.
TITLE OF INVENTION: REGULATORS OF G-PROTEIN SIGNALLING
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Fastseq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/568,258B
FILING DATE: January 12, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bleker-Brady, Kristina
REGISTRATION NUMBER: 39,109
REFERENCE/DOCKET NUMBER: 01997/216001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
TELEX:

INFORMATION FOR SEQ. ID NO. 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein

```

Query Match	25.88;	Score 165;	DB 2;	Length 119;
Best Local Similarity	32.88;	Pred. No. 2.2e-13;		
Matches 40;	Conservative 28;	Mismatches 46;	Indels 8;	Gaps 3

```

QY      1 WTKSHSLSLGQDAGVYETFLTEREKCVDTLDFMFACGPF--OMNLIKDKRTLVAARAY 58
QY      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      2 WSGSTERLLANQTQGVNGSFLKSEFSENEIEFWLACEDYKRTISDILLPCK---AEEIY 57
QY      59 KRYLENNSSVSKOLKPRATKTYIRGCIKKQQIGSVMPQAOETEIOAVENAYOVETLSDI 118
QY      58 KAFVHSD--AKQINIDRFRESTAKKIKAPPTPCGEDAOKVYITIMEKDSYPRFLKSDI 115
QY      119 YL 120
Db      116 YL 117

```

RESULT 3
US-08-460-505-31
; Sequence 31, Application US/08460505

```

1 Patent No. 60692296
2
3 GENERAL INFORMATION:
4
5 APPLICANT: Horvitz, Robert H.
6
7 APPLICANT: Koelle, Michael
8
9 TITLE OF INVENTION: REGULATORS OF G-PROTEIN SIGNALLING
10
11 NUMBER OF SEQUENCES: 37
12
13 CORRESPONDENCE ADDRESS:
14
15 ADDRESSEE: Fish & Richardson P.C.
16
17 STREET: 225 Franklin Street
18
19 CITY: Boston
20
21 STATE: MA
22
23 COUNTRY: USA
24
25 ZIP: 02110-2804
26
27 COMPUTER READABLE FORM:
28
29 MEDIUM TYPE: Floppy disk
30
31 COMPUTER: IBM PC compatible
32
33 OPERATING SYSTEM: PC-DOS/MS-DOS
34
35 SOFTWARE: PatentIn Release #1.0, Version #1.30
36
37 CURRENT APPLICATION DATA:
38
39 APPLICATION NUMBER: US/08/460,505
40
41 FILING DATE: 02-JUN-1995
42
43 CLASSIFICATION: 800
44
45 ATTORNEY/AGENT INFORMATION:
46
47 NAME: Bleker-Brady, Kristina
48
49 REGISTRATION NUMBER: 39,109
50
51 REFERENCE/DOCKET NUMBER: 01997/214001
52
53 TELECOMMUNICATION INFORMATION:
54
55 TELEPHONE: 617/542-5070
56
57 TELEFAX: 617/542-8906
58
59 TELEX: 200154
60
61 INFORMATION FOR SEQ ID NO: 31:
62
63 SEQUENCE CHARACTERISTICS:
64
65 LENGTH: 119 amino acids
66
67 TYPE: amino acid
68
69 STRANDEDNESS: not relevant
70
71 TOPOLOGY: linear
72
73 MOLECULE TYPE: protein
74
75 OS-08-460-505-31

```

US-08-460-505-31

Query Match	25.88;	Score 165;	DB 3;	Length 119;
Best Local Similarity	33.08;	Score 200;	DB 3;	Length 119;

Matches 40; Conservative 28; Mismatches 46; Indels 8; Gaps 3;

[illegible]

RESULT 4
PCT-US96-08295-31
; Sequence 31, Application PC/TUS9608295
GENERAL INFORMATION

APPLICANT: Massachusetts Institute of Technology
 TITLE OF INVENTION: REGULATORS OF G-PROTEIN SIGNALING
 NUMBER OF SEQUENCES: 41
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P. C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/08295
 FILING DATE: 31-MAY-1996
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/588,258
 FILING DATE: 12-JAN-96
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Bieker-Brady, Kristina
 REGISTRATION NUMBER: 39,109
 REFERENCE/DOCKET NUMBER: 01997/216001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-5070
 TELEFAX: 617/542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 31:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 119 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US96-08295-31

```

1 APPLICATION NUMBER:
2 FILING DATE:
3 ATTORNEY/AGENT INFORMATION:
4 NAME: Billings, Lucy J.
5 REGISTRATION NUMBER: 36,749
6 REFERENCE/DOCKET NUMBER: PR-0259 US
7 TELECOMMUNICATION INFORMATION:
8 TELEPHONE: 415-855-0555
9 TELEFAX: 415-845-4166
10 INFORMATION FOR SEQ ID NO: 5:
11 SEQUENCE CHARACTERISTICS:
12 LENGTH: 196 amino acids
13 TYPE: amino acid
14 STRANDEDNESS: single
15 TOPOLOGY: linear
16 IMMEDIATE SOURCE:
17 LIBRARY: GenBank
18 CLONE: 299705
19
20 US-08-829-110-5

```

TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 196 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 728966
US-08-748-483-3

Query Match
Best Local Similarity 32.8%; Score 165; DB 2; Length 196;
Matches 40; Conservative 28; Mismatches 46; Indels 8; Gaps 3;

OY 1 WTKSLHSLGDDGAYLFRFLERKCYDTLDFWFCNGFR--OMNLKDTYTLRVAKAIYR 58
Db 69 WSQLEKLANOTGONVGFSLKSESENIETFWLACEDYKTESDILPCK---AEIY 124
OY 59 KRYIENSVSKOLKPAKTYIRDGIRKQOIGSVFDOAQTEIOAVENAYOVFLTSDI 118
Db 125 KAFVHSDA--AKQINIDRRTRESTAKKIKAPTPTCFDEAKQVITTEKDSYPRFLKSDI 182
OY 119 YL 120
Db 183 YL 184

RESULT 7
US-08-829-110-3
Sequence 3; Application US/08829110
Patent No. 5882890
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL REGULATORS OF G-PROTEIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/829,110
FILING DATE: Filed Herewith
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PR-0259 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-845-4166
TELEFAX: 415-845-0555
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:

LIBRARY: THYMOT02
CLONE: 343504
US-08-829-110-3

Query Match
Best Local Similarity 25.0%; Score 160; DB 2; Length 243;
Matches 39; Conservative 30; Mismatches 49; Indels 4; Gaps 3;

OY 1 WTKSLHSLGDDGAYLFRFLERKCYDTLDFWFCNGFR--OMNLKDTYTLRVAKAIYR 60
Db 100 WASLENLEDEGVKRFREFLKESESENIETFWLACEDYKTESDILPCK---AEIY 158
OY 61 YIENSVSVKOLKPAKTYIRDGIRKQOIGSVFDOAQTEIOAVENAYOVFLTSDI 120
Db 159 FL--SSKASQVNVGQSRNLNKEILEEP-HPLMFQKLDQIFNLKDYSDYRFLKSDFL 215
OY 121 EY 122
Db 216 KH 217

RESULT 8
US-08-588-258B-32
Sequence 32; Application US/08588258B
Patent No. 5929207
GENERAL INFORMATION:
APPLICANT: H. Robert Horvitz et al.
TITLE OF INVENTION: REGULATORS OF G-PROTEIN SIGNALING
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,258B
FILING DATE: January 12, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER: 39,109
REFERENCE/DOCKET NUMBER: 01997/216001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-588-258B-32

Query Match
Best Local Similarity 24.7%; Score 158; DB 2; Length 121;
Matches 38; Conservative 20; Mismatches 59; Indels 2; Gaps 2;

OY 1 WTKSLHSLGDDGAYLFRFLERKCYDTLDFWFCNGFR--OMNLKDTYTLRVAKAIYR 60
Db 2 WSEAFDELLASKYGLAFAFRFLKSESENIETFWLACEDYKTESDILPCK---AEIY 119
OY 61 YIENSVSVKOLKPAKTYIRDGIRKQOIGSVFDOAQTEIOAVENAYOVFLTSDI 119

Db 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

RESULT 9

US-08-460-505-32

; Sequence 32, Application US/08460505

; Patent No. 6069296

; GENERAL INFORMATION:

; APPLICANT: Horvitz, Robert H.

; APPLICANT: Koellie, Michael

; TITLE OF INVENTION: REGULATORS OF G-PROTEIN SIGNALING

; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/460,505

; FILING DATE: 02-JUN-1995

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: Bieker-Brady, Kristina

; REGISTRATION NUMBER: 39,109

; REFERENCE/DOCKET NUMBER: 01997/214001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617/542-5070

; TELEFAX: 617/542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 32:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 121 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-460-505-32

Query Match 24.7%; Score 158; DB 3; Length 121;

Best Local Similarity 31.9%; Pred. No. 1.7e-12;

Matches 38; Conservative 20; Mismatches 39; Indels 2; Gaps 2;

Qy 1 WTKSLSLDGDGAVLFRFLERKCVDTLDFMFCNGFRONMLKDTKTLRVAKAIYKR 60

Db 2 WSEAFDELLASKYGLAFLKSECEENIEFWLACEDFKTKR-SPOKLSARKIYTD 60

Qy 61 YIENNSVSKQLPARKTYIRDCIKKQOIGSVFMDAQTEIOAVMEENAYOVLTSDIY 119

Db 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US96/08295

; FILING DATE: 31-MAY-1996

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/588,258

; FILING DATE: 12-JAN-96

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Bieker-Brady, Kristina

; REGISTRATION NUMBER: 39,109

; REFERENCE/DOCKET NUMBER: 01997/216001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617/542-5070

; TELEFAX: 617/542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 32:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 121 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: linear

; MOLECULE TYPE: protein

PCT-US96-08295-32

Query Match 24.7%; Score 158; DB 5; Length 121;

Best Local Similarity 31.9%; Pred. No. 1.7e-12;

Matches 38; Conservative 20; Mismatches 59; Indels 2; Gaps 2;

Qy 1 WTKSLSLDGDGAVLFRFLERKCVDTLDFMFCNGFRONMLKDTKTLRVAKAIYKR 60

Db 2 WSEAFDELLASKYGLAFLKSECEENIEFWLACEDFKTKR-SPOKLSARKIYTD 60

Qy 61 YIENNSVSKQLPARKTYIRDCIKKQOIGSVFMDAQTEIOAVMEENAYOVLTSDIY 119

Db 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNIQEAATSGCFTTAOKRVYSILMENNYPRLSESEFY 118

ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKEN NUMBER: PF-0157 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 181 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Consensus

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 7, 2001, 00:39:27 ; Search time 56.43 Seconds
(without alignments)
149.795 Million cell updates/sec

Title: US-09-587-574-2

Perfect score: 639
Sequence: 1 WTKSLSLSLGDDQGAYLFFRT.....VMEENAYOVFLTSDIYL 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	639	100.0	838	2	T08423	Axin homolog Ax11
2	407	63.7	832	2	T08422	negative regulator
3	172.5	27.0	519	2	S78089	G-protein signalin
4	167.5	26.2	211	2	IS3020	G-0/G-1 switch reg
5	160	25.0	173	2	S71812	RG501 protein - hu
6	158.5	24.8	533	2	T31002	hypothetical prote
7	158	24.7	196	2	S43436	B cell activation
8	155.5	24.3	205	2	S78221	G-protein signalin
9	143.5	22.5	181	2	JC7228	G-protein signalin
10	133	20.8	284	2	T15700	hypothetical prote
11	130	20.3	544	2	JC5503	G-protein signalin
12	124.5	19.5	558	2	T21468	hypothetical prote
13	121.5	19.0	169	2	T21034	hypothetical prote
14	121.5	19.0	181	2	T21035	hypothetical prote
15	115	18.0	1387	2	JC5502	G-protein signalin
16	112.5	17.6	244	2	T13580	hypothetical prote
17	107.5	16.8	251	2	S43576	C0585.7 protein (C
18	106	16.6	270	2	T22213	hypothetical prote
19	97.5	15.3	234	2	T2672	hypothetical prote
20	97	15.2	274	2	T22214	hypothetical prote
21	93.5	14.6	303	2	T29513	hypothetical prote
22	87.5	13.7	473	2	T19337	hypothetical prote
23	85	13.3	317	1	A42431	3-oxoacyl-lacyl-ca
24	85	13.3	1010	2	T41077	hypothetical struc
25	78.5	12.3	698	2	S55974	SSR2 protein - yea
26	78	12.2	843	2	H72204	pullulanase - Ther
27	76.5	12.0	719	2	S60771	developmental regu
28	75.5	11.8	216	2	T15317	hypothetical prote
29	73	11.4	469	2	T00429	probable peclnest

30	73	11.4	1276	2	T09204	probable tail-host
31	73	11.4	1291	2	T09273	probable tail-host
32	72.5	11.3	382	2	E64686	myosin-like prote
33	72.5	11.3	431	2	C71954	hypothetical prote
34	71.5	11.2	190	2	E71475	probable translati
35	71.5	11.2	1131	2	T41943	major DNA binding
36	71.5	11.2	1305	2	D82923	DNA-directed RNA p
37	71	11.1	157	2	I50817	MHC class I protei
38	70.5	11.0	268	2	S63621	cyma protein - Kie
39	70.5	11.0	413	2	S73643	MG349 homolog G12
40	70.5	11.0	421	2	T43406	cullin-3 - fission
41	70.5	11.0	785	2	T38359	cullin 3 homolog -
42	70.5	11.0	798	2	S62405	hypothetical prote
43	70.5	11.0	949	2	D82293	isolectin-CRNA syn
44	70.5	11.0	1607	2	T21982	hypothetical prote
45	70	11.0	190	2	B72021	translation elonga

ALIGNMENTS

RESULT 1
T08423
Axin homolog Ax11 - rat
N:Alternate names: Ax11
C:Species: Rattus norvegicus (Norway rat)
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jul-2000
C:Accession: T08423
R:Yamamoto, H.; Kishida, S.; Uochi, T.; Ikeda, S.; Koyama, S.; Asashima, M.; Kikuchi, M.; Cell. Biol. 18, 2867-2875, 1998
A:Title: Ax11, a member of the Axin family, interacts with both glycogen synthase kin
A:Reference number: Z16414; MUID:98226558
A:Accession: T08423
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-838 <YAM>
A:Cross-references: EMBL:AF017757; NID:93080758; PIDN:AMC40089.1; PID:93080759
A>Note: Interacts with GSK-3beta and beta-catenin
C:Keywords: phosphoprotein; signal transduction

Query Match 100.0%; Score 639; DB 2; Length 838;
Best local Similarity 100.0%; Pred. No. 7.6e-53;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WTKSLSLGDDQGAYLFFRTLEERKCVDTLDFWACNGFRQNNLKDPTLRVAKAIYKR 60
|||||
DB 78 WTKSLSLGDDQGAYLFFRTLEERKCVDTLDFWACNGFRQNNLKDPTLRVAKAIYKR 137
QY 61 YIENNSVSKQLPARKTYIRDCIKKQIGSVFDDAQRTIQAVMEENAYOVFLTSDIYL 120
|||||
DB 138 YIENNSVSKQLPARKTYIRDCIKKQIGSVFDDAQRTIQAVMEENAYOVFLTSDIYL 197
QY 121 EYV 123
|||
DB 198 EYV 200
RESULT 2
T08422
negative regulator axin [Imported] - rat
N:Alternate names: fAxin
C:Species: Rattus norvegicus (Norway rat)
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jul-2000
C:Accession: T08422
R:Ikeda, S.; Yamamoto, H.; Murali, H.; Kishida, S.; Kikuchi, A.
EMBO J. 17, 1371-1384, 1998
A:Title: Axin, a negative regulator of the Wnt signaling pathway, forms a complex wit
A:Reference number: Z16413; MUID:98151361
A:Accession: T08422
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-837 <IKE>

GenCore version 4.5
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OW protein - protein search, using sw model

Run on: June 7, 2001, 02:03:32 ; Search time 39.03 Seconds
(without alignments)
107.953 Million cell updates/sec

Title: US-09-587-574-2

Perfect score: 639
Sequence: 1 WTKSLHSLLGDDGAVLFRT.....VMEENAVQVFLTSIDYLEYV 123

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SWSwProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	639	100.0	838	1 AXN2_RAT	070240 ratu
2	639	100.0	840	1 AXN2_MOUSE	088566 mus musculu
3	624	97.7	843	1 AXN2_HUMAN	097271 homo sapien
4	560	87.6	812	1 AXN2_BRARE	P57095 brachydanto
5	420.5	65.8	835	1 AXN1_BRARE	P57094 brachydanto
6	420	65.7	842	1 AXN1_XENLA	Q9Y9Y0 xenopus lae
7	407	63.7	893	1 AXN1_RAT	070239 ratu
8	407	63.7	992	1 AXN1_MOUSE	035625 mus musculu
9	406	63.5	841	1 AXN1_CHICK	042400 gallu
10	401	62.8	900	1 AXN1_HUMAN	015169 homo sapien
11	172.5	27.0	519	1 RGS2_HUMAN	P49796 homo sapien
12	167.5	26.2	211	1 RGS2_HUMAN	P41220 homo sapien
13	162.5	25.4	211	1 RGS2_MOUSE	008849 mus musculu
14	160	25.0	167	1 RGS4_HUMAN	043665 mus musculu
15	158.5	24.8	745	1 AXN1_MOUSE	094407 drosophila
16	158	24.7	196	1 RGS1_HUMAN	008116 homo sapien
17	155.5	24.3	205	1 RGS4_HUMAN	P49798 homo sapien
18	154.5	24.2	181	1 RGS5_HUMAN	015539 homo sapien
19	152.5	23.9	205	1 RGS4_RAT	P49799 ratu
20	150.5	23.6	180	1 RGS8_HUMAN	P57771 ratu
21	149.5	23.4	180	1 RGS8_RAT	P49804 ratu
22	149.5	23.4	205	1 RGS4_MOUSE	008899 mus musculu
23	148.5	23.2	202	1 RGS6_MOUSE	046471 bos tauru
24	147.5	23.1	199	1 RGS6_BOVIN	P56700 ratu
25	145.5	22.8	181	1 RGS5_MOUSE	008850 mus musculu
26	143.5	22.5	181	1 RGS5_RAT	P49800 ratu
27	140.5	22.0	201	1 RGS6_MOUSE	P97428 mus musculu
28	140.5	22.0	216	1 GAIP_RAT	070221 ratu
29	139.5	21.8	217	1 GAIP_HUMAN	070221 ratu
30	136.5	21.4	159	1 RGS4_HUMAN	014921 homo sapien
31	136.5	21.4	202	1 RGS4_HUMAN	015492 homo sapien
32	133	20.8	284	1 YTN3_CAEL	018312 caenorhabd
33	130	20.3	544	1 RGS6_RAT	008773 ratu

ALIGNMENTS

RESULT 1	AXN2_RAT	STANDARD	PRT	838 AA.
AC	070240			
DT	01-OCT-2000 (Rel. 40, Created)			
DT	01-OCT-2000 (Rel. 40, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	AXIN 2 (AXIS INHIBITION PROTEIN 2) (CONDUCTIN) (AXIN-LIKE PROTEIN)			
DE	(AXIL)			
GN	AXIN2			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=98226558; PubMed=9566905;			
RA	Yamamoto H., Kishida S., Uochi T., Ikeda S., Koyama S., Asashima M., Kikuchi A.;			
RT	"Axil, a member of the Axin family, interacts with both glycogen synthase kinase 3beta and beta-catenin and inhibits axis formation of Xenopus embryos."			
RL	Mol. Cell. Biol. 18:2867-2875(1998).			
CC	-1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-CATENIN AND APC BY GSK-3B (BY SIMILARITY).			
CC	-1- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B) AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN OCCURS VIA THE ARADILLO REPEATS CONTAINED IN BETA-CATENIN.			
CC	TERMINAL COMPLEX.			
CC	-1- SUBCELLULAR LOCATION: CYTOPLASMIC.			
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN LUNG AND THYMUS.			
CC	-1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY PP2A.			
CC	-1- SIMILARITY: CONTAINS 1 RGS DOMAIN.			
CC	-1- SIMILARITY: CONTAINS 1 RGS DOMAIN.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.ebi.ac.uk/announce/ or send an email to license@ebi.ac.uk).			
CC	EMBL: AF017757; AAC40089.1; -			
CC	HSSP: P49799; JAGR.			
DR	InterPro: IPR000342; -			
DR	InterPro: IPR001158; -			
DR	PFam: PF00615; RGS_1.			
DR	PFam: PF00778; DIX_1.			
DR	PROSITE: PS50132; RGS_1.			
KW	Developmental protein; Phosphorylation.			
FT	DOMAIN 81 200 RGS			
FT	DOMAIN 327 413 GSK-3B BINDING SITE (BY SIMILARITY).			

34	130	20.3	547	1 RGS6_MOUSE	P97492 mus musculu
35	124.5	19.5	555	1 EGU1_CAEL	P49809 caenorhabd
36	121.5	19.0	169	1 YUJ1_CAEL	P49808 caenorhabd
37	118	18.5	467	1 RGS6_HUMAN	094810 homo sapien
38	118	18.5	675	1 RGS3_MOUSE	054528 mus musculu
39	118	18.5	677	1 RGS3_RAT	P49805 ratu
40	117	18.3	484	1 RGS2_BOVIN	046469 bos tauru
41	116.5	18.2	374	1 RGSX_BOVIN	P79348 bos tauru
42	115	18.0	674	1 RGS6_HUMAN	075916 homo sapien
43	115	18.0	1367	1 RGS6_RAT	008774 ratu
44	115	18.0	1447	1 RGS6_HUMAN	014924 homo sapien
45	107.5	16.8	254	1 YK07_CAEL	P34295 caenorhabd

FT	DOMAIN	413	476	BETA-CATENIN BINDING SITE (BY SIMILARITY).
FT	DOMAIN	469	474	POLY-HIS.
FT	DOMAIN	756	838	DIX.
SO	SEQUENCE	838 AA;	92947 MW;	45B825C13BA0F737 CRC64;
Query Match				
Best Local Similarity		100.0%;	Score 639;	DB 1; Length 838;
Matches 123;		Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	1	WTKSLHSLIGDGDGAYLFRPTFLERKECVDTLDFWFCACNGFROMNKIDTKTLRYAKAIYKR	60	
DB	78	WTKSLHSLIGDGDGAYLFRPTFLERKECVDTLDFWFCACNGFROMNKIDTKTLRYAKAIYKR	137	
QY	61	YIENSYSVKOLKPKTKYIRIDGIKKOQIGSMFPOAOTETIOAWNEENAYQFLTSDIYL	120	
DB	138	YIENSYSVKOLKPKTKYIRIDGIKKOQIGSMFPOAOTETIOAWNEENAYQFLTSDIYL	197	
QY	121	EYV	123	
DB	198	EYV	200	
RESULT				
AXIN2_MOUSE		STANDARD:	PRT;	840 AA.
ID	AXIN2_MOUSE	090XJ6;		
AC	088566;	090XJ6;		
DT	01-OCT-2000	(Rel. 40, Created)		
DT	01-OCT-2000	(Rel. 40, Last sequence update)		
DT	01-OCT-2000	(Rel. 40, Last annotation update)		
DE	AXIN 2 (AXIN INHIBITION PROTEIN 2) (CONDUCTIN) (AXIN-LIKE PROTEIN) (AXIL).			
GN	AXIN2.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=9621239; PubMed=9554852;			
RA	Behrens J., Jercchow B.-A., Muertel M., Grimm J., Asbrand C.,			
RA	Witz R., Kuehl M., Wedlich D., Birchmeier W.;			
RT	"Functional interaction of an axin homolog, conductin, with beta-			
RL	catenin, APC, and GSK3beta.";			
RL	Science 280:596-599(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G.,			
RA	Jenkins N.A., Warburton D., Costantini F.;			
RT	"Properties of mouse Axin2 and human AXIN2: chromosomal location,			
RT	expression pattern, interaction with Axin and effects on embryonic			
RT	axis formation.";			
RL	Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.			
CC	-1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES			
CC	BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-			
CC	CATENIN AND APC BY GSK-3B (BY SIMILARITY).			
CC	-1- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)			
CC	AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN			
CC	OCCURS VIA THE ARMA/DILLO REPEATS CONTAINED IN BETA-CATENIN.			
CC	TERNARY COMPLEX (BY SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).			
CC	-1- PM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY			
CC	PP2A (BY SIMILARITY).			
CC	-1- SIMILARITY: CONTAINS 1 RGS DOMAIN.			
CC	-1- SIMILARITY: CONTAINS 1 DIX DOMAIN.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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CC -----
DR DR EMBL; AF073768; AAC626047.1; -
DR DR EMBL; AF205889; AAF22800.1; -
DR DR MGI; MGI:1270862; Axin2.
DR DR HSSP; P49799; IAGR.
DR DR InterPro; IPR000342; -
DR DR InterPro; IPR001158; -
DR DR Pfam; PF00615; RGS; 1.
DR DR Pfam; PF00778; DIX; 1.
DR DR PRINTS; PRO1301; RGS-PROTEIN.
DR DR PROSITE; PS50132; RGS; 1.
DR DR Anti-oncogene; Phosphorylation.
RW RW DOMAIN 81 200 RGS.
FT FT 327 413 GSK-3B BINDING SITE (BY SIMILARITY).
FT FT DOMAIN 327 478 BETA-CATENIN BINDING SITE (BY
FT FT SIMILARITY).
FT FT POLY-HIS.
FT FT DIX.
FT FT 469 476 DIX.
FT FT DOMAIN 758 840 DIX.
FT FT CONFLICT 101 101 R -> K (IN REF. 2).
FT FT CONFLICT 474 474 H -> Y (IN REF. 2).
FT FT CONFLICT 484 484 S -> P (IN REF. 2).
FT FT CONFLICT 503 503 F -> S (IN REF. 2).
FT FT CONFLICT 603 603 G -> A (IN REF. 2).
SQ SEQUENCE 840 AA; 92934 MW; A07D5EBF25DE7277 CRC64;

Query Match 100.0%; Score 639; DB 1; Length 840;
Best Local Similarity 100.0%; Pred. No. 8,2e-53;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 WTKSLHSLGDDGAYLFERLEPERKCVDTLDFWFCNGFROMLKQDTLRYAAAIYR 60
Db 78 WTKSLHSLGDDGAYLFERLEPERKCVDTLDFWFCNGFROMLKQDTLRYAAAIYR 137
QY 61 YIENNSVYSKOLKPAATKYIYRDGIKKQIGSYMFPOAQEIOAVMEENAYQVELSDIYL 120
Db 138 YIENNSVYSKOLKPAATKYIYRDGIKKQIGSYMFPOAQEIOAVMEENAYQVELSDIYL 197
QY 121 EYV 123
Db 198 EYV 200

RESULT 3
AXN2_HUMAN STANDARD; PRT; 843 AA.
ID AXN2_HUMAN
AC Q9Y2T1; Q9UH84;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN 2 (AXIS INHIBITION PROTEIN 2) (CONDUCTIN) (AXIN-LIKE PROTEIN)
DE (AXIL).
GN AXIN2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99168905; PubMed=10049590;
RA Mai M., Qian C., Yokomizo A., Smith D.I., Liu W.;
RT "Cloning of the human homolog of conductin (AXIN2), a gene mapping to
RT chromosome 11q23-q24."
RL Genomics 55:341-344(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, and Lymphoblast;
RA Zhang T., Fagotto F., Heu W., Zeng L., Gilbert D., Copeland N.G.,
RA Jenkins N.A., Warburton D., Costantini F.;
RT "Properties of mouse Axin2 and human AXIN2: chromosomal location,
RT expression pattern, interaction with Axin and effects on embryonic
RT axis formation."

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Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.

CC - FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES

CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-

CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).

CC - SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)

CC AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN

CC OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN.

CC TERNARY COMPLEX (BY SIMILARITY).

CC - SUBCELLULAR LOCATION: CYTOPLASMIC.

CC - TISSUE SPECIFICITY: EXPRESSED IN BRAIN AND LYMPHOBLAST.

CC - PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY

CC PP2A (BY SIMILARITY).

CC - SIMILARITY: CONTAINS 1 RGS DOMAIN.

CC - SIMILARITY: CONTAINS 1 DIX DOMAIN.

CC -----

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CC -----

DR EMBL: AF078165; AAD20976.1; -

DR EMBL: AF205888; AAF22799.1; -

DR MIM: 604025; -

DR InterPro: IPR000342; -

DR InterPro: IPR001158; -

DR Pfam: PF00615; RGS; 1.

DR Pfam: PF00778; DIX; 1.

DR PRINTS: PR01301; RGS-PROTEIN.

DR PROSITE: PS50132; RGS; 1.

DR Developmental Protein: Phosphorylation.

FT DOMAIN 81 200

FT DOMAIN 327 413

FT DOMAIN 413 476

FT DOMAIN 469 474

FT DOMAIN 761 843

FT CONFLICT 37 62

FT CONFLICT 346 346

FT CONFLICT 572 636

FT CONFLICT 687 687

FT CONFLICT 696 696

FT SEQUENCE 843 AA; 93557 MW; F7B62BD6AB4664D CRC64;

Query Match 97.7%; Score 624; DB 1; Length 843;

Best Local Similarity 95.9%; Pred. No. 2.1e-51;

Matches 118; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 WTKSLSLDQDQAGVYLFRTLEKRCVDTLDWFACNGFRONMLKDTLRYAKAIYKR 60

DB 78 WTKSLSLDQDQAGVYLFRTLEKRCVDTLDWFACNGFRONMLKDTLRYAKAIYKR 137

QY 61 YIENNSVSKQLKPKATYTRDGIKQKQISVWFDAQTEIOAVMEENAVOVFLTSIYL 120

DB 138 YIENNSVSKQLKPKATYTRDGIKQKQISVWFDAQTEIOAVMEENAVOVFLTSIYL 197

QY 121 EYV 123

DB 198 EYV 200

RESULT 4

AXIN2_BRAE STANDARD; PRT; 812 AA.

AC P57095;

DT 01-OCT-2000 (Rel. 40, Created)

DT 01-OCT-2000 (Rel. 40, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE AXIN 2 (AXIS INHIBITION PROTEIN 2).

GN AXIN2.

OS Brachydanio rerio (zebrafish) (Zebra danio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;

OC Cypriniformes; Cyprinidae; Rasbora; Danio.

OX NCBI_TaxID=7955;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20171051; PubMed=10704853;

RA Shimizu T., Yamataka Y., Ryu S.-L., Hashimoto H., Yabe T., Hirata T.,

RA Bae Y.-K., Hibi M., Hirano T.;

RT Cooperative roles of Bozozok/Dharma and Nodal-related proteins in the

RT formation of the dorsal organizer in zebrafish.;

RL Mech. Dev. 91:293-303(2000)

CC - FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES

CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-

CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).

CC - SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

CC - PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY

CC PP2A (BY SIMILARITY).

CC - SIMILARITY: CONTAINS 1 RGS DOMAIN.

CC - SIMILARITY: CONTAINS 1 DIX DOMAIN.

CC -----

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CC -----

DR EMBL: AB032263; BAA92440.1; -

DR HSSP: P49799; IAGR.

DR InterPro: IPR000342; -

DR InterPro: IPR001158; -

DR Pfam: PF00615; RGS; 1.

DR Pfam: PF00778; DIX; 1.

DR PROSITE: PS50132; RGS; 1.

DR Developmental Protein: Phosphorylation.

FT DOMAIN 84 203

FT DOMAIN 329 415

FT DOMAIN 415 467

FT DOMAIN 412 419

FT DOMAIN 730 812

FT SEQUENCE 812 AA; 91496 MW; 46E5ADA6DE2240CC CRC64;

Query Match 87.6%; Score 560; DB 1; Length 812;

Best Local Similarity 86.2%; Pred. No. 2.2e-45;

Matches 106; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 1 WTKSLSLDQDQAGVYLFRTLEKRCVDTLDWFACNGFRONMLKDTLRYAKAIYKR 60

DB 81 WTKSLSLDQDQAGVYLFRTLEKRCVDTLDWFACNGFRONMLKDTLRYAKAIYKR 140

QY 61 YIENNSVSKQLKPKATYTRDGIKQKQISVWFDAQTEIOAVMEENAVOVFLTSIYL 120

DB 141 YIENNSVSKQLKPKATYTRDGIKQKQISVWFDAQTEIOAVMEENAVOVFLTSIYL 200

QY 121 EYV 123

DB 201 EYV 203

RESULT 5

AXIN1_BRAE STANDARD; PRT; 835 AA.

AC P57094;

DT 01-OCT-2000 (Rel. 40, Created)

DT 01-OCT-2000 (Rel. 40, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE AXIN 1 (AXIS INHIBITION PROTEIN 1).

GN AXIN1.
 OS Brachydanio rerio (zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 CC Cypriniformes; Cyprinidae; Rasbora; Danio.
 NCBI_TaxID=7955;
 RN NCBI
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2017051; PubMed=10704853;
 RA Shimizu T., Yamamoto Y., Ryu S.-L., Hashimoto H., Yabe T., Hirata T.,
 BA Bae Y.-K., Hibi M., Hirano T.,
 RT "Cooperative roles of Bozozok/Dharma and Nodal-related proteins in the
 RL formation of the dorsal organizer in zebrafish."
 Mech. Dev. 91:293-303(2000).
 CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
 CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
 CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- PPM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
 CC PP2A (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; AB032262; BAA92439.1; -
 DR HSSP; P49799; IAGR.
 DR InterPro: IPR000342; -
 DR InterPro: IPR001158; -
 DR Pfam; PF00615; RGS; 1.
 DR Pfam; PF00778; DIX; 1.
 DR PROSITE; PS50132; RGS; 1.
 KW Developmental protein; Phosphorylation.
 FT DOMAIN 92 214 RGS.
 FT 351 436 GSK-3B BINDING SITE (BY SIMILARITY).
 FT DOMAIN 437 512 BETA-CATENIN BINDING SITE (BY
 FT SIMILARITY).
 FT DOMAIN 753 835 DIX.
 FT SEQUENCE 835 AA; 94351 MW; 1c62fcf1f5937c87 CRC64;
 SQ
 Query Match 65.8%; Score 420.5; DB 1; Length 835;
 Best Local Similarity 63.2%; Pred. No. 3.2e-32;
 Matches 79; Conservative 20; Mismatches 23; Indels 3; Gaps 2;
 OY 1 WTKSLSLDGDGGAYLFTFLERKCVDTLDFWACNGFROMNLKD--TKTLRVAKATY 58
 DB 89 WAESLSLDDDDGHLFTFLFKQECADMLDFWACSGFRKQANDGNEKMLAKATY 148
 OY 59 KRYI-ENNSVSVSKQJLPAKTYIRDGIRKQKQIGSVMDQACTETQAVMENAAYVFLTS 117
 DB 149 KYIILDNNGIYSROIKPATKSFIRKQCVKMLHIDPAMFDQAGIETQVMEENTYPIFLKSD 208
 OY 118 IYLEY 122
 DB 209 IYLEY 213
 RESULT 6
 AXIN_XENLA STANDARD: PRT; 842 AA.
 ID AXN_XENLA
 AC O9YGYO.
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE AXIN (AXIS INHIBITION PROTEIN) (XAXIN).
 GN AXIN OR AXN.

OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 CC Xenopodidae; Xenopus.
 NCBI_TaxID=8355;
 RN NCBI
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99173782; PubMed=10072781;
 RA Hedgepeth C.M., Deardorff M.A., Klein P.S.;
 RT "Xenopus axin interacts with glycogen synthase kinase-3 beta and is
 RL expressed in the anterior midbrain."
 Mech. Dev. 80:147-151(1999).
 CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
 CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
 CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- DEVELOPMENTAL STAGE: WEAKLY AND UBICUOUSLY EXPRESSED THROUGHOUT
 CC EARLY DEVELOPMENT. AND HIGHLY EXPRESSED IN THE ANTERIOR
 CC MESENCEPHALON ADJACENT TO THE FOREBRAIN-MIDBRAIN BOUNDARY.
 CC -1- PPM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
 CC PP2A (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
 CC -----
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 CC -----
 DR EMBL; AF097313; AAC71036.1; -
 DR HSSP; P49799; IAGR.
 DR InterPro: IPR000342; -
 DR InterPro: IPR001158; -
 DR Pfam; PF00615; RGS; 1.
 DR Pfam; PF00778; DIX; 1.
 DR PROSITE; PS50132; RGS; 1.
 KW Developmental protein; Phosphorylation.
 FT DOMAIN 88 211 RGS.
 FT 348 433 GSK-3B BINDING SITE (BY SIMILARITY).
 FT DOMAIN 434 508 BETA-CATENIN BINDING SITE (BY
 FT SIMILARITY).
 FT DOMAIN 760 842 DIX.
 FT SEQUENCE 842 AA; 94459 MW; BDAL52734C97191E CRC64;
 SQ
 Query Match 65.7%; Score 420; DB 1; Length 842;
 Best Local Similarity 61.1%; Pred. No. 3.6e-32;
 Matches 77; Conservative 25; Mismatches 20; Indels 4; Gaps 2;
 OY 1 WTKSLSLDGDGGAYLFTFLERKCVDTLDFWACNGFROMNLKDKT--LRVARAI 57
 DB 85 WAESLSLDDDDGHLFTFLFKQECADMLDFWACSGFRLEPNDSKVERKLAAAI 144
 OY 58 KRYI-ENNSVSVSKQJLPAKTYIRDGIRKQKQIGSVMDQACTETQAVMENAAYVFLTS 116
 DB 145 YKYYLDSNGIYSROIKPATKSFIRKQCVKMLHIDPAMFDQAGIETQVMEENTYPIFLKSD 204
 OY 117 IYLEY 122
 DB 205 IYLEY 210
 RESULT 7
 AXIN_RAT STANDARD: PRT; 893 AA.
 ID AXN_RAT
 AC O70239.
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE AXIN 1 PROTEIN (AXIS INHIBITION PROTEIN 1) (RAXIN) (FRAGMENT).

GN AXIN1 OR AXIN.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 ON NCBI_TaxID=10116;
 [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE:Brain;
 RX MEDLINE=98151361; PubMed=9482734;
 RA Ikeda S., Kishida S., Yamamoto H., Murali H., Koyama S., Kikuchi A.;
 RT "Axin, a negative regulator of the Wnt signaling pathway, forms a
 RT complex with GSK-3beta and beta-catenin and promotes GSK-3beta-
 RT dependent phosphorylation of beta-catenin.";
 RL EMBL J. 17:1371-1384(1998).
 CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
 CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
 CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
 CC -1- SUBUNIT: INTERACTS WITH GSK-3B AND BETA-CATENIN. THE INTERACTION
 CC BETWEEN AXIN AND BETA-CATENIN OCCURS VIA THE ARMADILLO REPEATS
 CC CONTAINED IN BETA-CATENIN. TERNARY COMPLEX. ALSO BINDS TO
 CC PLAGIOLOBIN (GAMA-CATENIN), APC, DVL AND PP2A (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS, THYMUS AND LUNG
 CC FOLLOWED BY CEREBRUM, CEREBELLUM, HEART, KIDNEY, SKELETAL MUSCLE,
 CC SPLEEN AND LIVER.
 CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
 CC PP2A (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
 CC -----
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 CC -----
 CC EMBL: AF017756; AAC40066.1; ALT_INIT.
 DR HSSP: P49799; IAGR.
 DR InterPro: IPR000342; -
 DR InterPro: IPR001158; -
 DR Pfam: PF00615; RGS; 1.
 DR Pfam: PF00778; DIX; 1.
 DR PROSITE: PS50132; RGS; 1.
 DR Developmental protein; phosphorylation.
 KW NON_TER 1
 FT DOMAIN 154 277 RGS.
 FT DOMAIN 414 498 GSK-3B BINDING SITE.
 FT DOMAIN 499 567 BETA-CATENIN BINDING SITE.
 FT DOMAIN 811 893 DIX.
 SQ SEQUENCE 893 AA; 99188 MW; 3CDBD2224EDD384C CRC64;
 Query Match 63.7%; Score 407; DB 1; Length 893;
 Best Local Similarity 61.9%; Pred. No. 6.4e-31;
 Matches 78; Conservative 21; Mismatches 23; Indels 4; Gaps 2;

ID AXIN1_MOUSE STANDARD; PRT; 992 AA.
 AC 035625;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DE 01-OCT-2000 (Rel. 40, Last annotation update)
 DE AXIN 1 (AXIS INHIBITION PROTEIN 1) (FUSED PROTEIN) (FRAGMENT).
 GN AXIN1 OR AXIN OR FU.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 [1]
 RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RX MEDLINE=97373830; PubMed=9230313;
 RA Zeng L., Fagotto F., Zhang T., Hsu W., Vasilek T.J., Perry W.L. III,
 RA Lee J.J., Tillman S.M., Gumbiner B.M., Costantini F.;
 RT "The mouse fused locus encodes Axin, an inhibitor of the Wnt signaling
 RT pathway that regulates embryonic axis formation.";
 RL Cell 90:181-192(1997).
 CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
 CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
 CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
 CC -1- SUBUNIT: INTERACTS WITH GSK-3B AND BETA-CATENIN. THE INTERACTION
 CC BETWEEN AXIN AND BETA-CATENIN OCCURS VIA THE ARMADILLO REPEATS
 CC CONTAINED IN BETA-CATENIN. TERNARY COMPLEX. ALSO BINDS TO
 CC PLAGIOLOBIN (GAMA-CATENIN), APC, DVL AND PP2A (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN EMBRYONIC STEM CELLS.
 CC -1- DEVELOPMENTAL STAGE: WIDELY EXPRESSED AT E10.5 TO E16.5 DAY.
 CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
 CC PP2A.
 CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
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 CC -----
 CC EMBL: AF009011; AAC53285.1; -
 DR HSSP: P49799; IAGR.
 DR MGD: MGI:1096327; Axin.
 DR InterPro: IPR000342; -
 DR InterPro: IPR001158; -
 DR Pfam: PF00615; RGS; 1.
 DR Pfam: PF00778; DIX; 1.
 DR PROSITE: PS50132; RGS; 1.
 DR Developmental protein; phosphorylation; Alternative splicing.
 KW NON_TER 1
 FT DOMAIN 10 18 POLY-ALA.
 FT DOMAIN 217 340 RGS.
 FT DOMAIN 477 561 GSK-3B BINDING SITE (BY SIMILARITY).
 FT DOMAIN 562 630 BETA-CATENIN BINDING SITE (BY
 FT SIMILARITY).
 FT DOMAIN 910 992 DIX.
 FT VARSPLIC 860 895 MISSING (IN ISOFORM 2).
 SQ SEQUENCE 992 AA; 109917 MW; 70EBB53D387BD26F CRC64;
 Query Match 63.7%; Score 407; DB 1; Length 992;
 Best Local Similarity 61.9%; Pred. No. 7.2e-31;
 Matches 78; Conservative 21; Mismatches 23; Indels 4; Gaps 2;

Db 274 YRKYLDSNGICVSRQKATKSFITKDCVMKQOIPDMFDOAQOTELQSTMEENTYPSFLKS 333
QY 117 DILEY 122
Db 334 DILEY 339

RESULT 9

AXN_CHICK STANDARD: PRT: 841 AA.
ID AXN_CHICK
AC 042400;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN (AXIS INHIBITION PROTEIN).
GN AXIN OR AXN.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;

[1]
SEQUENCE FROM N.A.
RP TISSUE-Embryo;
RX MEDLINE=9373830; PubMed=9230313;
RA Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perry W.L. III,
Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F.;
"The mouse fused locus encodes Axin, an inhibitor of the Wnt signaling
pathway that regulates embryonic axis formation.";
RT Cell 90:181-192(1997).
RL -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CATENIN AND APC BY GSK-3B (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT STAGE 12 TO 15.
CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
PP2A (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.

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or send an email to license@sib-sib.ch).
CC
CC EMBL; AF009012; AAC60245.1; -
DR HSP: P49799; IAGR.
DR InterPro: IPR000158;
DR Pfam: PF00615; RGS; 1.
DR ProSITE: PS50132; RGS; 1.
KW Developmental protein; Phosphorylation.
FT DOMAIN 88 211 RGS.
FT DOMAIN 348 433 GSK-3B BINDING SITE (BY SIMILARITY).
FT DOMAIN 434 508 BETA-CATENIN BINDING SITE (BY
SIMILARITY).
FT DIX.
FT SEQUENCE 841 AA; 94931 MW; 400DC90E72506FE CRC64;

Query Match 63.5%; Score 406; DB 1; Length 841;
Best Local Similarity 61.1%; Pred. No. 7.5e-31;
Matches 77; Conservative 22; Mismatches 23; Indels 4; Gaps 2;

OY 1 WTKSLHSLGDDGAYLPTETLEKCVDTLDWFAKNGEFGMN--LKDITLRARAKAI 57
Db 85 WAESLHSLDQDDGINTLPTFLKQEDCADLDFWACSGFRLEPCVNEERKLAKAI 144

OY 58 YKRRI-ENNSVSKQKLPATKTYIDGKKQOIGSVMDAQOTELQWMEENAYOVFLTS 116
Db 145 YKKYILDNNNGISQIKPATKSFITKDCVMKLIQIPDMFDOAQOTELQCMETDTPFLKS 204
QY 117 DILEY 122
Db 205 DILEY 210

RESULT 10

AXN1_HUMAN STANDARD: PRT: 900 AA.
ID AXN1_HUMAN
AC 015169;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN 1 (AXIS INHIBITION PROTEIN 1) (HAXIN) (FRAGMENT).
GN AXIN1 OR AXIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
OX [1]

SEQUENCE FROM N.A.
RX MEDLINE=9373830; PubMed=9230313;
RA Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perry W.L. III,
Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F.;
"The mouse fused locus encodes Axin, an inhibitor of the Wnt signaling
pathway that regulates embryonic axis formation.";
RT Cell 90:181-192(1997).
RL -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CATENIN AND APC BY GSK-3B.

CC -1- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)
AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN
OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN.
CC TERNARY COMPLEX. MAY ALSO BINDS TO PLACOGLOBIN (GAMA-CATENIN),
APC, DVL AND PP2A.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: UBQUITOUSLY EXPRESSED.
CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
PP2A.

CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC
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or send an email to license@sib-sib.ch).
CC
CC EMBL; AF009674; AAC51624.1; -
DR HSP: P49799; IAGR.
DR InterPro: IPR000342;
DR Pfam: PF00615; RGS; 1.
DR ProSITE: PS50132; RGS; 1.
KW Developmental protein; Phosphorylation.
FT NON_TER 1 1
FT DOMAIN 125 248 RGS.
FT DOMAIN 385 470 GSK-3B BINDING SITE (BY SIMILARITY).
FT DOMAIN 471 540 BETA-CATENIN BINDING SITE (BY
SIMILARITY).
FT DIX.
FT SEQUENCE 900 AA; 99803 MW; EEF990B11FC7B3B CRC64;

Query Match 62.8%; Score 401; DB 1; Length 900;
Best Local Similarity 62.7%; Pred. No. 2.4e-30;

Matches 79; Conservative 17; Mismatches 26; Indels 4; Gaps 2;

QY 1 WTKSLSLGDDGAVLFPFLERKCVDTLDFWACNGFROMLKDT---KTLVAKAI 57
 DB 122 WAKSLSLGDDGAVLFPFLERKCVDTLDFWACNGFROMLKDT---KTLVAKAI 181
 QY 58 YKRYI-ENNSVSVSKQLPARKTYIRDIKKGQISVWFOAQETIOAVMEENAYQVFLTS 116
 DB 182 YKRYIENNSVSVSKQLPARKTYIRDIKKGQISVWFOAQETIOAVMEENAYQVFLTS 241
 QY 117 DYLEY 122
 DB 242 DYLEY 247

RESULT 11
 RGS3_HUMAN STANDARD; PRT; 519 AA.
 AC P49796;
 DT 01-OCT-1996 (rel. 34, Last sequence update)
 DT 01-OCT-1996 (rel. 34, Last sequence update)
 DE REGULATOR OF G-PROTEIN SIGNALING 3 (RGS3). (RGP3).
 GN RGS3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96178495; PubMed=8602223;
 RA Druey K.M., Blumer K.J., Kang V.H., Kehrl J.H.:
 RT "Inhibition of G-protein-mediated MAP kinase activation by a new
 RT mammalian gene family".
 RL Nature 379:742-746(1996).
 CC -1- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
 CC ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO
 CC THEIR INACTIVE GDP-BOUND FORM.
 CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
 CC
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 CC
 CC EMBL: U27655; AAC50394.1; -
 CC DR HSSP: P49799; JAGR.
 CC DR MIM: 602189; -
 CC DR InterPro: IPR000342; -
 CC DR Pfam: PF00615; RGS; 1.
 CC DR PRINTS: PRO1301; RGS-PROTEIN.
 CC DR PROSITE: PS50132; RGS; 1.
 CC KW Signal transduction inhibitor.
 CC FT DOMAIN 394 510
 CC FT SEQUENCE 519 AA; 56601 MW; FICFE3F27D4673A0 CRC64;

Query Match 27.0%; Score 172.5; DB 1; Length 519;
 Best Local Similarity 32.5%; Pred. No. 4.5e-09;
 Matches 40; Conservative 24; Mismatches 56; Indels 3; Gaps 2;

QY 1 WTKSLSLGDDGAVLFPFLERKCVDTLDFWACNGFROMLKDTKTLVAKAIYKR 60
 DB 391 WGSLEKLLVHKYGLAVFOAFLTERSEENLEWLAECDEPKKYK-SQSKASAKAKIFAE 449
 QY 61 YIENNSVSVSKQLPARKTYIRDIKKGQISVWFOAQETIOAVMEENAYQVFLTS 120
 DB 450 YIAIOACKEVNLDVYTRHTKML--QSVTRCGCFDLAOKRIFGLMERKDSYPRFLRSDLYL 507
 QY 121 EVY 123

DB 508 DLI 510

RESULT 12
 RGS2_HUMAN STANDARD; PRT; 211 AA.
 AC P41220;
 DT 01-FEB-1995 (rel. 31, Last sequence update)
 DT 01-FEB-1995 (rel. 31, Last sequence update)
 DE REGULATOR OF G-PROTEIN SIGNALING 2 (RGS2) (G0/G1 SWITCH REGULATORY
 DE PROTEIN 8).
 GN RGS2 OR G0S8.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=94235158; PubMed=8179820;
 RA Siderovski D.P., Heximer S.P., Forsdyke D.R.:
 RT "A human gene encoding a putative basic helix-loop-helix
 RT phosphoprotein whose mRNA increases rapidly in cycloneximide-treated
 RT blood mononuclear cells".
 RL DNA Cell Biol. 13:123-147(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Baggaley C.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP CHARACTERIZATION.
 RX MEDLINE=95371353; PubMed=7643615;
 RA Wu H.-K., Heng H.H., Shi X.-M., Forsdyke D.R., Tsui L.-C., Mak T.W.,
 RA Minden M.D., Siderovski D.P.:
 RT "Differential expression of a basic helix-loop-helix phosphoprotein
 RT gene, G0S8, in acute leukemia and localization to human chromosome
 RT 1q31".
 RL Leukemia 9:1291-1298(1995).
 CC -1- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
 CC ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO
 CC THEIR INACTIVE GDP-BOUND FORM. MAY PLAY A ROLE IN LEUKEMOGENESIS.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ACUTE MYELOGENOUS LEUKEMIA (AML)
 CC AND IN ACUTE LYMPHOBLASTIC LEUKEMIA (ALL).
 CC -1- PTM: COULD BE PHOSPHORYLATED. MIGHT BE FUNCTIONALLY REGULATED BY
 CC PROTEIN KINASE(S).
 CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
 CC
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 CC
 CC EMBL: L13391; AAA20680.1; -
 CC DR EMBL: L13463; AAC37587.1; -
 CC DR EMBL: AL035407; CAB62512.1; -
 CC DR HSSP: P49799; JAGR.
 CC DR MIM: 600861; -
 CC DR InterPro: IPR000342; -
 CC DR Pfam: PF00615; RGS; 1.
 CC DR PRINTS: PRO1301; RGS-PROTEIN.
 CC DR PROSITE: PS50132; RGS; 1.
 CC KW Signal transduction inhibitor; Cell cycle; Phosphorylation.
 CC FT DOMAIN 83 199
 CC FT SEQUENCE 211 AA; 24382 MW; EFFE4A47EP9AD8F CRC64;

Query Match 26.2%; Score 167.5; DB 1; Length 211;
 Best Local Similarity 32.8%; Pred. No. 4.8e-09;

Matches 39; Conservative 20; Mismatches 57; Indels 3; Gaps 2;

OY 1 WTKSHSLGDDGAYLFTFLERKCVDTLDFWFCNGFRONMLKDKTKTLRVAKAIYKR 60
 DB 80 WSEAFDELLASKYGLAARAFLEKSECEENIEFWLACEDFFKTK-SPOKLSKARKITYTD 138
 OY 61 YIENNSVSVKOLKPAKTYIRDGIRKQOIGSVWFDQATEIOAVMEENAYOVFLSDIY 119
 DB 139 FIEKAPKEINIDFOTKSLIAONI--QEAATSGCFTTAQKRVYSIMENNSYPRLESEFY 195

RESULT 13
 RGS2_MOUSE STANDARD; PRT; 211 AA.

AC 008849; 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE REGULATOR OF G-PROTEIN SIGNALING 2 (RGS2).
 GN RGS2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97236828; PubMed=9079700;
 RA Chen C., Zheng B., Han J., Lin S.C.;
 RT "Characterization of a novel mammalian RGS protein that binds to
 RT Galpha proteins and inhibits pheromone signalling in yeast."
 RL J. Biol. Chem. 272:8679-8685(1997).
 CC -1- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
 CC ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO
 CC THEIR INACTIVE GDP-BOUND FORM. MAY PLAY A ROLE IN LEUKEMOGENESIS.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
 CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
 CC -----
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 CC -----
 CC EMBL; U67187; AAB50617.1; -
 DR HSEF; P49799; IACR.
 DR MGD; MGI:1098271; Rgs2.
 DR InterPro; IPR000342; -
 DR Pfam; PF00615; RGS; 1.
 DR PRINTS; PR01301; RGSPPROTEIN.
 DR PROSITE; PS50132; RGS; 1.
 KM Signal transduction inhibitor; Cell cycle.
 FT DOMAIN 83 199 RGS.
 FT SEQUENCE 211 AA; 24297 MW; 61FAA2DC9B0C4DF9 CRC64;

Query Match 25.4%; Score 162.5; DB 1; Length 211;
 Best Local Similarity 31.9%; Pred. No. 1.4e-08;
 Matches 38; Conservative 20; Mismatches 58; Indels 3; Gaps 2;

AC 043665;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE REGULATOR OF G-PROTEIN SIGNALING 10 (RGS10).
 GN RGS10.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chatterjee T.K., Fisher R.A.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
 CC ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO
 CC THEIR INACTIVE GDP-BOUND FORM. ASSOCIATES SPECIFICALLY WITH THE
 CC ACTIVATED FORMS OF THE G PROTEIN SUBUNITS G-ALPHA(1) AND G-
 CC ALPHA(2) BUT FAILS TO INTERACT WITH THE STRUCTURALLY AND
 CC FUNCTIONALLY DISTINCT G-ALPHA(S) SUBUNIT.
 CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
 CC -----
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 CC -----
 CC EMBL; AF045229; AAC03783.1; -
 DR MIM; 602856; -
 DR InterPro; IPR000342; -
 DR Pfam; PF00615; RGS; 1.
 DR PRINTS; PR01301; RGSPPROTEIN.
 DR PROSITE; PS50132; RGS; 1.
 KM Signal transduction inhibitor
 FT DOMAIN 27 142 RGS.
 FT SEQUENCE 167 AA; 19608 MW; EF36915F1AA23F3B CRC64;

Query Match 25.0%; Score 160; DB 1; Length 167;
 Best Local Similarity 32.0%; Pred. No. 1.9e-08;
 Matches 39; Conservative 30; Mismatches 49; Indels 4; Gaps 3;

OY 1 WTKSHSLGDDGAYLFTFLERKCVDTLDFWFCNGFRONMLKDKTKTLRVAKAIYKR 60
 DB 24 WAAISLENLEDEGVKRRFRELKFESEENVLFWLACEDFFKMDK-TQOMKAKEIYWT 82
 OY 61 YIENNSVSVKOLKPAKTYIRDGIRKQOIGSVWFDQATEIOAVMEENAYOVFLSDIYL 120
 DB 83 FL--SSKASSQVWVGOSRLNEKILEEP-HPLMFQKLDQIFNLMKYDSYRFLSDLEL 139
 OY 121 EX 122
 DB 140 KH 141

RESULT 15
 AXN_DROME STANDARD; PRT; 745 AA.

AC Q9V407; Q9XYC1; 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE AXIN (AXIS INHIBITION PROTEIN) (DAXIN) (D-AXIN).
 GN AXN OR CG7926.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]

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OM protein - protein search, using sw model

Run on: June 7, 2001, 02:02:17 ; Search time 81.06 Seconds

(without alignments)
177.851 Million cell updates/sec

Title: US-09-587-574-2

Perfect score: 639
Sequence: 1 WTSLSLSLGDGDGAYLFRT.....VMEENAYOVLTSDIYLEYV 123Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008
Listing first 45 summaries

Database :

SPREMBL.15:*

- 1: sp.archaea:*
- 2: sp.bacteria:*
- 3: sp.fungi:*
- 4: sp.human:*
- 5: sp.invertebrate:*
- 6: sp.mammal:*
- 7: sp.mhc:*
- 8: sp.organelle:*
- 9: sp.phage:*
- 10: sp.plant:*
- 11: sp rodent:*
- 12: sp.unclassified:*
- 13: sp.vertebrate:*
- 14: sp.virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	639	100.0	838	11 070240	070240 rattus norv
2	639	100.0	840	11 088366	088366 mus musculu
3	636	99.5	840	11 090XJ6	090XJ6 mus musculu
4	624	97.7	777	4 090H84	090H84 homo sapien
5	624	97.7	843	4 09Y2T1	09Y2T1 homo sapien
6	420	65.7	842	13 09YGY0	09YGY0 xenopus lae
7	407	63.7	832	11 070239	070239 rattus norv
8	407	63.7	992	11 035625	035625 mus musculu
9	406	63.5	841	13 042400	042400 gallus gall
10	401	62.8	900	4 015169	015169 homo sapien
11	336	52.6	706	13 09PTP2	09PTP2 xenopus lae
12	186.5	29.2	235	4 09NS28	09NS28 homo sapien
13	167.5	26.2	192	11 09JL23	09JL23 mus musculu
14	167.5	26.2	297	11 09JL22	09JL22 mus musculu
15	166.5	26.1	211	11 09JHX0	09JHX0 rattus norv
16	163	25.5	196	11 09JL25	09JL25 mus musculu
17	162.5	25.4	211	11 09JL24	09JL24 mus musculu
18	161.5	25.3	204	13 0919D9	0919D9 xenopus lae
19	158.5	24.8	533	5 022998	022998 caenorhabd

20	158.5	24.8	743	5 09XYC1	09XYC1 drosophila
21	158.5	24.8	745	5 09Y407	09Y407 drosophila
22	144.5	22.6	829	5 09UB06	09UB06 drosophila
23	144.5	22.6	872	5 09NG00	09NG00 drosophila
24	144.5	22.6	1175	5 09YXX8	09YXX8 drosophila
25	144.5	22.6	1175	5 09VCX2	09VCX2 drosophila
26	143.5	22.5	181	11 09JKD7	09JKD7 rattus norv
27	127.5	20.0	208	4 09JUS8	09JUS8 homo sapien
28	127.5	20.0	218	4 09UGC6	09UGC6 homo sapien
29	126.5	19.8	210	11 09QZB0	09QZB0 mus musculu
30	126.5	19.8	239	11 09QZB2	09QZB2 mus musculu
31	126.5	19.8	239	11 09QZB1	09QZB1 mus musculu
32	123.5	19.3	210	13 09PMA0	09PMA0 gallus gall
33	123.5	19.3	217	4 076081	076081 homo sapien
34	123.5	19.3	218	13 09PMA1	09PMA1 gallus gall
35	123.5	19.2	271	5 09V888	09V888 drosophila
36	122	19.1	438	11 09Z2H1	09Z2H1 mus musculu
37	121.5	19.0	181	5 09TVK0	09TVK0 caenorhabd
38	115.5	18.1	108	13 09W7I6	09W7I6 gallus gall
39	115	18.0	443	4 075573	075573 homo sapien
40	112.5	17.6	244	5 096842	096842 drosophila
41	112	17.5	346	4 075577	075577 homo sapien
42	112	17.5	472	4 09Y245	09Y245 homo sapien
43	112	17.5	490	4 09Y647	09Y647 homo sapien
44	109	17.1	409	11 09Z2H2	09Z2H2 mus musculu
45	107.5	16.8	201	5 09NHP9	09NHP9 caenorhabd

ALIGNMENTS

RESULT	ID	1	PRELIMINARY:	PRT:	838 AA.
070240	070240				
AC	070240				
DT	01-AUG-1998 (TREMBLrel. 07, Created)				
DT	01-AUG-1998 (TREMBLrel. 07, Last sequence update)				
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)				
DE	AXIL.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Rattus.				
OX	NCBI_TaxID=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=98226558; PubMed=9566905;				
RA	Yamamoto H., Kishida S., Uochi T., Ikeda S., Koyama S., Asashima M.,				
RA	Kikuchi A.;				
RT	*Axil, a member of the Axin family, interacts with both glycogen				
RT	synthase kinase 3beta and beta-catenin and inhibits axis formation of				
RT	Xenopus embryos.*;				
RL	Mol. Cell. Biol. 18:2867-2875(1998).				
DR	EMBL: AF017757; AAC40089.1; -				
DR	HSSP: P49799; IAGR.				
DR	INTERPRO: IPR000342; -				
DR	INTERPRO: IPR001158; -				
DR	PFAM: PF00615; RGS; 1.				
DR	PFAM: PF00778; DIX; 1.				
DR	PRODOM: PD001580; -; 1.				
DR	PRODOM: PD003639; -; 1.				
SO	SEQUENCE 838 AA; 92947 MW; 458825C13BA07F37 CRC64;				
Query Match 100.0%; Score 639; DB 11; Length 838;					
Best local Similarity 100.0%; Pred. No. 7.7e-53;					
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	WTSLSLSLGDGDGAYLFRTLEKRCVDTLDFWFCNGFRONKMDTKTLRYAKAYKR	60		
DB	78	WTSLSLSLGDGDGAYLFRTLEKRCVDTLDFWFCNGFRONKMDTKTLRYAKAYKR	137		
QY	61	YIINNSVSVSKOLKPAATKYTRDGIKKQIGSVMEFDQOTFIQVMEENAYOVLTSDIYL	120		

DB 137 YIENNSIVSKOLKPAKTYIRBGIKKQIDSIWFDQAOTIEIOSVMEENAYOMFLTSDIYL 196

QY 121 EYV 123

DB 197 EYV 199

RESULT 5

Q9Y2T1 PRELIMINARY: PRT: 843 AA.

AC Q9Y2T1: 01-NOV-1999 (TREMBlrel. 12, Created)

DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)

DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)

DE CONDUCTIN.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxId=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99168905; PubMed=10049590;

RA Mai M., Qian C., Yokomizo A., Smith D.I., Liu W.;

RT "Cloning of the human homolog of conductin (AXIN2), a gene mapping to

chromosome 17q23-q24."

RL Genomics 55:341-344(1999).

DR HSSP; P49799; IAGR.

DR INTERPRO: IPR000342; -.

DR INTERPRO: IPR001158; -.

DR PFAM; PF00615; RGS; 1.

DR PFAM; PF00778; DIX; 1.

SQ SEQUENCE 843 AA; 93557 MW; F7B62BED6A664D CRC64;

Query Match 97.7%: Score 624; DB 4; Length 843;

Best Local Similarity 95.9%: Pred. No. 2.1e-51;

Matches 118; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 WTKSLHSLGDGDGAVLFTFLEREKCVDTLDWFACNGFRQNLKDTYLRVAKAIYKR 60

DB 78 WTKSLHSLGDGDGAVLFTFLEREKCVDTLDWFACNGFRQNLKDTYLRVAKAIYKR 137

QY 61 YIENNSIVSKOLKPAKTYIRBGIKKQIDSIWFDQAOTIEIOSVMEENAYOMFLTSDIYL 120

DB 138 YIENNSIVSKOLKPAKTYIRBGIKKQIDSIWFDQAOTIEIOSVMEENAYOMFLTSDIYL 197

QY 121 EYV 123

DB 198 EYV 200

RESULT 6

Q9YGV0 PRELIMINARY: PRT: 842 AA.

AC Q9YGV0: 01-MAY-1999 (TREMBlrel. 10, Created)

DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)

DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)

DE AXIN.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae;

OC Xenopodinae; Xenopus.

OX NCBI_TaxId=8355;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99173782; PubMed=10072781;

RA Hedgpeth C.M., Dearioff M.A., Klein P.S.;

RT "Xenopus axin interacts with glycogen synthase kinase-3 beta and is

expressed in the anterior midbrain."

RT Mech. Dev. 80:147-151(1999).

DR EMBL; AF097313; AAC71036.1; -.

DR HSSP; P49799; IAGR.

DR INTERPRO: IPR000342; -.

DR INTERPRO: IPR001158; -.

DR PFAM; PF00615; RGS; 1.

DR PFAM; PF00778; DIX; 1.

DR PRODOM; PD001580; -; 1.

DR PRODOM; PD003639; -; 1.

SQ SEQUENCE 842 AA; 94459 MW; BDA152734C97191E CRC64;

Query Match 65.7%: Score 420; DB 13; Length 842;

Best Local Similarity 61.1%: Pred. No. 5.9e-32;

Matches 77; Conservative 25; Mismatches 20; Indels 4; Gaps 2;

QY 1 WTKSLHSLGDGDGAVLFTFLEREKCVDTLDWFACNGFRQNLKDTYLRVAKAI 57

DB 85 WTKSLHSLGDGDGAVLFTFLEREKCVDTLDWFACNGFRQNLKDTYLRVAKAI 144

QY 58 YKRYT-ENNSVSKOLKPAKTYIRBGIKKQIDSIWFDQAOTIEIOSVMEENAYOMFLTSDIYL 116

DB 145 YKRYT-ENNSVSKOLKPAKTYIRBGIKKQIDSIWFDQAOTIEIOSVMEENAYOMFLTSDIYL 204

QY 117 DITLEY 122

DB 205 DITLEY 210

RESULT 7

Q7O239 PRELIMINARY: PRT: 832 AA.

AC Q7O239: 01-AUG-1998 (TREMBlrel. 07, Created)

DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)

DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)

DE RAXIN.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxId=10116;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98151361; PubMed=9482734;

RA Ikeda S., Yamamoto H., Murai H., Kishida S., Kikuchi A.;

RT "Axin, a negative regulator of the Wnt signaling pathway, forms a

complex with GSK-3beta and beta-catenin and promotes GSK-3beta-

dependent phosphorylation of beta-catenin."

RL EMBL; AF017756; AAC40066.1; -.

DR HSSP; P49799; IAGR.

DR INTERPRO: IPR000342; -.

DR INTERPRO: IPR001158; -.

DR PFAM; PF00615; RGS; 1.

DR PFAM; PF00778; DIX; 1.

DR PRODOM; PD001580; -; 1.

DR PRODOM; PD003639; -; 1.

SQ SEQUENCE 832 AA; 92856 MW; B489504C7B594347 CRC64;

Query Match 63.7%: Score 407; DB 11; Length 832;

Best Local Similarity 61.9%: Pred. No. 1e-30; 23; Indels 4; Gaps 2;

Matches 78; Conservative 21; Mismatches 23; Indels 4; Gaps 2;

QY 1 WTKSLHSLGDGDGAVLFTFLEREKCVDTLDWFACNGFRQNLKDTYLRVAKAI 57

DB 90 WTKSLHSLGDGDGAVLFTFLEREKCVDTLDWFACNGFRQNLKDTYLRVAKAI 149

QY 58 YKRYT-ENNSVSKOLKPAKTYIRBGIKKQIDSIWFDQAOTIEIOSVMEENAYOMFLTSDIYL 116

DB 150 YKRYT-ENNSVSKOLKPAKTYIRBGIKKQIDSIWFDQAOTIEIOSVMEENAYOMFLTSDIYL 209

QY 117 DITLEY 122

DB 205 DITLEY 210

RA Reif K., Cyster J.G.;
RT "RGS molecule expression in murine B lymphocytes and ability to down-
RT regulate chemotaxis to lymphoid chemokines.";
RL J. Immunol. 164:4720-4723(2000).
DR EMBL: AF215670; AAF34627.1; -
FT NON_TER 1
SO SEQUENCE 297 AA; 33683 MW; ADF80985150B525C CRC64;

Query Match 26.2%; Score 167.5; DB 11; Length 297;
Best Local Similarity 31.7%; Pred. No. 2.2e-08;
Matches 39; Conservative 26; Mismatches 55; Indels 3; Gaps 2;

OY 1 WTKSLHSLIGDGDGAYLRFLEKREKCVDTLDFWACNGFRQNLKDTKTLRVAKAIYKR 60
DB 169 WSESLKLLHKGLEVFQAFRTFEESENELEFWLACEDFKRK-SQSKMAKAKKIFAE 227
OY 61 YIENNSVSVSKQKPKATKYIRDGIRKQKQIGSVMPDQOTEIOAVMENAYOVFLTSDIYL 120
DB 228 FTAIOACEKVNLDSTYREHTKENTL--QSTTRGCFDLAQRIFGLMKDSTYPRFLRSDIYL 285
OY 121 EKV 123
DB 286 DLI 288

RESULT 15

O9JHXO PRELIMINARY; PRT: 211 AA.

AC 09JHXO;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE REGULATOR OF G-PROTEIN SIGNALING PROTEIN 2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE DAWLEY; TISSUE=THORACIC AORTA SMOOTH MUSCLE;
RA Grant S.L., Lasegue B., Griending K.K.;
RT "RGS2 regulates angiotensin II signaling in vascular smooth muscle.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF279918; AAF85981.1; -
SO SEQUENCE 211 AA; 24323 MW; 84B5525CB41EA964 CRC64;

Query Match 26.1%; Score 166.5; DB 11; Length 211;
Best Local Similarity 32.8%; Pred. No. 1.8e-08;
Matches 39; Conservative 19; Mismatches 58; Indels 3; Gaps 2;

OY 1 WTKSLHSLIGDGDGAYLRFLEKREKCVDTLDFWACNGFRQNLKDTKTLRVAKAIYKR 60
DB 80 WEAEDELLASRYGLAARAFILKSECEENLEFWLACEDFKRK-SPQKLSKARKIYTD 138
OY 61 YIENNSVSVSKQKPKATKYIRDGIRKQKQIGSVMPDQOTEIOAVMENAYOVFLTSDIYL 119
DB 139 FIEKEAPKEINIDFQTKLIAONT--QDATSCFTYAKRKVYSIMENSYPRFLESERY 195

Search completed: June 7, 2001, 02:09:39
Job time: 442 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 7, 2001, 02:01:15 ; Search time 80.96 Seconds
(without alignments)
38.128 Million cell updates/sec

Title: US-09-587-574-3
Sequence: 1 ANGVSLPHPRTRHRLPKEM.....RLEKIKLELSRHSLEERLQ 54

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues
Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : A_Geneseq_0401.*
1: /SID52/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID52/gcgdata/geneseq/geneseq/AA1981.DAT.*
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8: /SID52/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SID52/gcgdata/geneseq/geneseq/AA1988.DAT.*
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11: /SID52/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SID52/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SID52/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SID52/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SID52/gcgdata/geneseq/geneseq/AA1994.DAT.*
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21: /SID52/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID52/gcgdata/geneseq/geneseq/AA2001.DAT.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	272	100.0	840	20	W93570 Human conductin pr
2	272	100.0	840	20	W93569 Human conductin pr
3	142.5	52.4	992	20	W96265 Mus
4	141.5	52.0	900	20	W96264 Human axin. Homo
5	65	23.9	462	16	R78230 Candida antarctica
6	65	23.9	463	15	R48084 C. antarctica lipas
7	61.5	22.6	995	20	Y04658 L.lactis Hsdr subu
8	58	21.3	1816	21	Y95440 Caenorhabditis ele
9	57	21.0	115	21	B27999 Human secreted pro
10	57	21.0	260	21	G56044 Arabidopsis thalia
11	57	21.0	260	21	G61383 Arabidopsis thalia

12	57	21.0	306	21	G56043 Arabidopsis thalia
13	57	21.0	306	21	G61382 Arabidopsis thalia
14	57	21.0	321	21	G56042 Arabidopsis thalia
15	57	21.0	321	21	G61381 Arabidopsis thalia
16	56.5	20.8	534	17	R91309 Fungal signal reco
17	56.5	20.8	535	17	R91310 Fungal signal reco
18	56	20.6	349	19	W78102 Chimeric receptor
19	55	20.2	856	21	B40894 Human ORF ORF658
20	54.5	20.0	398	19	W98441 H. pylori GHPO 511
21	54	19.9	578	18	W10422 Penicillium chryso
22	53.5	19.7	267	21	B42487 Human ORF ORF2251
23	53.5	19.7	439	20	W88235 Human prothrombina
24	53.5	19.7	626	20	Y06292 Human transcriptio
25	53.5	19.7	824	19	W68093 Human neuronal PAs
26	53	19.5	347	17	W05394 Mouse SH3p13 prote
27	53	19.5	406	20	Y31719 Human fibronogen d
28	53	19.5	406	20	Y23627 A human growth fac
29	53	19.5	406	20	Y05393 Human TIE ligand N
30	53	19.5	406	21	B28212 Novel TIE ligand N
31	53	19.5	406	21	B12426 Human TIE ligand N
32	53	19.5	406	21	Y54496 Human muscle angio
33	53	19.5	406	21	Y86289 Human secreted pro
34	53	19.5	453	22	B53070 Human angiogenesis
35	53	19.5	758	21	B11540 SEN virus protein
36	53	19.5	900	17	R88615 TNF-R p55IC-Bindin
37	53	19.5	908	18	W15473 Human P100 protein
38	53	19.5	1257	20	Y06427 Mouse circadian re
39	52.5	19.3	1047	18	W01535 Cellular homologue
40	52	19.1	422	14	R39819 ZMPK1 homologue pr
41	52	19.1	478	20	W92950 WO9905287 Seq ID 1
42	52	19.1	722	19	W55104 Streptococcus pneu
43	52	19.1	803	21	B00066 KIAA0160 polypepti
44	52	19.1	2234	21	Y81502 Streptococcus pneu
45	51.5	18.9	149	14	R39358 rzpp.149. Sus scr

ALIGNMENTS

RESULT 1	
W93570	W93570 standard; Protein: 840 AA.
XX	
AC	W93570;
XX	
DT	17-JUN-1999 (first entry)
XX	
DE	Human conductin protein.
XX	
KW	Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour;
KW	therapy: cytoplasmic degradation; blockade; Wnt signalling pathway;
KW	Wingless signalling pathway; Adenomatous Polyposis Coll.; APC;
KW	tumour suppressor.
XX	
OS	Homo sapiens.
XX	
PN	W09911780-A2.
XX	
PD	11-MAR-1999.
XX	
PF	01-SEP-1998; 98MO-DE02621.
XX	
PR	02-SEP-1997; 97DE-1038205.
XX	
PA	(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX	
PI	Behrens J, Birchmeier W;
XX	
DR	WPI: 1999-214706/18.
XX	
PT	N-PSDB; X23370.
XX	
PT	Tumor-suppressing protein conductin - used for treatment and diagnosis of tumors

XX Claim 11; Fig 3; 22pp; German.
PS
CC This invention describes a novel human conductin protein which has
CC anti-tumour activity. Detecting the presence or amount of conductin,
CC at protein or nucleic acid levels, is used to diagnose tumours, while
CC agents that (re)activate conductin are used for tumour therapy.
CC Conductin binds to beta-catenin and induces its cytoplasmic degradation,
CC resulting in blockade of the Wnt/Wingless signalling pathway in
CC vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC)
CC fragments and, in conjunction with APC, acts as a tumour suppressor.
XX
SQ Sequence 840 AA:

Query Match 100.0%; Score 272; DB 20; Length 840;
Best Local Similarity 100.0%; Pred. No. 4.9e-25;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ANGOVSLPHFPRTTRLPKEMTPVEPAFAFAELISRLKIKLESLERHSLEERLQ 54
|||||
Db 343 angvslphfprthrlpkemtpvepaafaelsrlkiklesrhsleerlq 396

RESULT 2
ID W93569 standard; Protein; 840 AA.
XX W93569;
AC
XX 17-JUN-1999 (first entry)
DT
XX
DE Human conductin protein.
XX
KW Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour;
KW therapy; cytoplasmic degradation; blockade; wnt signalling pathway;
KW Wingless signalling pathway; Adenomatous Polyposis Coli; APC;
KW tumour suppressor.
XX
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT Domain /note= "Regulator of G protein signalling domain as
FT described in claim 12"
FT Binding-site 343..396
FT /note= "GSK-3-beta binding region as described in
FT claim 13"
FT Binding-site 397..465
FT /note= "Beta-catenin binding domain as described in
FT claim 14"
FT Region 783..833
FT /note= "Dishevelled homology region as described in
FT claim 15"
FT
FT
XX WO9911780-A2.
XX
XX 11-MAR-1999.
XX
XX 01-SEP-1998; 98WO-DE02621.
XX
XX 02-SEP-1997; 97DE-1038205.
XX
XX (DELB-) DELBRUECK CENT MOLKULARE MEDIZIN MAX.
XX
XX Behrens J, Birchmeier W;
XX
XX WPI; 1999-214706/18.
XX
XX N-PSDB; X23369.
XX
XX Tumour-suppressing protein conductin - used for treatment and
XX diagnosis of tumors
XX

PS Claim 11; Fig 1; 22pp; German.
XX
CC This invention describes a novel human conductin protein which has
CC anti-tumour activity. Detecting the presence or amount of conductin,
CC at protein or nucleic acid levels, is used to diagnose tumours, while
CC agents that (re)activate conductin are used for tumour therapy.
CC Conductin binds to beta-catenin and induces its cytoplasmic degradation,
CC resulting in blockade of the Wnt/Wingless signalling pathway in
CC vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC)
CC fragments and, in conjunction with APC, acts as a tumour suppressor.
XX
SQ Sequence 840 AA:

Query Match 100.0%; Score 272; DB 20; Length 840;
Best Local Similarity 100.0%; Pred. No. 4.9e-25;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ANGOVSLPHFPRTTRLPKEMTPVEPAFAFAELISRLKIKLESLERHSLEERLQ 54
|||||
Db 343 angvslphfprthrlpkemtpvepaafaelsrlkiklesrhsleerlq 396

RESULT 3
ID W96265 standard; Protein; 992 AA.
XX W96265;
AC
XX 14-JUN-1999 (first entry)
DT
XX
DE Murine axlin.
XX
KW Axlin; cancer; breast cancer; colorectal cancer;
KW gastrointestinal cancer; esophageal cancer; carcinoma; melanoma;
KW diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;
KW beta-catenin.
XX
XX Mus musculus.
OS
XX
XX WO9902179-A1.
XX
XX 21-JAN-1999.
XX
XX 09-JUL-1998; 98WO-US14414.
XX
XX 10-JUL-1997; 97US-0890865.
XX
XX (UYCO) UNIV COLUMBIA NEW YORK.
XX
XX Constantini F, Zeng L;
XX
XX WPI; 1999-120510/10.
XX
XX N-PSDB; X09013.
XX
XX Newly isolated nucleic acid encoding "axis inhibition" protein
XX (Axin) - useful for detecting, diagnosing and treating cancer
XX
XX Claim 8; Figure 8; 95pp; English.
XX
XX Nucleic acids encoding mutant and wild type Axin and
XX oligonucleotides derived from them are useful for detecting
XX mutations in the Axin gene and for determining whether a subject is
XX likely to develop cancer (including breast, colorectal,
XX gastrointestinal, esophageal, carcinomas or melanomas). The wild
XX type Axin and homologues of Axin are useful for treating subjects
XX who are likely to develop cancer (thyroid carcinomas). The nucleic
XX acids are also useful for diagnosing cancer and for detecting
XX mutations in cancerous cells. Wild type Axin, its antisense
XX molecule and identified compounds form pharmaceutical compositions
XX in the treatment of cancer. The compositions are also useful for
XX treating cancer by inhibiting tumorigenesis (by inducing degradation
XX of beta-catenin). The nucleic acid encoding Axin acts through
XX

OY 1 ANGOVSLPHFPR--THRLPKEMTPVEPA 27
 | : | | | | | : | | | : | | |
 DB 336 asytsvypkpfiflwhalpdelpvypgaa 364

RESULT 6
 ID R48084 standard; Protein; 463 AA.
 XX R48084;
 AC R48084;

DT 19-JUL-1994 (first entry)
 XX
 DE C. antarctica lipase A.

XX Lipase A; thermostability; specific activity; mechanical pulp;
 KW ester hydrolysis; ester synthesis; interesterification; acid pH;
 KM pitch; paper-making; detergent; digestive enzyme; cystic fibrosis.
 XX

OS Candida antarctica.

PN WO9401541-A.

PD 20-JAN-1994.

PF 05-JUL-1993; 93WO-DK00225.

PR 06-JUL-1992; 92DK-0000888.

PA (NOVO) NOVO-NORDISK AS.

PI Borch K, Clausen G, Egel-Mitani M, Hansen M, Pathar S;
 PI Svendsen A;

XX WPI: 1994-035050/04.

DR N-PSDB; 055463.

XX New lipase variants, partic. from Candida antarctica - have amino acid
 PT substitutions to increase specific activity against substrates
 PT compared to parent lipase(s)

PS Claim 15; Page 39-40; 60pp; English.

XX This sequence represents the C. antarctica lipase A protein. This
 CC lipase has high thermostability and is active at acid pH. A variant
 CC of the mature lipase A in which phe139 has been replaced by a Trp
 CC residue has increased specific activity compared to the parent
 CC lipase. The lipase or variant may be used in ester hydrolysis,
 CC ester synthesis or interesterification. They can also be used for
 CC avoiding pitch trouble in the process for the production of
 CC mechanical pulp or a paper-making process using mechanical pulp.
 CC They can also be used in detergents or as a digestive enzyme, eg. in
 CC the treatment of cystic fibrosis.

XX Sequence 463 AA;
 SQ

Query Match 23.9%; Score 65; DB 15; Length 463;
 Best Local Similarity 48.3%; Pred. No. 4.9;

Matches 14; Conservative 5; Mismatches 8; Indels 2; Gaps 1;

OY 1 ANGOVSLPHFPR--THRLPKEMTPVEPA 27
 | : | | | | | : | | | : | | |
 DB 336 asytsvypkpfiflwhalpdelpvypgaa 364

RESULT 7
 ID Y04658 standard; Protein; 995 AA.
 XX Y04658;
 AC Y04658;
 XX

DT 22-JUN-1999 (first entry)

XX L.lactis HsdR subunit #1.

DE HsdR; HsdM; HsdS; restriction/modification; bacteriophage; resistance;
 KW lactic acid bacterium.
 XX Lactococcus lactis.

XX FR2767831-A1.

PN 05-MAR-1999.

PD 02-SEP-1997; 97FR-0010885.

PF 02-SEP-1997; 97FR-0010885.

PR (INRG) INRA INST NAT RECH AGRONOMIQUE.

PA Chopin MC, Clier F, Ehrlich SD, Gautier M, Schouler C;
 PI Chopin MC, Clier F, Ehrlich SD, Gautier M, Schouler C;

XX WPI: 1999-183265/16.

DR N-PSDB; X29768.

XX Bacteriophage resistance mechanism subunit polypeptides - of lactic
 PT acid bacteria, especially Lactococcus lactis

PS Claim 3; Page 18-22; 65pp; French.

XX The invention relates to polypeptides that constitute the HsdR, HsdM or
 CC HsdS subunit of a R/M [restriction/modification] type Ic bacteriophage
 CC resistance mechanism active against the phages of lactic acid bacteria,
 CC especially Lactococcus lactis. This sequence represents the Lactococcus
 CC lactic HsdR subunit. Nucleic acids encoding the HsdR, HsdM or HsdS
 CC fragment can be used for expression of at least one bacteriophage
 CC resistance mechanism in a lactic acid bacterium.

XX Sequence 995 AA;
 SQ

Query Match 22.6%; Score 61.5; DB 20; Length 995;
 Best Local Similarity 29.6%; Pred. No. 31;

Matches 16; Conservative 17; Mismatches 10; Indels 11; Gaps 3;

OY 11 PTHRLPKEMTPV--EPAAFAELISRLK-----LKLLEBSRSLERLQ 54
 | : | : | | | | | | | | | | : | | | : | | | : | : |
 DB 732 pqsnglpr-lpavgelkafagedtsqprgeklkgfvtlgtqnglqg 784

RESULT 8
 ID Y95440 standard; Protein; 1816 AA.
 XX Y95440;
 AC Y95440;

XX 10-OCT-2000 (first entry)
 DT
 DE Caenorhabditis elegans polypeptide at the c05c12.3 locus.

XX SOC/CRAC; calcium channel; store operated channel;
 KW calcium release activated channel; therapy; diagnosis;
 KW lymphocyte proliferative disorder.

XX Caenorhabditis elegans.

OS WO2000040614-A2.

PN 13-JUL-2000.

PD 20-DEC-1999; 99WO-US29996.

PF 30-DEC-1998; 98US-0114220.

PR 29-JAN-1999; 99US-0120018.

PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139452.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
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PR 19-JUL-1999; 99US-0144333.
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PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 22-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 21.0%; Score 57; DB 21; Length 321;
Best Local Similarity 37.5%; Pred. No. 30;

Matches 15; Conservative 10; Mismatches 11; Indels 4; Gaps 2;

Oy 17 PKEMTPVEPPAFA--AAELISRLKLELSEGRHSLEERLQ 54
Db 102 pkelipdpasypnpyaylwkie--dipeerthlllqile 139

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OW protein - protein search, using sw model

Run on: June 7, 2001, 02:02:09 ; Search time 40.76 Seconds
(without alignments)
25.451 Million cell updates/sec

Title: US-09-587-574-3

Perfect score: 272
Sequence: 1 ANGOVSLPFRPHRLPKEM.....RLKKLKLKLESLRRRLQ 54

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*
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5: /cgn2_6/ptodata/2/1aa/PCITUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	23.9	462	1	US-08-458-023B-2
2	65	23.9	463	3	US-09-111-556A-2
3	65	23.9	463	3	US-08-360-758-2
4	56.5	20.8	534	2	US-08-317-401E-2
5	56.5	20.8	552	2	US-08-317-401E-4
6	56	20.6	2584	3	US-08-936-135-4
7	56	20.6	2588	3	US-08-936-135-2
8	53.5	19.7	824	2	US-08-785-310A-7
9	53.5	19.7	824	2	US-08-816-693A-52
10	53.5	19.7	824	3	US-08-885-291-52
11	53	19.5	406	3	US-08-934-494-2
12	53	19.5	406	3	US-09-143-068-2
13	53	19.5	853	3	US-08-699-103B-10
14	53	19.5	908	3	US-08-699-103B-12
15	53	19.5	1257	4	US-09-220-641-3
16	53	19.5	3218	1	US-08-764-100-27
17	52.5	19.3	338	2	US-09-004-502-5
18	52	19.1	722	4	US-08-961-083-84
19	51.5	18.9	576	2	US-08-533-306A-2
20	51.5	18.9	576	2	US-08-742-923A-2
21	51.5	18.9	1358	1	US-08-404-665-4
22	51.5	18.9	1358	1	US-08-404-667-4
23	51.5	18.9	1358	1	US-08-404-781-4
24	51	18.8	346	3	US-08-960-507-19
25	51	18.8	347	3	US-09-004-502-1
26	50.5	18.6	477	4	US-08-704-711A-20
27	50.5	18.6	477	4	US-08-448-489-15

28	50.5	18.6	2089	1	US-08-418-893D-23	Sequence 23, Appl
29	50.5	18.6	2089	1	US-08-418-893D-24	Sequence 24, Appl
30	50	18.4	396	1	US-08-769-309A-15	Sequence 15, Appl
31	50	18.4	396	3	US-08-994-570-15	Sequence 15, Appl
32	50	18.4	446	2	US-08-748-947A-2	Sequence 2, Appl
33	50	18.4	453	1	US-08-769-309A-14	Sequence 14, Appl
34	50	18.4	453	3	US-08-994-570-14	Sequence 14, Appl
35	50	18.4	624	2	US-08-756-317-9	Sequence 9, Appl
36	50	18.4	651	1	US-08-769-309A-17	Sequence 17, Appl
37	50	18.4	651	3	US-08-994-570-17	Sequence 17, Appl
38	50	18.4	673	4	US-09-078-347A-2	Sequence 2, Appl
39	50	18.4	1780	1	US-08-769-309A-5	Sequence 5, Appl
40	50	18.4	1780	3	US-08-994-570-5	Sequence 5, Appl
41	49.5	18.2	140	6	5164490-8	Patent No. 5164490
42	49.5	18.2	196	5	PCIT-US91-09055-5	Sequence 5, Appl
43	49.5	18.2	226	3	US-08-966-318-1	Sequence 1, Appl
44	49.5	18.2	226	4	US-09-216-619-1	Sequence 1, Appl
45	49.5	18.2	739	2	US-08-836-943-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-458-023B-2
; Sequence 2, Application US/08458023B
; Patent No. 5667990
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Yoder, Wendy
; APPLICANT: Takagi, Shinobu
; APPLICANT: Booninathan, Karuppan C.
; TITLE OF INVENTION: ASPERGILLUS EXPRESSION SYSTEM
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 56679900 No. 5667990disk of No. 5667990th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,023B
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney Dr., Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4086,010-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 462 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-458-023B-2

Query Match 23.9% Score 65; DB 1; Length 462;
Best Local Similarity 48.3%; Pred. No. 1.6;
Matches 14; Conservative 5; Mismatches 8; Indels 2; Gaps 1;
Oy 1 ANGOVSLPFRPHRLPKEMTPVEPAA 27
Db 336 ASYTVSVPRFPRIMHAIIDELIVQDPA 364

CORRESPONDENCE ADDRESS:
ADDRESSEE: NO. 60748630 No. 6074863disk of No. 6074863th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,758
FILING DATE: 22-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK PCT/DK93/00225
FILING DATE: 03-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Landitis, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3748, 204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-360-758-2

Query Match 23.9%; Score 65; DB 3; Length 463;
Best Local Similarity 48.3%; Pred. No. 1.6;
Matches 14; Conservative 5; Mismatches 8; Indels 2; Gaps 1;

OY 1 LANGVSLPFRP--THRLPKENTPEPPAA 27
|: ||: ||| | : ||: | : |||
Db 336 ASYYSVKFPRFWHATPDELVPYQPAA 364

RESULT 4
US-08-317-401E-2
Sequence 2, Application US/08317401E
Patent No. 5922561
GENERAL INFORMATION:
APPLICANT: Thompson, Sheryl Ann
APPLICANT: Yaver, Debbie Sue
TITLE OF INVENTION: GENES ENCODING SIGNAL RECOGNITION PARTICLE OF
TITLE OF INVENTION: ASPERGILLUS NIGER
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: NO. 59225610 No. 5922561disk of No. 5922561th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,401E
FILING DATE: 03-October-1994
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711

REFERENCE/DOCKET NUMBER: 4248-000-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 534 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Aspergillus niger
US-08-317-401E-2

Query Match 20.8%; Score 56.5; DB 2; Length 534;
Best Local Similarity 33.3%; Pred. No. 21;
Matches 13; Conservative 8; Mismatches 13; Indels 5; Gaps 1;

OY 20 MTPVEPAFAAEILSRLEKLEL-----ESRHSLEERL 53
DB 164 LTQTDPAIVAAEGVAKFKRERETIIIVDTSGRHKQEEEL 202

RESULT 5
US-08-317-401E-4
Sequence 4, Application US/08317401E
Patent No. 5922561
GENERAL INFORMATION:

APPLICANT: Thompson, Sheryl Ann
TITLE OF INVENTION: GENES ENCODING SIGNAL RECOGNITION PARTICLE OF
TITLE OF INVENTION: ASPERGILLUS NIGER
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 59225610 No. 59225610 of No. 59225610 America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08317.401E
FILING DATE: 03-October-1994
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 4248-000-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Aspergillus niger
US-08-317-401E-4

Query Match 20.8%; Score 56.5; DB 2; Length 552;
Best Local Similarity 33.3%; Pred. No. 22;
Matches 13; Conservative 8; Mismatches 13; Indels 5; Gaps 1;

OY 20 MTPVEPAFAAEILSRLEKLEL-----ESRHSLEERL 53
DB 160 LTQTDPAIVAAEGVAKFKRERETIIIVDTSGRHKQEEEL 218

RESULT 6
US-08-936-135-4
Sequence 4, Application US/08936135
Patent No. 6054293
GENERAL INFORMATION:

APPLICANT: Tessier-Lavigne, Marc
APPLICANT: He, Zhigang
TITLE OF INVENTION: Semaphorin Receptors
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94010

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,135
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 0097-288-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2584 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-936-135-4

Query Match 20.6%; Score 56; DB 3; Length 2584;
Best Local Similarity 47.8%; Pred. No. 1.5e+02;
Matches 11; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

OY 2 NCQVSLPFPRTTRLPKENTPVE 24
DB 1790 NSERGLPHEPRTTRRYRGLYPHE 1812

RESULT 7
US-08-936-135-2
Sequence 2, Application US/08936135
Patent No. 6054293
GENERAL INFORMATION:

APPLICANT: Tessier-Lavigne, Marc
APPLICANT: He, Zhigang
TITLE OF INVENTION: Semaphorin Receptors
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA

Query Match 20.8%; Score 56.5; DB 2; Length 552;
Best Local Similarity 33.3%; Pred. No. 22;
Matches 13; Conservative 8; Mismatches 13; Indels 5; Gaps 1;

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: ZIP: 94010
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/936,135
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: OSMAN, RICHARD A
: REGISTRATION NUMBER: 36,627
: REFERENCE/DOCKET NUMBER: UC97-288-2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (650) 343-4341
: TELEFAX: (650) 343-4342
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2588 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-936-135-2

Query Match 20.6%; Score 56; DB 3; Length 2588;
Best Local Similarity 47.8%; Pred. NO. 1.5e+02;
Matches 11; Conservative 3; Mismatches 9; Indels 0; Gaps 0.

OY 2 NGVSLPHFPRTHRLKEMTPVE 24
db 1792 NSERGLPHEPRTHRLKGLYPHE 1814

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RESULT      8
US-08-785-310A-7
: Sequence 7, Application US/08785310A
: Patent No. 5840532
: GENERAL INFORMATION:
: APPLICANT: McKNIGHT, Steven L.
: APPLICANT: Russell, David W.
: TITLE OF INVENTION: Neuronal PAS Domain Protein
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
: STREET: 266 BUSH STREET, SUITE 3200
: CITY: SAN FRANCISCO
: STATE: CALIFORNIA
: COUNTRY: USA
: ZIP: 94104
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/785,310A
: FILING DATE: 21-JAN-1997
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: OSMAN, RICHARD A
: REGISTRATION NUMBER: 36,627
: REFERENCE/DOCKET NUMBER: UTSD:1226
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 343-4341
: TELEFAX: (415) 343-4342
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 824 amino acids
: TYPE: amino acid
: STRANDEDNESS: single

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;      TOPOLOGY: linear
;      MOLECULE TYPE: peptide
US-08-785-310A-7
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Query Match	19.7%;	Score 53.5;	DB 2;	Length 824;
Best Local Similarity	20.0%;	Pred. No. 84;		
Matches	20;	Conservative	12;	Mismatches 17;
				Indels 51;
				Gaps 3;

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QY      4  QVSLPSPHPTRIPLKEM-----TPVPPAAF 28
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Db      436 EASTPALPRSTATQPELPVPGLSAATMPAPLPSPGLSCDITQOOLLPTVLTQSTPAPMAOF 495
QY      29  AAEILSRLEKLELSESR-----HSLERL 53
      : | : | : | | | | | : | | : |
Db      496 SAQ-FSMQITKDQLEQRTIRLIANIRMQDEELHKIOEOL 534

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RESULT 9
US-08-816-693A-52
; Sequence 52, Application US/08816693A

: APPLICANT: Takahashi, Joseph S
 : APPLICANT: Turek, Fred W
 : APPLICANT: Pinto, Lawrence H
 : TITLE OF INVENTION: Clock Gene and Gene Product
 : NUMBER OF SEQUENCES: 53
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Dressler, Rocky, Milnamow & Katz
 : STREET: Two Prudential Plaza, Suite 4700

STATE: Illinois
COUNTRY: USA
ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US
APPLICATION NUMBER: 05/08/816,693A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5874241thrup, Thomas E
REGISTRATION NUMBER: 33,268
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 824 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
OS-08-816-693A-52

Query Match	19.7%;	Score 53.5;	DB 2;	Length 824;
Best Local Similarity	20.0%;	Pred. No. 84;		
Matches	20;	Mismatches	17;	Gaps 3

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QY      4 QVSLPHFPPRTHRLPKEM-----TPVERAAF 28
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Db    436 EASIPALPKRATLPQGLPVPGLSQATMPAPLPLSPLSCDLTQQLLPQTVLQSTPAPMAQF 495

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QY      29 AAELISRLKLEKLEES-----HSLERL 53
      :|: | : : | | | | | | | | | |
Db      496 SAQ-FNSFQITDQLEQRTILQANIRMQQEEIHKIQQL 534

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2001, 02:03:20 ; Search time 56.43 Seconds

(without alignments)
65.764 Million cell updates/sec

Title: US-09-587-574-3

Perfect score: 272

Sequence: 1 ANGVSLPHPRTRHRLPKEM.....RLKLESLRSLERLQ 54

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database :

PIR 67: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	272	100.0	838	2	T08423	Axin homolog Ax11
2	142.5	52.4	832	2	T08422	negative regulator
3	64.5	23.7	268	2	C83442	hypothetical prote
4	63	23.2	141	2	D69857	conserved hypothet
5	62.5	23.0	251	2	T12864	probable antitrepre
6	62	22.8	333	2	C48423	homeotic protein e
7	61.5	22.6	539	2	S55190	hypothetical prote
8	60	22.1	377	2	T46149	protein kinase ATN
9	59.5	21.9	369	2	S56638	mitogen-activated
10	59.5	21.9	964	2	E70826	probable membrane
11	59.5	21.9	7862	2	T38346	elastic titin - hu
12	59	21.7	231	2	S30438	homeotic protein e
13	58.5	21.5	601	2	A82461	hypothetical prote
14	58.5	21.5	725	2	T19994	hypothetical prote
15	58	21.3	171	2	S35638	homeotic protein E
16	58	21.3	1707	2	T18951	hypothetical prote
17	57.5	21.1	254	2	D70406	DMSO reductase cha
18	57.5	21.1	978	2	A70387	conserved hypothet
19	57	21.0	392	2	B48423	homeotic protein e
20	57	21.0	401	2	A48423	engrailed homeodom
21	57	21.0	722	2	T26297	hypothetical prote
22	56.5	20.8	526	2	T39748	probable ser/thr p
23	56.5	20.8	534	2	UC4572	signal recognition
24	56	20.6	261	1	S30437	homeotic protein e
25	56	20.6	489	1	SYBS85	glutamate--tRNA 11
26	56	20.6	501	2	T39801	hypothetical sh3-c
27	56	20.6	545	2	C83379	probable dehydroge
28	56	20.6	840	2	D82615	hypothetical prote
29	56	20.6	1258	2	D75453	5-methyltetrahydro

30	55.5	20.4	349	2	S32040	homeotic protein e
31	55.5	20.4	1325	2	S16129	dynlein-associated
32	55.5	20.4	1364	2	T40839	hypothetical prote
33	55	20.2	239	2	T02984	myb-related prote
34	55	20.2	416	2	T30946	hypothetical prote
35	55	20.2	1553	2	T09361	hypothetical prote
36	54.5	20.0	312	2	C71136	hypothetical prote
37	54.5	20.0	324	2	S44956	lmbi protein - str
38	54.5	20.0	370	2	C64645	hypothetical prote
39	54.5	20.0	510	2	PC4054	cardiac C-protein
40	54.5	20.0	662	2	I36792	hypothetical prote
41	54.5	20.0	1063	2	T03743	bifocal protein -
42	54	19.9	375	2	T01468	hypothetical prote
43	54	19.9	591	2	F82234	aspartyl-tRNA synt
44	54	19.9	602	2	T29386	hypothetical prote
45	53.5	19.7	183	2	D81296	hypothetical prote

ALIGNMENTS

RESULT 1
T08423
Axin homolog Ax11 - rat
N:Alternate names: Ax11
C:Species: Rattus norvegicus (Norway rat)
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jul-2000
C:Accession: T08423
R:Yamamoto, H.; Kishida, S.; Uochi, T.; Ikeda, S.; Koyama, S.; Asashima, M.; Kikuchi, M.; Cell. Biol. 18, 2867-2875, 1998
A:Title: Ax11, a member of the Axin family, interacts with both glycogen synthase kin
A:Reference number: T08423
A:Accession: T08423
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-838 <YAM>
A:Cross-references: EMBL:AF017757; NID:g3080758; PIDN:AC40089.1; PID:g3080759
A:Note: Interacts with GSK-3beta and beta-catenin
C:Keywords: phosphoprotein; signal transduction

Query Match 100.0%; Score 272; DB 2; Length 838;
Best Local Similarity 100.0%; Pred. No. 7.1e-24;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ANGVSLPHPRTRHRLPKEMTPVPPAFALISRLKLESLRSLERLQ 54
|||||
Db 343 ANGVSLPHPRTRHRLPKEMTPVPPAFALISRLKLESLRSLERLQ 396

RESULT 2
T08422
negative regulator axin [Imported] - rat
N:Alternate names: rAxin
C:Species: Rattus norvegicus (Norway rat)
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jul-2000
C:Accession: T08422
R:Ikeda, S.; Yamamoto, H.; Mural, H.; Kishida, S.; Kikuchi, A.
EMBO J. 17, 1371-1384, 1998
A:Title: Axin, a negative regulator of the Wnt signaling pathway, forms a complex wit
A:Reference number: Z16413; MIMD:98151361
A:Accession: T08422
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-832 <IKE>
A:Cross-references: EMBL:AF017756; NID:g2982197; PIDN:AC40066.1; PID:g2982198
A:Note: GSK-3beta interacting protein
C:Keywords: phosphoprotein; signal transduction

Query Match 52.4%; Score 142.5; DB 2; Length 832;
Best Local Similarity 56.6%; Pred. No. 9.2e-09;
Matches 30; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

```

Oy      2 NGVGSLLPFRHTRLPKEMTPVEPPAAFAELISLREKLTAEASHSHSEPTLO 54
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      368 NGRVPLPHIPTTYMPKEIR-VEPOKFAEELIHLRLLEAVQRTREAERKLEERLK 419

RESULT      3
C83442
Hypothetical protein PA1624 [Imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: C83442
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Laribig, K.; Lim, J.; Loiy, S.; Olson, M.V.
Nature 406, 959-964, 2000
A>Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A:Reference number: A82950; MUID:20437337
A:Accession: C83442
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-268 <STO>
A:Cross-references: GB:AE004590; GB:AE004091; MID:g9947587; PIDN:AAG05013.1; GSPDB:GN001
A:Experimental source: strain PA01
A:Genetics:
A:Gene: PA1624

Query Match      23.7%; Score 64.5; DB 2; Length 268;
Best Local Similarity 32.1%; Pred. No. 3.3;
Matches 18; Conservative 9; Mismatches 14; Indels 15; Gaps 2;

Oy      1 ANGVSLLPFRHTRLPKEMTPVEPPAAFAELISLREKLT---KLEESRSLEER 52
        |||::|| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      195 ANGELITLSH-----VPAPAGSMLEILVTRTLRLDTGVRVELSGKAQENR 239

RESULT      4
D69857
Conserved hypothetical protein yk1A - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C:Accession: D69857
R:Kunst, F.; Ogawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertet, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capiano, V.; Carter, N.M.; Chaitin, E.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Furuta, S.; Galizzi, A.; Gallenbach, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holtsappel, S.; Hosono, S.; Huilo, M.F.; Jeck, T.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Koetter, P.; Konigstein, G.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee, S.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, T.; Schlegel, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Toignoni, A.; Tosato, V.; Uchlyama, T.; Winfers, P.; Wipolt, A.; Yamamoto, H.; Yanane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A>Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033
A:Accession: D69857
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-141 <KUN>
A:Cross-references: GB:D29110; GB:AL009126; MID:g26343472; PIDN:CAB13171.1; PID:g2633668
A:Experimental source: strain 168
A:Genetics:
A:Gene: yk1A
C:Superfamily: hypothetical protein yk1A

Query Match      23.2%; Score 63; DB 2; Length 141;
Best Local Similarity 33.3%; Pred. No. 2.4;
Matches 16; Conservative 11; Mismatches 13; Indels 8; Gaps 2;

```

OY 5 VSLHFRHTLHPKEMTPVE--PAFAA-----ELLSRLKEKLLE 44
|::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 31 VAMGTSPRAKLEKATNPDEQLFAGYAACFPASQALVARTERVAVE 78

RESULT 5
T12864
probable antirepressor - Bacillus subtilis phage SPBC2
C:Species: Bacillus subtilis phage SPBC2
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 20-Jun-2000
C:Accession: T12864; D65919
R:Lazarevic, V.; Ducrest-Hoeft, A.; Soldo, B.; Hilbert, H.; Mauel, C.; Karmata, D.
submitted to the EMBL Data Library, August 1997
A:description: The complete nucleotide sequence of the Bacillus subtilis spBactac2 pro
A:Reference number: Z17583
A:Accession: T12864
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-251 <LMZ>
A:Cross-references: EMBL:AF020713; NID:q3025478; PID:g3025578; PIDN:AAC13073.1
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azavedo, V.; Ber
C.: Bron, S.; Broiliet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.: Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
A:Authors: Foulger, C.R.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizi, A.; Gal
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holappel, S.; Hosono, S.; Hulio, M
Koetter, P.; Konigstein, G.; Krogh, S.; Kunano, M.; Kurita, K.; Lapidus, A.; Lardino
A:Authors: Lauber, U.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
Y., M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portere
Rieger, M.; Rivolta, C.; Roche, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scall
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terstira, P.; Togonoi, A.; Tosato, V.; Uchiya
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamané, K.; Yasumoto, K.; Yata, K.; Yoshida
A:Authors: Yoshikawa, H.F.; Zunstein, E.; Yoshikawa, H.; Danchin, A.
A:title: The complete genome sequence of the Gram-positive bacterium Bacillus subtil
A:Reference number: A69580; MUID:98044033
A:Accession: D69919
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-251 <KUN>
A:Cross-references: GB:z99114; GB:z99115; GB:AL009126; NID:q2634478; PIDN:CAB13985.1;
A:Experimental source: strain 168
C:Genetics:
A:Gene: yocD
C:superfamily: phage P1 kila protein

Query Match 23.0%; Score 62.5; DB 2; Length 251;
Best Local Similarity 32.1%; Pred. No. 5.3;
Matches 17; Conservative 13; Mismatches 18; Indels 5; Gaps 2;

OY 1 LANGGVSLPHFRTH---LPKEMTPVEPPAPFAAEILSRLEKLLESRSLSL 49
|::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 62 ATGR-SLKHFHLTRGCDVMANKMGAKGVLTQTQYVSKEFEEMEKALKARPSL 113

RESULT 6
C48423
homeotic protein engrailed 1 - chicken
C:Species: Gallus gallus (chicken)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Oct-1997
C:Accession: C48423
R:Irligan, C.; Hanks, M.C.; Noble-Topham, S.; Nallanathan, D.; Provant, N.J.; Joyner,
Dev. Genet. 13, 345-358, 1992
A:title: Cloning and sequence comparison of the mouse, human, and chicken engrailed g
A:Reference number: A48423; MUID:93185339
A:Accession: C48423
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-333 <LOG>
C:Superfamily: unassigned homeobox proteins; homeobox homolog
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

F:245-301/Domain: homeobox homology <HOX>

Query Match 22.8%; Score 62; DB 2; Length 333;
 Best Local Similarity 38.8%; Pred. No. 8.2;
 Matches 19; Conservative 9; Mismatches 13; Indels 8; Gaps 3;

OY 11 PRTNRLPKEMTPVEP-----AAFAELISRLKLELE-SRHSLEPRIQ 54
 DB 230 PRTNRLKPKTEKEDKRPRTAFTAE---OLQRLKAEEQANRYITEQRQ 275

RESULT 7
 S55190

hypothetical protein YJR003C - yeast (Saccharomyces cerevisiae)
 M:Alternate names: hypothetical protein J1415; hypothetical protein YJR03.30
 C:Species: Saccharomyces cerevisiae
 C:Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 04-Mar-2000

R:de Haan, M.; Smits, P.H.M.; Grivell, L.A.
 submitted to the EMBL Data Library, May 1995
 A:Reference number: S55183

A:Accession: S55190
 A:Molecule type: DNA

A:Residues: 1-539 <DEH>
 A:Cross-references: EMBL:X87611; NID:g854567; PIDN:CAA60924.1; PID:g854575

R:de Haan, M.; Grivell, L.A.; Smits, P.H.M.
 submitted to the Protein Sequence Database, September 1995

A:Reference number: S56771
 A:Accession: S57018

A:Molecule type: DNA
 A:Residues: 1-539 <ZAG>

A:Cross-references: EMBL:Z49503; NID:g1015623; PIDN:CAA89525.1; PID:g1015624; MIPS:YJR003C
 C:Genetics:

A:Map position: 10R
 C:Superfamily: Saccharomyces cerevisiae hypothetical protein YJR003C

Query Match 22.6%; Score 61.5; DB 2; Length 539;
 Best Local Similarity 34.3%; Pred. No. 16;
 Matches 12; Conservative 10; Mismatches 12; Indels 1; Gaps 1;

OY 8 PHF-PRTNRLPKEMTPVEPAAFAELISRLKLE 41
 DB 56 PSFDPTRHLPEDITIDYDSQNYSTLNRLEV 90

RESULT 8
 T46149

protein kinase ATN1-like protein - Arabidopsis thaliana
 M:Alternate names: protein T3A5.100
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 17-Mar-2000

R:Blöcker, H.; Mewes, H.W.; Mayer, K.F.X.; Lemcke, K.; Schueller, C.; Quettler, F.; Salz
 submitted to the Protein Sequence Database, December 1999
 A:Reference number: Z25024

A:Accession: T46149
 A:Status: Preliminary

A:Molecule type: DNA
 A:Residues: 1-377 <BLD>

A:Cross-references: EMBL:AL132979

A:Experimental source: cultivar Columbia; BAC clone T3A5
 C:Genetics:

A:Map position: 3
 A:Introns: 66/2; 111/3; 177/1; 217/3; 269/3

A:Note: T3A5.100
 C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote

Query Match 22.1%; Score 60; DB 2; Length 377;
 Best Local Similarity 30.6%; Pred. No. 16;
 Matches 15; Conservative 11; Mismatches 15; Indels 8; Gaps 2;

OY 5 VSLPHF-----PRTNRLPKEMTPVEPAAFAELISRLKLELES 45
 DB 261 ISIPYFVNOGKRPSLSNIDEVVPILECCWADSKRTLEFKDTITLES 309

RESULT 9
 S56638

mitogen-activated protein kinase 1 homolog (clone AspK9) - oat
 M:Alternate names: MAP1 kinase
 C:Species: Avena sativa (oat)

C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 18-Jun-1999
 A:Accession: S56638

R:Huttely, A.K.; Phillips, A.L.
 Plant Mol. Biol. 27, 1043-1052, 1995

A:Title: Gibberellin-regulated expression in oat aleurone cells of two kinases that s

A:Reference number: S56638; MUID:95284341
 A:Accession: S56638

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA
 A:Residues: 1-369 <HUT>

A:Cross-references: EMBL:X79993; NID:g871983; PIDN:CAA56314.1; PID:g871984

C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: ATP; phosphotransferase; protein kinase

F:33-322/Domain: protein kinase homology <KIN>
 F:42-50/Region: protein kinase ATP-binding motif

Query Match 21.9%; Score 59.5; DB 2; Length 369;
 Best Local Similarity 35.8%; Pred. No. 18;
 Matches 19; Conservative 7; Mismatches 18; Indels 9; Gaps 3;

OY 7 LPHFPTNRLPKEMTPVEPAAFAELISRLKLELESRHSLEERT 53
 DB 276 LPQFPR-RPFCQFQPKVQPAAL--DLIERMIFENPLQRTVEBALEHPLYERL 325

RESULT 10
 E70826

probable membrane protein - Mycobacterium tuberculosis (strain H37Rv)
 C:Species: Mycobacterium tuberculosis

C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
 C:Accession: E70826

R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
 et al.; Connor, R.; Davies, R.; Devlin, K.; Felkwell, T.; Gentles, S.; Hamlin, N.; Holroyd,

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skellon, S.; Squares, S.
 Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno

A:Reference number: A70500; MUID:9829587

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
 A:Residues: 1-964 <COI>

A:Cross-references: GB:AI021943; GB:AL123456; NID:g3261530; PIDN:CA17459.1; PID:el25

A:Experimental source: strain H37Rv
 C:Genetics:

Query Match 21.9%; Score 59.5; DB 2; Length 964;
 Best Local Similarity 31.2%; Pred. No. 53;
 Matches 15; Conservative 10; Mismatches 18; Indels 5; Gaps 1;

OY 7 LPHFPTNRLPKEMTPVEPAAFAELISRLKLELESRHSLEERTQ 54
 DB 621 LPLMQRLDILMPQLTAMMP-----EMIQTKSKQAQMLSHSTQEBLQ 663

RESULT 11
 I38346

elastic titin - human (fragment)
 C:Species: Homo sapiens (man)

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FT DOMAIN 413 476 BETA-CATENIN BINDING SITE (BY
FT DOMAIN 469 474 POLY-HIS.
FT DOMAIN 756 838 DIX.
SQ SEQUENCE 838 AA; 92947 MW; 45B825C13BA07F37 CRC64;

Query Match 100.0%; Score 272; DB 1; Length 838;
Best Local Similarity 100.0%; Pred. No. 1.7e-24;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANGVSLPFPFTRHLPKEMTPVEPAFAFAELISRLKLESLERHSLEERLQ 54
DQ 343 ANGVSLPFPFTRHLPKEMTPVEPAFAFAELISRLKLESLERHSLEERLQ 396

RESULT 2
ID AXN2_MOUSE STANDARD; PRT; 840 AA.
AC 088566; 090XJ6;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN 2 (AXIS INHIBITION PROTEIN 2) (CONDUCTIN) (AXIN-LIKE PROTEIN)
DE (AXIL).
GN AXIN2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-9821239; PubMed-954852;
RA Behrens J., Jerchow B.-A., Wuerstele M., Grimm J., Asbrand C.,
Witz R., Kuehl M., Wedlich D., Birchmeier W.;
RT "Functional interaction of an axin homolog, conductin, with beta-
catenin, APC, and GSK3beta.";
RL Science 280:596-599(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G.,
Jenkins N.A., Warburton D., Costantini F.;
RT "Properties of mouse Axin2 and human AXIN2: chromosomal location,
RT expression pattern, interaction with Axin and effects on embryonic
RT axis formation.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATENIN AND APC BY GSK-3B (BY SIMILARITY).
CC -1- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)
CC AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN
CC OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN.
CC TERMARY COMPLEX (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC PP2A (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -----
CC CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF073788; AAC26047.1; -
DR EMBL: AF205889; AA222860.1; -
DR MGD: MG1:1270862; AXIN2.
DR HSSP: P49799; IAGR.
DR InterPro: IPR000342; -
DR InterPro: IPR001158; -

DR Pfam: PF00615; RGS; 1.
DR Pfam: PF00778; DIX; 1.
DR PRINTS: PR01301; RGS-PROTEIN.
DR PROSITE: PS01332; RGS; 1.
KW Anti-oncogene; Phosphorylation.
FT DOMAIN 81 200
FT DOMAIN 327 413 GSK-3B BINDING SITE (BY SIMILARITY).
FT DOMAIN 413 478 BETA-CATENIN BINDING SITE (BY
FT SIMILARITY).
FT DOMAIN 469 476 POLY-HIS.
FT DOMAIN 758 840 DIX.
FT CONFLICT 101 101 R -> K (IN REF. 2).
FT CONFLICT 474 474 H -> Y (IN REF. 2).
FT CONFLICT 484 484 S -> P (IN REF. 2).
FT CONFLICT 503 503 F -> S (IN REF. 2).
FT CONFLICT 603 603 G -> A (IN REF. 2).
SQ SEQUENCE 840 AA; 92934 MW; A07D5EF825DE7277 CRC64;

Query Match 100.0%; Score 272; DB 1; Length 840;
Best Local Similarity 100.0%; Pred. No. 1.8e-24;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANGVSLPFPFTRHLPKEMTPVEPAFAFAELISRLKLESLERHSLEERLQ 54
DQ 343 ANGVSLPFPFTRHLPKEMTPVEPAFAFAELISRLKLESLERHSLEERLQ 396

RESULT 3
ID AXN2_HUMAN STANDARD; PRT; 843 AA.
AC 09Y2T1; 09UH84;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN 2 (AXIS INHIBITION PROTEIN 2) (CONDUCTIN) (AXIN-LIKE PROTEIN)
DE (AXIL).
GN AXIN2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99168905; PubMed-10049590;
RA Mai M., Qian C., Yokomizo A., Smith D.I., Liu W.;
RT "Cloning of the human homolog of conductin (AXIN2), a gene mapping to
RT chromosome 17q23-q24.";
RL Genomics 55:341-344(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G.,
Jenkins N.A., Warburton D., Costantini F.;
RT "Properties of mouse Axin2 and human AXIN2: chromosomal location,
RT expression pattern, interaction with Axin and effects on embryonic
RT axis formation.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATENIN AND APC BY GSK-3B (BY SIMILARITY).
CC -1- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)
CC AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN
CC OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN.
CC TERMARY COMPLEX (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN AND LYMPHOBLAST.
CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC PP2A (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -----
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DR EMBL: AF078165; AAD20976.1; -
DR EMBL: AF205888; AAF22799.1; -
DR MIM: 604025; -
DR InterPro: IPR000342; -
DR InterPro: IPR001158; -
DR Pfam: PF00615; RGS; 1.
DR Pfam: PF00778; DIX; 1.
DR PRINTS: PR01301; RGS-PROTEIN.
DR PROSITE: PS50132; RGS; 1.
KW Developmental protein; Phosphorylation.
FT DOMAIN 81 200 RGS.
FT DOMAIN 327 413 BETA-CATENIN BINDING SITE (BY
FT DOMAIN 413 476 SIMILARITY).
FT DOMAIN 469 474 POLY-HIS.
FT DOMAIN 761 843 DIX.
FT CONFLICT 37 62 OPGVGKGVTRKPMYSVSNTRNEDGL -> HHGCGPGHOT
FT CONFLICT 346 346 Q -> R (IN REF. 2).
FT CONFLICT 572 636 MISSING (IN REF. 2).
FT CONFLICT 687 687 P -> S (IN REF. 2).
FT CONFLICT 696 696 Q -> H (IN REF. 2).
SQ SEQUENCE 843 AA; 93557 MW; F7B62BED6A664D CRC64;

Query Match 98.5%; Score 268; DB 1; Length 843;
Best Local Similarity 98.1%; Pred. No. 5.2e-24;
Matches 53; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ANGVSLPFPRTTHRLPKEMTPVEPAFAELISRLKLESHSLERLQ 54
DB 343 ANGVSLPFPRTTHRLPKEMTPVEPAFAELISRLKLESHSLERLQ 396

RESULT 4
AXN2_BRARE STANDARD; PRT: 812 AA.
AC P57095;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN 2 (AXIS INHIBITION PROTEIN 2).
CN AXIN2.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20171051; PubMed=10704853;
RA Shintzu T., Yamana Y., Ryu S.-L., Hashimoto H., Yabe T., Hirata T.,
RA Bae Y.-K., Hibi M., Hirano T.;
RT "Cooperative roles of Berezovskiy/Dharma and Nodal-related proteins in the
RT formation of the dorsal organizer in zebrafish.";
RL Mech. Dev. 91:293-303(2000).
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC PP2A (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -----
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DR EMBL: AB032263; BAA92440.1; -
DR HSSP: P49799; IAGR.
DR InterPro: IPR000342; -
DR InterPro: IPR001158; -
DR Pfam: PF00615; RGS; 1.
DR Pfam: PF00778; DIX; 1.
DR PROSITE: PS50132; RGS; 1.
KW Developmental protein; Phosphorylation.
FT DOMAIN 84 203 RGS.
FT DOMAIN 329 415 BETA-CATENIN BINDING SITE (BY
FT DOMAIN 415 467 SIMILARITY).
FT DOMAIN 412 419 POLY-SER.
FT DOMAIN 730 812 DIX.
SQ SEQUENCE 812 AA; 91496 MW; 46E5ADA6DE2240CC CRC64;

Query Match 75.0%; Score 204; DB 1; Length 812;
Best Local Similarity 79.2%; Pred. No. 1.8e-16;
Matches 42; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 2 NGVSLPFPRTTHRLPKEMTPVEPAFAELISRLKLESHSLERLQ 54
DB 346 NGVSLPFPRTTHRLPKEMTPVEPAFAELISRLKLESHSLERLQ 398

RESULT 5
AXN2_BRARE STANDARD; PRT: 841 AA.
AC 042400;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN (AXIS INHIBITION PROTEIN).
CN AXIN OR AXN.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Embryo;
RA MEDLINE=97373830; PubMed=9230313;
RA Zeng L., Fagotto F., Zhang T., Hsu W., Vasilek T.J., Perry W.L. III,
RA Lee J.D., Tildeman S.M., Gumbiner B.M., Costantini F.;
RT "The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling
RT pathway that regulates embryonic axis formation.";
RL Cell 90:181-192(1997).
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT STAGE 12 TO 15.
CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC PP2A (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -----
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CC -----
DR EMBL: AF009012; AAC60245.1; -
DR HSSP; P49799; IAGR.
DR InterPro: IPR000342; -
DR Pfam; PF00615; RGS; 1.
DR Pfam; PF00778; DIX; 1.
DR PROSITE; PS50132; RGS; 1.
KM Developmental protein; Phosphorylation.
FT DOMAIN 88 211
FT DOMAIN 348 433 GSK-3B BINDING SITE (BY SIMILARITY).
FT DOMAIN 434 508 BETA-CATENIN BINDING SITE (BY
FT SIMILARITY).
FT DOMAIN 759 841 DIX
SQ SEQUENCE 841 AA; 94931 MW; 400DCC90E72506FE CRC64;

Query Match 57.9%; Score 157.5; DB 1; Length 841;
Best Local Similarity 59.3%; Pred. No. 5.5e-11;
Matches 32; Conservative 11; Mismatches 10; Indels 1; Gaps 1;

QY 1 ANGVSLPPTPTHTRLPKEMTPVEPAFAELISRLKLELSRHSLEERLQ 54
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 362 ANGVPLPHIPTNTKRPDI-HVEPEKFAELISRLKLELSRHSLEERLQ 414

RESULT 6
AXNI_BRARE STANDARD; PRT; 835 AA.
AC P57094;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN 1 (AXIS INHIBITION PROTEIN 1).
GN AXIN1.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20171051; PubMed=10704853;
RA Shimizu T., Yamanaka Y., Ryu S.-L., Hashimoto H., Yabe T., Hirata T.,
Bae Y.-K., Hibi M., Hirano T.;
RT "Cooperative roles of Bozozok/Dharma and Nodal-related proteins in the
formation of the dorsal organizer in zebrafish.";
RL Mech. Dev. 91:293-303(2000).
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CATENIN AND APC BY GSK-3B (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
PP2A (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -----
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CC -----
DR EMBL; AB032262; BAA92439.1; -
DR HSSP; P49799; IAGR.
DR InterPro: IPR000342; -
DR InterPro: IPR001158; -
DR Pfam; PF00615; RGS; 1.
DR Pfam; PF00778; DIX; 1.
DR PROSITE; PS50132; RGS; 1.
KM Developmental protein; Phosphorylation.
FT DOMAIN 154 277 RGS.
```

```
FT DOMAIN 92 214 RGS.
FT DOMAIN 351 436 GSK-3B BINDING SITE (BY SIMILARITY).
FT DOMAIN 437 512 BETA-CATENIN BINDING SITE (BY
FT SIMILARITY).
FT DOMAIN 753 835 DIX.
SQ SEQUENCE 835 AA; 94351 MW; 1C62FCF1F5937C87 CRC64;

Query Match 55.3%; Score 150.5; DB 1; Length 835;
Best Local Similarity 60.4%; Pred. No. 3.7e-10;
Matches 32; Conservative 9; Mismatches 11; Indels 1; Gaps 1;

QY 2 NGVSLPPTPTHTRLPKEMTPVEPAFAELISRLKLELSRHSLEERLQ 54
|||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 366 NGRVPLPHIPTNTKRPDI-HVEPEKFAELISRLKLELSRHSLEERLQ 417

RESULT 7
AXNI_BRAT STANDARD; PRT; 893 AA.
AC Q70239;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN 1 PROTEIN (AXIS INHIBITION PROTEIN 1) (RAXIN) (FRAGMENT).
GN AXIN1 OR AXIN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Brain;
RC MEDLINE=98151361; PubMed=9482734;
RA Ikeda S., Kishida S., Yamamoto H., Murai H., Koyama S., Kikuchi A.;
RT "Axin, a negative regulator of the Wnt signaling pathway, forms a
complex with GSK-3beta and beta-catenin and promotes GSK-3beta-
dependent phosphorylation of beta-catenin.";
RL EMBO J. 17:1371-1384(1998).
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CATENIN AND APC BY GSK-3B (BY SIMILARITY).
CC -1- SUBUNIT: INTERACTS WITH GSK-3B AND BETA-CATENIN. THE INTERACTION
BETWEEN AXIN AND BETA-CATENIN OCCURS VIA THE ARMADILLO REPEATS
CONTAINED IN BETA-CATENIN. TERNARY COMPLEX. ALSO BINDS TO
PLAKOGLOBIN (GAMMA-CATENIN), APC, DVL AND PP2A (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS, THYMUS AND LUNG
FOLLOVED BY CEREBRUM, CEREBELLUM, HEART, KIDNEY, SKELETAL MUSCLE,
SPLEEN AND LIVER.
CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
PP2A (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -----
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CC -----
DR EMBL; AF017756; AAC40066.1; ALT_INIT.
DR HSSP; P49799; IAGR.
DR InterPro: IPR000342; -
DR InterPro: IPR001158; -
DR Pfam; PF00615; RGS; 1.
DR Pfam; PF00778; DIX; 1.
DR PROSITE; PS50132; RGS; 1.
KM Developmental protein; Phosphorylation.
FT DOMAIN 154 277 RGS.
```


FT DOMAIN 471 540 BETA-CATENIN BINDING SITE (BY
FT DOMAIN 818 900 SIMILARITY).
SQ SEQUENCE 900 AA; 99803 MW; EEF990B11FC7B3B CRC64;

Query Match 52.0%; Score 141.5; DB 1; Length 900;
Best Local Similarity 56.6%; Pred. No. 4.6e-09;
Matches 30; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

2 NGQVSLPHPRTHRLPKEMTPVEPAFAAELISRLKLESHSLERLQ 54
Db 400 NGKVPPLHPRTYHMPKDI-HVDEKFAELISRLKLESHSLERLQ 414

RESULT 10
AXN_XENLA STANDARD; PRT; 842 AA.

ID AXN_XENLA STANDARD; PRT; 842 AA.
AC 09YGT0;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN (AXIS INHIBITION PROTEIN) (AXIN).
GN AXIN OR AXN.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;

RM [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9173782; PubMed=10072781;
RA Hedgepeth C.M., Deardorff M.A., Klein P.S.;
RT "Xenopus axin interacts with glycogen synthase kinase-3 beta and is
RL Mech. Dev. 80:147-151(1999)."
RT expressed in the anterior midbrain."

CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATENIN AND APC BY GSK-3B (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- DEVELOPMENTAL STAGE: WEAKLY AND UBQUITOUSLY EXPRESSED THROUGHOUT
CC EARLY DEVELOPMENT, AND HIGHLY EXPRESSED IN THE ANTERIOR
CC MESENCEPHALON ADJACENT TO THE FOREBRAIN-MIDBRAIN BOUNDARY.

CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC PP2A (BY SIMILARITY).

CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.

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CC EMBL; AF097313; AAC71036.1; -
CC HSP; P49799; IAGR.
CC InterPro: IPR000342; -
CC InterPro: IPR001158; -
CC Pfam; PF00615; RGS; 1.
CC ProSite; PS50132; RGS; 1.
CC ProSite; PS50132; RGS; 1.
CC Developmental protein: Phosphorylation.

FT DOMAIN 88 211 RGS
FT DOMAIN 348 433 GSK-3B BINDING SITE (BY SIMILARITY).
FT DOMAIN 434 508 BETA-CATENIN BINDING SITE (BY
SIMILARITY).
FT DOMAIN 760 842 DIX.
SQ SEQUENCE 842 AA; 94459 MW; BDAL52734C97191E CRC64;

Query Match 50.2%; Score 136.5; DB 1; Length 842;

Best Local Similarity 53.7%; Pred. No. 1.7e-08;
Matches 29; Conservative 10; Mismatches 14; Indels 1; Gaps 1;

OY 1 ANGQVSLPHPRTHRLPKEMTPVEPAFAAELISRLKLESHSLERLQ 54
Db 362 ANGKVPPLHPRTYHMPKDI-HVDEKFAELISRLKLESHSLERLQ 414

RESULT 11
HMEI_CHICK STANDARD; PRT; 333 AA.

ID HMEI_CHICK STANDARD; PRT; 333 AA.
AC 005916;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HOMEOBOX PROTEIN ENGRAILED-1 (GG-EN-1).
GN EN1 OR EN-1.
OS Gallus gallus (chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;

RM [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9318539; PubMed=1363401;
RA Logan C., Hanks M.C., Noble-Topham S., Nallathattan D.,
RA Provart N.J., Joyner A.L.;
RT "Cloning and sequence comparison of the mouse, human, and chicken
RT engrailed genes reveal potential functional domains and regulatory
RT regions."
RL Dev. Genet. 13:345-358(1992).
RT -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: BELONGS TO THE ENGRAILED FAMILY OF HOMEOBOX PROTEINS.

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CC EMBL; L12694; AAA53435.1; -
CC EMBL; L12695; AAA53436.1; -
CC HSP; P02836; IHDD.
CC TRANSFAC: T02014; -
CC InterPro: IPR000747; -
CC InterPro: IPR001356; -
CC Pfam; PF00046; homeobox; 1.
CC PRINTS; PR00024; HOMEOBOX.
CC PRINTS; PR00026; ENGRAILED.
CC PROSITE; PS00027; HOMEOBOX_1; 1.
CC PROSITE; PS00027; HOMEOBOX_2; 1.
CC PROSITE; PS00033; ENGRAILED; 1.
CC Homeobox; DNA-binding; Developmental protein; Nuclear protein.

FT DOMAIN 22 29 POLY-GLY.
FT DOMAIN 36 65 PRO-RICH.
FT DOMAIN 59 65 POLY-PRO.
FT DOMAIN 97 104 POLY-GLY.
FT DNA_BIND 244 303 HOMEOBOX.
SQ SEQUENCE 333 AA; 34515 MW; DQFLIF917ELFBAD CRC64;

Query Match 24.3%; Score 66; DB 1; Length 333;
Best Local Similarity 38.5%; Pred. No. 1.2; Indels 8; Gaps 3;
Matches 20; Conservative 9; Mismatches 15; Indels 8; Gaps 3;

OY 8 PHPRTHRLPKEMTPVEPAFAAELISRLKLESHSLERLQ 54
Db 227 PSSPRTKLKKKTEKEDKPRRTAFATAE--QLQRLAKAEQANRYITEGRQ 275

RESULT 12

RESULT 15

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TX28_HUMAN          STANDARD;          PRT;          410 AA.
ID   TX28_HUMAN
AC   O15482;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   TESTIS-SPECIFIC PROTEIN TEX28.
CN   CXORF2 OR TEX28.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX   NCBI_TaxID:9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=97422617; PubMed=9268643;
RA   Hanna M.C., Platts J.T., Kirkness E.F.;
RT   "Identification of a gene within the tandem array of red and green
RT   color pigment genes."
RL   Genomics 43:384-386(1997).
CC   -!- TISSUE SPECIFICITY: TESTIS-SPECIFIC.
CC   -!- SIMILARITY: SOME, TO HUMAN KIAA0481.
CC   -----
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CC   or send an email to license@sib-sib.ch).
CC   -----
DR   EMBL: U93720; AAB71379.1; -
DR   MIM: 300092; -
SQ   SEQUENCE 410 AA; 46131 MW; 8E455A761D52A660 CRC64;

```

Query Match 21.9%; Score 59.5; DB 1; Length 410;

Best Local Similarity 32.4%; Pred. No. 8.9; Mismatches 20; Indels 17; Gaps 2;

```

QY   2 NGQVSLPFPFTRRLP-----KEMTPVEPAFAFAELISRLKLEL-----E 44
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB   162 DGPYNLPHASRPFLFSFQSLQGTCTLEFDVAQQQNLILQKVALELEAKRHISLGE 221
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
QY   45 SRHSLEER 52
      | | | | |
DB   222 SYHSLKER 229

```

Search completed: June 7, 2001, 02:10:31
Job time: 419 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 7, 2001, 02:09:39 ; Search time 81.06 seconds
(without alignments)
78.081 Million cell updates/sec

Title: US-09-587-574-3

Perfect score: 272
Sequence: 1 ANGVSLPHPRTRHRLPKEM.....RLKIKLELSRHSLSERLQ 54

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues
Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP:REMBL_15:*
2: sp.archaea:*
3: sp.bacteria:*
4: sp.fungi:*
5: sp.human:*
6: sp.invertebrate:*
7: sp.mammal:*
8: sp.mhc:*
9: sp.organelle:*
10: sp.phage:*
11: sp.plant:*
12: sp.rodent:*
13: sp.unclassified:*
14: sp.vertebrate:*
15: sp.virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	272	100.0	838	11 070240	070240 rattus norv
2	272	100.0	840	11 088566	088566 mus musculu
3	272	100.0	840	11 090X06	090X06 mus musculu
4	268	98.5	843	4 09Y2T1	09Y2T1 homo sapien
5	264	97.1	777	4 09UH84	09UH84 homo sapien
6	157.5	57.9	841	13 042400	042400 gallus gall
7	144	52.9	706	13 09PTP2	09PTP2 xenopus lae
8	142.5	52.4	832	11 070239	070239 rattus norv
9	142.5	52.4	992	11 035625	035625 mus musculu
10	141.5	52.0	900	4 015169	015169 homo sapien
11	136.5	50.2	842	13 09YGY0	09YGY0 xenopus lae
12	68	25.0	2590	13 09W7R4	09W7R4 brachydanio
13	64	23.5	226	2 09R810	09R810 acinetobact
14	62.5	23.0	251	2 034449	034449 bacillus su
15	62.5	23.0	251	9 064113	064113 bacterioph
16	61.5	22.6	234	5 096565	096565 junonia coe
17	61.5	22.6	995	2 068167	068167 lactococcus
18	60.5	22.2	369	10 081599	081599 triticum ae
19	60	22.1	377	10 09SC04	09SC04 arabidopsis

20	59.5	21.9	129	8 047954	047954 trypanosoma
21	59.5	21.9	369	10 043379	043379 arena sativ
22	59.5	21.9	442	4 09NZJ2	09NZJ2 homo sapien
23	59.5	21.9	2715	11 09WTS6	09WTS6 mus musculu
24	59.5	21.9	7962	4 010465	010465 homo sapien
25	59	21.7	363	2 09ZG07	09ZG07 myxococcus
26	59	21.7	884	4 09UPX6	09UPX6 homo sapien
27	59	21.7	1327	2 09RUK4	09RUK4 streptomyce
28	58.5	21.5	601	2 09PAT1	09PAT1 xylella fas
29	58.5	21.5	883	4 09UL19	09UL19 homo sapien
30	58.5	21.5	1061	4 09N0V6	09N0V6 homo sapien
31	58	21.3	259	13 09YGU2	09YGU2 brachydanio
32	58	21.3	1707	5 017652	017652 caenorhabdl
33	57.5	21.1	254	2 067279	067279 aquifex aeo
34	57.5	21.1	978	2 067124	067124 aquifex aeo
35	57.5	21.1	1454	10 09X117	09X117 arabidopsis
36	57	21.0	156	5 022757	022757 caenorhabdl
37	57	21.0	287	10 09SSL8	09SSL8 caenorhabdl
38	57	21.0	435	5 09V539	09V539 drosophila
39	57	21.0	722	5 09XU77	09XU77 caenorhabdl
40	56.5	20.8	90	14 074750	074750 human immun
41	56.5	20.8	207	10 09M8W6	09M8W6 arabidopsis
42	56.5	20.8	483	2 087270	087270 bartonella
43	56.5	20.8	526	3 09USX7	09USX7 schizosacch
44	56.5	20.8	1100	10 09XIM3	09XIM3 arabidopsis
45	56	20.6	501	3 09UUD0	09UUD0 schizosacch

ALIGNMENTS

RESULT	ID	PRELIMINARY:	PRT:	838 AA.
070240	070240			
AC	070240			
DT	01-AUG-1998 (T-REMBLrel. 07, Created)			
DT	01-AUG-1998 (T-REMBLrel. 07, Last sequence update)			
DT	01-OCT-2000 (T-REMBLrel. 15, Last annotation update)			
DE	AXIL.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-98226558; PubMed-9566905;			
RA	Yamanoto H., Kishida S., Uochi T., Ikeda S., Koyama S., Asashima M.,			
RA	Kikuchi A.;			
RT	"Axil, a member of the Axin family, interacts with both glycogen			
RT	synthase kinase 3beta and beta-catenin and inhibits axis formation of			
RT	Xenopus embryos."			
RL	MOL. Cell. Biol. 18:2867-2875(1998).			
DR	EMBL; AF017757; AAC40089.1; -			
DR	HSSP; P49799; 1AGR.			
DR	INTERPRO; IPR000342; -			
DR	INTERPRO; IPR001158; -			
DR	PFAM; PF00615; RGS; 1.			
DR	PFAM; PF00778; DIX; 1.			
DR	PRODOM; PD001580; -; 1.			
DR	PRODOM; PD003639; -; 1.			
SO	SEQUENCE 838 AA; 92947 MW; 45B825C13BA07F37 CRC64;			

Query Match 100.0%; Score 272; DB 11; Length 838;
Best Local Similarity 100.0%; Pred. No. 3e-23;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 ANGVSLPHPRTRHRLPKEMTPVPAFAELISRLKIKLELSRHSLSERLQ 54
DB 343 ANGVSLPHPRTRHRLPKEMTPVPAFAELISRLKIKLELSRHSLSERLQ 396
RESULT 2

088566
ID 088566 PRELIMINARY; PRT: 840 AA.
AC 088566;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE CONDUCTIN.
GN AXIN2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98221239; PubMed=9554852;
RA Behrens J., Jerchow B.A., Wuttele M., Grimm J., Asbrand C., Wirtz R.,
Kuhl M., Wedlich D., Birchmeier W.,
RT "Functional interaction of an axin homolog, conductin, with beta-
catenin, APC, and GSK3beta."
RL Science 280:596-599(1998).
DR EMBL: AF073788; AAC26047.1; -.
DR HSSP: P49799; IAGR.
DR MGD: MGI:1270862; Axin2.
DR INTERPRO: IPR000342; -.
DR INTERPRO: IPR001158; -.
DR PFAM: PF00615; RGS; 1.
DR PFAM: PF00778; DIX; 1.
DR PRODOM: PD001580; -; 1.
DR PRODOM: PD003639; -; 1.
SQ SEQUENCE 840 AA; 92934 MW; A07D5FEB25DE7277 CRC64;

Query Match 100.0%; Score 272; DB 11; Length 840;
Best Local Similarity 100.0%; Pred. No. 3e-23;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ANGOVSLPFPRTTHLPKEMTPVEPAFAELISRLKIKLELSRHSLEERLQ 54
Db 343 ANGOVSLPFPRTTHLPKEMTPVEPAFAELISRLKIKLELSRHSLEERLQ 396
|||||

RESULT 3
ID 090XJ6 PRELIMINARY; PRT: 840 AA.
AC 090XJ6;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE AXIN2.
GN AXIN2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G.,
Jenkins N.A., Warburton D., Costantini F.,
RT "Properties of mouse Axin2 and human AXIN2: chromosomal location,
RT expression pattern, interaction with Axin and effects on embryonic
RT axis formation."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF205889; AAF22800.1; -.
DR HSSP: P49799; IAGR.
DR INTERPRO: IPR000342; -.
DR INTERPRO: IPR001158; -.
DR PFAM: PF00615; RGS; 1.
DR PFAM: PF00778; DIX; 1.
DR PRINTS: PR01301; RGS-PROTEIN.
SQ SEQUENCE 840 AA; 92896 MW; 767D546B43C921C5 CRC64;

Query Match 100.0%; Score 272; DB 11; Length 840;

Best Local Similarity 100.0%; Pred. No. 3e-23;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ANGOVSLPFPRTTHLPKEMTPVEPAFAELISRLKIKLELSRHSLEERLQ 54
Db 343 ANGOVSLPFPRTTHLPKEMTPVEPAFAELISRLKIKLELSRHSLEERLQ 396
|||||

RESULT 4
ID 09Y2T1 PRELIMINARY; PRT: 843 AA.
AC 09Y2T1;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE CONDUCTIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99168905; PubMed=10049590;
RA Mai M., Qian C., Yokomizo A., Smith D.I., Liu W.,
RT "Cloning of the human homolog of conductin (AXIN2), a gene mapping to
RT chromosome 17q23-q24."
RL Genomics 55:341-344(1999).
DR EMBL: AF078165; AAD20976.1; -.
DR HSSP: P49799; IAGR.
DR INTERPRO: IPR000342; -.
DR INTERPRO: IPR001158; -.
DR PFAM: PF00615; RGS; 1.
DR PFAM: PF00778; DIX; 1.
SQ SEQUENCE 843 AA; 93557 MW; F7B62BED6A464D CRC64;

Query Match 98.5%; Score 268; DB 4; Length 843;
Best Local Similarity 98.1%; Pred. No. 8.6e-23;
Matches 53; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ANGOVSLPFPRTTHLPKEMTPVEPAFAELISRLKIKLELSRHSLEERLQ 54
Db 343 ANGOVSLPFPRTTHLPKEMTPVEPAFAELISRLKIKLELSRHSLEERLQ 396
|||||

RESULT 5
ID 09UH84 PRELIMINARY; PRT: 777 AA.
AC 09UH84;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE AXIN2.
GN AXIN2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN; LYMPHOBLAST.
RA Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G.,
Jenkins N.A., Warburton D., Costantini F.,
RT "Properties of mouse Axin2 and human AXIN2: chromosomal location,
RT expression pattern, interaction with Axin and effects on embryonic
RT axis formation."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF205888; AAF22799.1; -.
DR HSSP: P49799; IAGR.
DR INTERPRO: IPR000342; -.
DR INTERPRO: IPR001158; -.
DR PFAM: PF00615; RGS; 1.
DR PFAM: PF00778; DIX; 1.

DR PRINTS: PRO1301: RGSPROTEIN.
S0 SEQUENCE 777 AA: 86857 MW: 3A4943ABF430BBD3 CRC64:

Query Match 97.1%; Score 264; DB 4; Length 777;
Best Local Similarity 96.3%; Pred. No. 2,3e-22;
Matches 52; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 ANGOVSLPHFPRTNRLPKEMTPVEPAFAELISRLKLESLRHSLEERLQ 54
DB 342 ANGRVPLPHFPRTNRLPKEMTPVEPAFAELISRLKLESLRHSLEERLQ 395

RESULT 6
ID 042400 PRELIMINARY; PRT: 841 AA.

AC 042400;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE AXIN.
GN Gallus gallus (Chicken).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archaeoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97373830; PubMed=9230313;
RA Zeng L., Fagotto F., Zhang T., Hsu W., Vasilek T.J., Perry W.L.,
RA Iit Lee J.J., Tligman S.M., Gumbiner B.M., Costantini F.,
RA "The mouse fused locus encodes Axin, an inhibitor of the Wnt signaling
RT pathway that regulates embryonic axis formation."
RL Cell 90:181-192(1997).
DR EMBL: AF009012; AAC60245.1; -
DR HSSP: P49799; IAGR.
DR INTERPRO: IPR000342; -
DR INTERPRO: IPR001158; -
DR PFM: PF00778; RCS: 1.
DR PFM: PF00778; DIX: 1.
DR PRODOM: PD001580; -; 1.
DR PRODOM: PD003639; -; 1.
SQ SEQUENCE 841 AA: 94931 MW: 4000DC90E72506FE CRC64:

Query Match 57.9%; Score 157.5; DB 13; Length 841;
Best Local Similarity 59.3%; Pred. No. 4,8e-10;
Matches 32; Conservative 11; Mismatches 10; Indels 1; Gaps 1;

OY 1 ANGOVSLPHFPRTNRLPKEMTPVEPAFAELISRLKLESLRHSLEERLQ 54
DB 362 ANGRVPLPHFPRTNRLPKEMTPVEPAFAELISRLKLESLRHSLEERLQ 414

RESULT 7
ID 09PTP2 PRELIMINARY; PRT: 706 AA.

AC 09PTP2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE AXIN-RELATED PROTEIN.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodidae; Xenopus.
GN NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RA Itoh K., Antipova A., Ratcliffe M., Sokol S.;
RT "Dishevelled transduces a signal by displacing GSK3 from axin-GSK3

RT complex."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF140243; AAF22574.1; -
DR INTERPRO: IPR000342; -
DR INTERPRO: IPR001158; -
DR PFM: PF00778; DIX: 1.
DR PRINTS: PRO1301: RGSPROTEIN.
SQ SEQUENCE 706 AA: 79196 MW: C3D0AF0D9540F162 CRC64:

Query Match 52.9%; Score 144; DB 13; Length 706;
Best Local Similarity 55.6%; Pred. No. 1,5e-08;
Matches 30; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

OY 1 ANGOVSLPHFPRTNRLPKEMTPVEPAFAELISRLKLESLRHSLEERLQ 54
DB 303 ANGRVPLPHFPRTNRLPKEMTPVEPAFAELISRLKLESLRHSLEERLQ 356

RESULT 8
ID 070239 PRELIMINARY; PRT: 832 AA.

AC 070239;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96151361; PubMed=9482734;
RA Ikeda S., Yamamoto H., Murai H., Kishida S., Kikuchi A.;
RA "Axin, a negative regulator of the Wnt signaling pathway, forms a
RT complex with GSK-3beta and beta-catenin and promotes GSK-3beta-
RT dependent phosphorylation of beta-catenin."
RL EMBL: AF017756; AAC40066.1; -
DR HSSP: P49799; IAGR.
DR INTERPRO: IPR000342; -
DR INTERPRO: IPR001158; -
DR PFM: PF00778; RCS: 1.
DR PFM: PF00778; DIX: 1.
DR PRODOM: PD001580; -; 1.
DR PRODOM: PD003639; -; 1.
SQ SEQUENCE 832 AA: 92856 MW: B489504C7E594347 CRC64:

Query Match 52.4%; Score 142.5; DB 11; Length 832;
Best Local Similarity 56.6%; Pred. No. 2,6e-08;
Matches 30; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

OY 2 NGOVSLPHFPRTNRLPKEMTPVEPAFAELISRLKLESLRHSLEERLQ 54
DB 368 NGRVPLPHFPRTNRLPKEMTPVEPAFAELISRLKLESLRHSLEERLQ 419

RESULT 9
ID 035625 PRELIMINARY; PRT: 992 AA.

AC 035625;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE AXIN (FRAGMENT).
GN AXIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=97373830; PubMed=9230313;
RA Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perry W.L.,
RA Iii Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F.;
RT "The mouse fused locus encodes Axin, an inhibitor of the Wnt signaling
RT pathway that regulates embryonic axis formation.";
RL Cell 90:181-192(1997).
DR EMBL: AF009011; AAC53285.1; -.
DR HSSP: P49799; IAGR.
DR MGD: MGI:1096327; Axin.
DR INTERPRO: IPRO00342; -.
DR INTERPRO: IPRO01158; -.
DR PFAM: PF00615; RGS; 1.
DR PFAM: PF00778; DIX; 1.
DR PRINTS: PR01301; RGSPROTEIN.
FT NON_TER
SQ SEQUENCE 992 AA; 109917 MW; 70EEB53D387BD26F CRC64;

OY 2 NGVSLPHPEPTTHRLPKEMTPVEPAFAAELISRLKLESHRSLSERLQ 54
   ||| ||| |||||::|||:: ||| ||| ||| :: | : |||||:
Db 492 NGRVPLPIPIPTYRMFKRIR-VEPQFAEELLHRLAVQRTREAEKKLERLK 543

RESULT 10
O15169 PRELIMINARY; PRT; 900 AA.
ID O15169 AC O15169 DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE AXIN (FRAGMENT).
GN AXIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606; [1]
RP RP SEQUENCE FROM N.A.
RX MEDLINE=97373830; PubMed=9230313;
RA Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perry W.L.,
RA Iii Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F.;
RT "The mouse fused locus encodes Axin, an inhibitor of the Wnt signaling
RT pathway that regulates embryonic axis formation.";
RL Cell 90:181-192(1997).
DR EMBL: AF009674; AAC51624.1; -.
DR HSSP: P49799; IAGR.
DR INTERPRO: IPRO00342; -.
DR INTERPRO: IPRO01158; -.
DR PFAM: PF00615; RGS; 1.
DR PFAM: PF00778; DIX; 1.
DR PRINTS: PR01301; RGSPROTEIN.
FT NON_TER
SQ SEQUENCE 900 AA; 99803 MW; EE5F990B11FC7B3B CRC64;

Query Match 52.0%; Score 141.5; DB 4; Length 900;
Best Local Similarity 56.6%; Pred. No. 3.6e-08;
Matches 30; Conservative 8; Mismatches 14; Indels 1; Gaps 1;.

OY 2 NGVSLPHPEPTTHRLPKEMTPVEPAFAAELISRLKLESHRSLSERLQ 54
   ||| ||| |||||::|||:: ||| ||| ||| :: | : |||||:
Db 400 NGRVPLPIPIPTYRMFKRIR-VEPQFAEELLHRLAVQRTREAEKKLERLK 451

RESULT 11
O15169 PRELIMINARY; PRT; 842 AA.
ID O15169 AC O15169 DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE AXIN (FRAGMENT).
GN AXIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606; [1]
RP RP SEQUENCE FROM N.A.
RX MEDLINE=97373830; PubMed=9230313;
RA Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perry W.L.,
RA Iii Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F.;
RT "The mouse fused locus encodes Axin, an inhibitor of the Wnt signaling
RT pathway that regulates embryonic axis formation.";
RL Cell 90:181-192(1997).
DR EMBL: AF009674; AAC51624.1; -.
DR HSSP: P49799; IAGR.
DR INTERPRO: IPRO00342; -.
DR INTERPRO: IPRO01158; -.
DR PFAM: PF00615; RGS; 1.
DR PFAM: PF00778; DIX; 1.
DR PRINTS: PR01301; RGSPROTEIN.
FT NON_TER
SQ SEQUENCE 900 AA; 99803 MW; EE5F990B11FC7B3B CRC64;

Query Match 52.0%; Score 141.5; DB 4; Length 900;
Best Local Similarity 56.6%; Pred. No. 3.6e-08;
Matches 30; Conservative 8; Mismatches 14; Indels 1; Gaps 1;.

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01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE AXIN.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=99173782; PubMed=10072781;
RX Hedgepeth C.M., Dearnorff M.A., Klein P.S.;
RA "Xenopus axin interacts with glycogen synthase kinase-3 beta and is
RT expressed axin interact with glycogen synthase kinase-3 beta and is
RL Mech. Dev. 80:147-151(1999).
DR EMBL; AF097313; AAC71036.1; -.
DR HSSP; P49799; IAGR.
DR INTERPRO; IPR000342; -.
DR INTERPRO; IPR001158; -.
DR PFAM; PF00615; GGS; 1.
DR PFAM; PF00778; DIG; 1.
DR PRODOM; PD001580; -; 1.
DR PRODOM; PD003639; -; 1.
SO SEQUENCE 842 AA; 94459 MW; BDA152734C97191E CRC64;

Query Match 50.2%; Score 136.5; DB 13; Length 842;
Best Local Similarity 53.7%; Pred. No. 1.3e-07;
Matches 29; Conservative 10; Mismatches 14; Indels 1; Gaps 1;

QY 1 ANGVSLPHFPRTHRLPKEMTPVEPAAFAELISLLEKIKLELESRHSLERLQ 54
    |||: ||| |||: |||: |: ||||| |||: |: ||| |||:
DB 362 ANGRSPLPHIPRTYHMPKDI-HVDEKFAAELISRLGVLRDREAQKLEERLK 414

RESULT 12
Q9W7R4 ID Q9W7R4 PRELIMINARY; PRT. 2590 AA.
AC Q9W7R4;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE TEN-M3.
GN TEN-M3.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RN SEQUENCE FROM N.A.
RP Mleda M., Kikuchi Y., Hirate Y., Aoki M., Okamoto H.;
RT "Compartmentalized expression of zebrafish ten-m3 and ten-m4,
RT homologues of the Drosophila tenm /odd Oz gene, in the central nervous
RT system."
RL Mech. Dev. 0:0-0(1999).
DR EMBL; AB026979; BAA81892.1; -.
DR HSSP; P02468; IKLO.
DR INTERPRO; IPR000561; -.
DR INTERPRO; IPR002049; -.
DR PFAM; PF00008; EGF; 5.
DR PRINTS; PR00011; EGF_LAMININ.
DR PROSITE; PS00022; EGF_1; UNKNOWN_8.
DR PROSITE; PS01186; EGF_2; 7.
SO SEQUENCE 2590 AA; 288587 MW; 597592866219148D CRC64;

Query Match 25.0%; Score 68; DB 13; Length 2590;
Best Local Similarity 31.0%; Pred. No. 33;
Matches 22; Conservative 6; Mismatches 19; Indels 24; Gaps 2;

3 GOVSLPHFPRTHRLPKEMTPVEPAAFAAELISRLLEKLE-----PVEPAAFAAELISRLLEKLE----- 42

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DB 76 GGGTLPVPPPHNQPSVVALNHNLSRRNVPAPPALPALQTPPSVPLQDSWVLG 135
OY 43 -----LESRHS 49
DB 136 SNVPLESRHFL 146

RESULT 13
ID Q9RB10 PRELIMINARY; PRT; 226 AA.
AC Q9RB10;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
OS PUTATIVE 2-COMPONENT REGULATORY PROTEIN.
OC Acinetobacter sp. ADP1.
OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
OC Acinetobacter.
OX NCBI_TaxID=62977;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ADP1;
RT Jones R.M., Collier L.S., Neidie E.L., Williams P.A.;
RT "arABC genes determine the catabolism of aryl esters in Acinetobacter
RT sp. strain ADP1."
RL J. Bacteriol. 181:4568-4575(1999).
DR EMBL; AF150928; AAF04314.1; -
DR HSSP; P08402; 1B00.
DR INTERPRO: IPR001789; -
DR PFAM; PF00072; response_reg.1.
DR PFAM; PF00486; trans_reg_C.1.
SQ SEQUENCE 226 AA; 26423 MW; B3C1E64105C74DB CRC64;

Query Match 23.5%; Score 64; DB 2; Length 226;
Best Local Similarity 31.4%; Pred. No. 7.6;
Matches 16; Conservative 11; Mismatches 22; Indels 2; Gaps 1;

OY 3 GOVSLPHFPRTHRLPKEMTPVEPAFAELISRLKLELSRHSLEERT 53
DB 135 GOVOL--FPNTHRLTKDGPINSTKEMSTLEPMVMYVQDIFSKMLEERT 183

RESULT 14
ID 034449 PRELIMINARY; PRT; 251 AA.
AC 034449;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE YOOD. PROTEIN.
GN YOOD.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Scaphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RC MEDLINE=98044033; PubMed=9384377;
RA Kunze F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bartero M.G., Bessieres P., Bolotin A., Borcherdt S.,
RA Bourlès R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conerton I.F., Cummins N.J., Daniel R.A.,
RA Denzot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Eutlan K.D., Erington J., Fabre C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Gallitz A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Hatach J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

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RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koertter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic C.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medjerg C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Portolillo S., Prescott A.M.,
RA Presacan E., Puig P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sorokin A., Taccioni E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpsita P., Toognoni K.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler E., Welzenegger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kunze F., Ogasawara N., Yoshikawa H., Danchin A.;
RA Submitted (Nov-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z89114; CAB13959.1; -
DR EMBL; Z89115; CAB13985.1; -
SQ SEQUENCE 251 AA; 28593 MW; BE79F500A3A0E3C8 CRC64;

Query Match 23.0%; Score 62.5; DB 2; Length 251;
Best Local Similarity 32.1%; Pred. No. 13;
Matches 17; Conservative 13; Mismatches 18; Indels 5; Gaps 2;

OY 1 ANGVSLPHFPRTHR----LPKEMTPVEPAFAELISRLKLELSRHS 49
DB 62 ATGR-SLKHHHLRKGDVANKMTGAKGVLFPAQVYSKREMEKALKARPSL 113

RESULT 15
ID 064113 PRELIMINARY; PRT; 251 AA.
AC 064113;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DE 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE PUTATIVE ANTIREPRESSOR.
GN YOOD.
OS Bacteriophage SPBc2.
OC viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae.
OX NCBI_TaxID=66797;
RN [1]
RP SEQUENCE FROM N.A.
RA Lazarevic V., Dusterhoft A., Soldo B., Hilbert H., Mauel C.,
RA Karamata D.;
RU Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF020713; AAC13073.1; -
SQ SEQUENCE 251 AA; 28593 MW; BE79F500A3A0E3C8 CRC64;

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Query Match 23.0%; Score 62.5; DB 9; Length 251;
Best Local Similarity 32.1%; Pred. No. 13;
Matches 17; Conservative 13; Mismatches 18; Indels 5; Gaps 2;

OY 1 ANGVSLPHFPRTHR----LPKEMTPVEPAFAELISRLKLELSRHS 49
DB 62 ATGR-SLKHHHLRKGDVANKMTGAKGVLFPAQVYSKREMEKALKARPSL 113

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Search completed: June 7, 2001, 02:09:41
 Job time: 444 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 7, 2001, 02:01:17 ; Search time 80.96 Seconds
(without alignments)
48.719 Million cell updates/sec

Title: US-09-587-574-4

Perfect score: 360
Sequence: 1 QHDEEKEEGSEQALSSRDG.....VLKPGCGSPGVGRSPSR 69

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A.Geneseq-0401:*

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2: /SID2/gcgdata/geneseq/AA1981.DAT:*
3: /SID2/gcgdata/geneseq/AA1982.DAT:*
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5: /SID2/gcgdata/geneseq/AA1984.DAT:*
6: /SID2/gcgdata/geneseq/AA1985.DAT:*
7: /SID2/gcgdata/geneseq/AA1986.DAT:*
8: /SID2/gcgdata/geneseq/AA1987.DAT:*
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11: /SID2/gcgdata/geneseq/AA1990.DAT:*
12: /SID2/gcgdata/geneseq/AA1991.DAT:*
13: /SID2/gcgdata/geneseq/AA1992.DAT:*
14: /SID2/gcgdata/geneseq/AA1993.DAT:*
15: /SID2/gcgdata/geneseq/AA1994.DAT:*
16: /SID2/gcgdata/geneseq/AA1995.DAT:*
17: /SID2/gcgdata/geneseq/AA1996.DAT:*
18: /SID2/gcgdata/geneseq/AA1997.DAT:*
19: /SID2/gcgdata/geneseq/AA1998.DAT:*
20: /SID2/gcgdata/geneseq/AA1999.DAT:*
21: /SID2/gcgdata/geneseq/AA2000.DAT:*
22: /SID2/gcgdata/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	360	100.0	840	W93570	Human conductin pr
2	360	100.0	840	W93569	Human conductin pr
3	139.5	38.8	992	W96265	Murine axlin. Mus
4	113.5	31.5	900	W96264	Human axlin. Homo
5	68.5	19.0	441	R41875	Steroid hormone re
6	68.5	19.0	441	R89214	Peroxisome prolif
7	68.5	19.0	441	R05472	Human PPAR-delta p
8	68.5	19.0	1132	R77417	Human cell cycle p
9	68	18.9	397	W29659	Homo sapiens BP202
10	63.5	17.6	382	W44865	Human TPC3 telomer
11	63.5	17.6	434	W73959	Human TPC3 protein

12	63.5	17.6	605	21	Y57950	Human transmembran
13	62.5	17.4	1042	21	B11732	Cryptosporidium pa
14	62.5	17.4	1837	21	B11726	Cryptosporidium pa
15	62	17.2	303	21	G59725	Arabidopsis thalia
16	62	17.2	348	17	W01437	Murine cyclin-depe
17	62	17.2	375	21	G59724	Arabidopsis thalia
18	62	17.2	390	21	G59723	Arabidopsis thalia
19	61.5	17.1	144	21	G27248	Arabidopsis thalia
20	61.5	17.1	172	21	G21146	Zea mays protein f
21	61.5	17.1	917	21	G53920	Zea mays protein f
22	61	16.9	95	20	Y76563	A Bcl-2 associated
23	61	16.9	138	21	G10503	Human ovarian tumo
24	61	16.9	202	21	G10502	Arabidopsis thalia
25	61	16.9	204	21	G10501	Arabidopsis thalia
26	61	16.9	1490	22	B65644	Novel protein kina
27	60.5	16.8	474	20	Y40494	T. pallidum yael p
28	59.5	16.5	181	21	G33818	Arabidopsis thalia
29	59.5	16.5	186	21	G33817	Arabidopsis thalia
30	59.5	16.5	192	21	G33816	Arabidopsis thalia
31	59.5	16.5	216	21	G24174	Arabidopsis thalia
32	59.5	16.5	221	21	G24173	Arabidopsis thalia
33	59	16.4	700	12	R11354	Cellular Receptor
34	59	16.4	1498	16	R77085	Hamster sulphonylu
35	58	16.4	1582	16	R77088	Hamster sulphonylu
36	58	16.1	214	21	Y93216	Amino acid sequenc
37	58	16.1	567	16	R71700	Spleen necrosis vi
38	58	16.1	1498	16	R77084	Rat sulphonylurea
39	58	16.1	1582	16	R77087	Rat sulphonylurea
40	57.5	16.0	104	21	G40674	Zea mays protein f
41	57.5	16.0	104	21	G40680	Zea mays protein f
42	57.5	16.0	105	21	G12626	Zea mays protein f
43	57.5	16.0	129	21	G12625	Zea mays protein f
44	57.5	16.0	129	21	G40672	Zea mays protein f
45	57.5	16.0	138	21	Y79574	Human calpain 10h.

ALIGNMENTS

RESULT 1	W93570	W93570 standard; Protein: 840 AA.
XX	W93570;	
AC	17-JUN-1999	(first entry)
XX		
DE	Human conductin protein.	
XX		
KW	Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour;	
KW	therapy; cytoplasmic degradation; blockade; Wnt signalling pathway;	
KW	Wingless signalling pathway; Adenomatous Polyposis Coll.; APC;	
KW	tumour suppressor.	
XX		
OS	Homo sapiens.	
XX		
PN	W09911780-A2.	
XX		
PD	11-MAR-1999.	
XX		
PF	01-SEP-1998; 98MO-DE02621.	
XX		
PR	02-SEP-1997; 97DE-1038205.	
XX		
PA	(DELB-) DELBRUECK CENT MOLECULAR MEDIZIN MAX.	
XX		
PI	Behrens J, Birchmeier W;	
XX	WPI; 1999-214706/18.	
DR	N-PSDB; X23370.	
XX		
PT	Tumor-suppressing protein conductin - used for treatment and	
	diagnosis of tumors	

XX Claim 11; Fig 3; 22pp; German.
PS This invention describes a novel human conductin protein which has
XX anti-tumour activity. Detecting the presence or amount of conductin,
CC at protein or nucleic acid levels, is used to diagnose tumours, while
CC agents that (re)activate conductin are used for tumour therapy.
CC Conductin binds to beta-catenin and induces its cytoplasmic degradation,
CC resulting in blockade of the Wnt/Wingless signalling pathway in
CC vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC)
CC fragments and, in conjunction with APC, acts as a tumour suppressor.
XX Sequence 840 AA;
SQ

Query Match 100.0%; Score 360; DB 20; Length 840;
Best Local Similarity 100.0%; Pred. No. 2.9e-35;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QIREDEKEGSEQALSRDGAPOHPLALPESGYEDPOTITLDDHLSRVLTGCGSPG 60
DB 397 qiredeekesqalsrdsdgpvqphlallpsgsyedpqtllldhlsrvlktpcgspg 456
OY 61 VGRYSRPR 69
DB 457 vgrysprsr 465

RESULT 2
W93569
ID W93569 standard; Protein; 840 AA.
XX W93569;
XX 17-JUN-1999 (first entry)
DT
XX Human conductin protein.
DE
XX Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour;
KW therapy; cytoplasmic degradation; blockade; Wnt signalling pathway;
KW Wingless signalling pathway; Adenomatous Polyposis Coli; APC;
KW tumour suppressor.
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FT 78..200
FT /note= "Regulator of G protein signalling domain as
FT described in claim 12"
FT Binding-site 343..396
FT /note= "GSK 3-beta binding region as described in
FT claim 13"
FT Binding-site 397..465
FT /note= "Beta-catenin binding domain as described in
FT claim 14"
FT Region 783..833
FT /note= "Dishevelled homology region as described in
FT claim 15"
FT
FT
XX W09911780-A2.
XX
XX
XX 11-MAR-1999.
XX
XX 01-SEP-1998; 98WO-DE02621.
XX
XX 02-SEP-1997; 97DE-1038205.
XX
XX
XX (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX Behrens J, Birchmeier W;
XX WPI: 1999-214706/18.
XX
XX N-PSDB: X23369.
DR

XX Tumor-suppressing protein conductin - used for treatment and
PT diagnosis of tumors
XX
XX Claim 11; Fig 1; 22pp; German.
PS
XX This invention describes a novel human conductin protein which has
CC anti-tumour activity. Detecting the presence or amount of conductin,
CC at protein or nucleic acid levels, is used to diagnose tumours, while
CC agents that (re)activate conductin are used for tumour therapy.
CC Conductin binds to beta-catenin and induces its cytoplasmic degradation,
CC resulting in blockade of the Wnt/Wingless signalling pathway in
CC vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC)
CC fragments and, in conjunction with APC, acts as a tumour suppressor.
XX Sequence 840 AA;
SQ

Query Match 100.0%; Score 360; DB 20; Length 840;
Best Local Similarity 100.0%; Pred. No. 2.9e-35;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QIREDEKEGSEQALSRDGAPOHPLALPESGYEDPOTITLDDHLSRVLTGCGSPG 60
DB 397 qiredeekesqalsrdsdgpvqphlallpsgsyedpqtllldhlsrvlktpcgspg 456
OY 61 VGRYSRPR 69
DB 457 vgrysprsr 465

RESULT 3
W96265
ID W96265 standard; Protein; 992 AA.
XX W96265;
XX 14-JUN-1999 (first entry)
DT
XX Murine axin.
DE
XX Axin; cancer; breast cancer; colorectal cancer;
KW gastrointestinal cancer; esophageal cancer; carcinoma; melanoma;
KW diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;
KW beta-catenin.
XX
XX Mus musculus.
OS
XX
XX W09902179-A1.
XX
XX 21-JAN-1999.
XX
XX 09-JUL-1998; 98WO-US14414.
XX
XX 10-JUL-1997; 97US-0890865.
XX
XX (UYCO) UNIV COLUMBIA NEW YORK.
XX
XX Constantini F, Zeng L;
XX WPI: 1999-120510/10.
XX
XX N-PSDB: X09013.
XX
XX Newly isolated nucleic acid encoding "axis inhibition" protein
XX (Axin) - useful for detecting, diagnosing and treating cancer
XX
XX Claim 8; Figure 8; 95pp; English.
XX
XX Nucleic acids encoding mutant and wild type Axin and
CC oligonucleotides derived from them are useful for detecting
CC mutations in the axin gene and for determining whether a subject is
CC likely to develop cancer (including breast, colorectal,
CC gastrointestinal, esophageal, carcinomas or melanomas). The wild

CC type Axin and homologues of Axin are useful for treating subjects
 CC who are likely to develop cancer (thyroid carcinomas). The nucleic
 CC acids are also useful for diagnosing cancer and for detecting
 CC mutations in cancerous cells. Wild type Axin, its antisense
 CC molecule and identified compounds form pharmaceutical compositions
 CC in the treatment of cancer. The compositions are also useful for
 CC treating cancer by inhibiting tumorigenesis (by inducing degradation
 CC of beta-catenin). The nucleic acid encoding Axin acts through
 CC negative regulation of the Wnt pathway in the Nieuwkoop Center.
 XX
 SQ Sequence 992 AA:

Query Match 38.8%; Score 139.5; DB 20; Length 992;
 Best Local Similarity 35.3%; Pred. No. 2,4e-08;
 Matches 30; Conservative 14; Mismatches 20; Indels 21; Gaps 2;

OY 1 QIRDEDEKESQALSRDGAAPVQHPLALPS-----GSYEEDPQTIL 43
 Db 544 ryvmeeggedgemp-----sgymashkliprvpawhfprryvdmgsglrdahenpestll 599
 OY 44 DDLHSRLVLTGPGCQSPGVGRYSPRS 68
 Db 600 dehvgrvmrtpgcgspgphrpsds 624

RESULT 4

W96264 W96264 standard; Protein: 900 AA.

AC W96264;

DT 14-JUN-1999 (first entry)

XX Human axin.

XX Axin: cancer; breast cancer; colorectal cancer;

KM gastrointestinal cancer; esophageal cancer; carcinoma; melanoma;
 KM diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;
 KW beta-catenin.

XX Homo sapiens.

OS Homo sapiens.

PN W09902179-A1.

PD 21-JAN-1999.

XX 09-JUL-1998; 98MO-US14414.

XX 10-JUL-1997; 97US-0890865.

PA (UYCO) UNIV COLUMBIA NEW YORK.

PI Constantini F, Zeng L;

XX WPI: 1999-120510/10.

DR N-PSDB; X09012.

XX Newly isolated nucleic acid encoding "axis inhibition" protein
 PT (Axin) - useful for detecting, diagnosing and treating cancer
 PT
 XX
 PS Disclosure: Figure 11; 95pp; English.

CC Nucleic acids encoding mutant and wild type Axin and
 CC oligonucleotides derived from them are useful for detecting
 CC mutations in the Axin gene and for determining whether a subject is
 CC likely to develop cancer (including breast, colorectal,
 CC gastrointestinal, esophageal, carcinomas or melanomas). The wild
 CC type Axin and homologues of Axin are useful for treating subjects
 CC who are likely to develop cancer (thyroid carcinomas). The nucleic
 CC acids are also useful for diagnosing cancer and for detecting
 CC mutations in cancerous cells. Wild type Axin, its antisense
 CC molecule and identified compounds form pharmaceutical compositions

CC in the treatment of cancer. The compositions are also useful for
 CC treating cancer by inhibiting tumorigenesis (by inducing degradation
 CC of beta-catenin). The nucleic acid encoding Axin acts through
 CC negative regulation of the Wnt pathway in the Nieuwkoop Center.
 XX
 SQ Sequence 900 AA:

Query Match 31.5%; Score 113.5; DB 20; Length 900;
 Best Local Similarity 34.4%; Pred. No. 3.1e-05;
 Matches 33; Conservative 10; Mismatches 22; Indels 31; Gaps 3;

OY 3 REDEEK-----EGSQALSRDGAAPVQHPLALPS----- 32
 Db 440 reeeekleerlkvrmeeggedgdpssgppgpc-hklppapawhfprrlwtacaglr 498
 OY 33 GSYEDDPQTILDDLHSRLVLTGPGCQSPGVGRYSPRS 68
 Db 499 dahenpestlldehvgrvrlrttgrrgspgphrpsds 534

RESULT 5

R41875 R41875 standard; Protein: 441 AA.

XX R41875;

DT 13-APR-1994 (first entry)

XX Steroid hormone receptor (NUC1).

KM Steroid; hormone; receptor; osteosarcoma; superfamily.

XX Homo sapiens.

PN GB2265376-A.

XX 29-SEP-1993.

XX 23-MAR-1993; 93GB-0006043.

XX 24-MAR-1992; 92US-0857055.

PA (MERI) MERCK & CO INC.

XX Rodan GA, Rutledge SJ, Schmidt A, Vogel RJ;

DR WPI: 1993-305586/39.

XX N-PSDB; Q48939.

XX New human steroid hormone receptor NUC1 - used to assay and
 PT evaluate ligands binding to the receptor
 PT
 XX
 PS Claim 5; Page 39-40; 62pp; English.

CC The steroid hormone receptor (designated NUC1) is used in assays to
 CC identify and evaluate chemical entities that bind to it.
 CC
 XX

SQ Sequence 441 AA:

Query Match 19.0%; Score 68.5; DB 14; Length 441;
 Best Local Similarity 30.3%; Pred. No. 3.8;
 Matches 23; Conservative 10; Mismatches 26; Indels 17; Gaps 4;

OY 1 QIRDEDEKESQALSRDGAAPVQH--PLALPESYEE-----DPQTILDDLHSRLVLT 53
 Db 10 evreeekkeevaa-----egapelnsgpqhlpssytdlstrsspslldq-----1q 59
 OY 54 PGCGSPGVGRYSPRSR 69
 Db 60 mcydgagsgslnmecr 75

```
RESULT 6
R89214
ID R89214 standard; Protein; 441 AA.
XX
AC R89214;
XX
DT 03-APR-1996 (first entry)
XX
DE Peroxisome proliferator activated receptor hNUC1B.
XX
KM hNUC1B; peroxisome proliferator activated receptor; hyperlipidemia;
KW hypercholesterolemia; hyperlipoproteinemia.
XX
OS Homo sapiens.
XX
PN M09601430-A2.
XX
PD 18-JAN-1996.
XX
PF 29-JUN-1995; 95MO-US08328.
XX
PR 01-JUL-1994; 94US-0270635.
XX
PA (LIGA-) LIGAND PHARM INC.
XX
PI Mukherjee R;
XX
DR WPI: 1996-087756/09.
DR N-PSDB; T10583.
XX
PT Screening methods for identifying NUC protein inhibitors - for use
PT as potential agents for the treatment of hyperlipidemia,
PT hypercholesterolemia and hyperlipoproteinemia
XX
PS Claim 44; Page 29-31; 45pp; English.
XX
CC A novel human peroxisome proliferator activated receptor (PPAR),
CC designated hNUC1B (R89214), is expressed from a cDNA clone (T10583)
CC isolated from a human kidney cDNA library. hNUC1B is a member of
CC the PPAR family and can be used to screen NUC protein inhibitors.
XX
SQ Sequence 441 AA;

Query Match 19.0%; Score 68.5; DB 17; Length 441;
Best Local Similarity 30.3%; Pred. No. 3.8;
Matches 23; Conservative 10; Mismatches 26; Indels 17; Gaps 4;

OY 1 QIREDEKEGSEQALSSRDGAPVQH--PLALLPSGSYE-----DPQTLLDDHLSRVLKT 53
   ::||:|||||:|:|||||:| ||| ||:|:|
DB 10 evreeeekveeaea---egapelngpqpahlpsssyldlrrssppslldq-----1q 59
OY 54 PGCQSPGVGRYSPPRSR 69
   ||| | : |
DB 60 mgcdgascgslnmeqr 75

RESULT 7
Y05472
ID Y05472 standard; Protein; 441 AA.
XX
AC Y05472;
XX
DT 07-JUL-1999 (first entry)
XX
DE Human PPAR-delta protein sequence.
XX
KM Nuclear receptor agonist; antagonist; identification; PPAR;
KW peroxisome proliferator activated receptor.
XX
OS Homo sapiens.
XX
```

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PN M09918124-A1.
XX
PD 15-APR-1999.
XX
PF 06-OCT-1998; 98MO-US21049.
XX
PR 07-OCT-1997; 97US-0061385.
XX
PA (MERI ) MERCK & CO INC.
XX
PI Cummings RT, Hermes JD, Moller DE, Zhou G;
XX
DR WPI: 1999-263998/22.
DR N-PSDB; X36523.
XX
PT Identifying nuclear receptor agonists and antagonists
XX
PS Disclosure; Fig 10a; 60pp; English.
XX
CC This sequence is the human peroxisome proliferator activated
CC receptor delta (PPAR-delta).
CC The invention relates to a method for identifying nuclear receptor
CC agonists and antagonists comprising measuring fluorescent resonance energy
CC transfer between fluorescent-labelled nuclear receptors and
CC co-activators. The method can be used for identifying agonists and
CC antagonist of nuclear receptors.
XX
SQ Sequence 441 AA;

Query Match 19.0%; Score 68.5; DB 20; Length 441;
Best Local Similarity 30.3%; Pred. No. 3.8;
Matches 23; Conservative 10; Mismatches 26; Indels 17; Gaps 4;

OY 1 QIREDEKEGSEQALSSRDGAPVQH--PLALLPSGSYE-----DPQTLLDDHLSRVLKT 53
   ::||:|||||:|:|||||:| ||| ||:|:|
DB 10 evreeeekveeaea---egapelngpqpahlpsssyldlrrssppslldq-----1q 59
OY 54 PGCQSPGVGRYSPPRSR 69
   ||| | : |
DB 60 mgcdgascgslnmeqr 75

RESULT 8
R77417
ID R77417 standard; Protein; 1132 AA.
XX
AC R77417;
XX
DT 08-AUG-1996 (first entry)
XX
DE Human cell cycle protein min1.
XX
KM Human; MIN1; cell cycle; G2/M border; progression; cdc2 kinase; yeast;
KW functional complementation; weel; mik1; mutant; cancer; development;
KW antimitotic factor; mitosis.
XX
OS Homo sapiens.
XX
PN JF07274971-A.
XX
PD 24-OCT-1995.
XX
PF 05-APR-1994; 94JP-0093033.
XX
PR 05-APR-1994; 94JP-0093033.
XX
PA (SHKJ ) SHINGIJUTSU JIGYODAN.
XX
KM WPI: 1995-399339/51.
DR N-PSDB; T05406.
XX
PT Human derived cell cycle gene encoding an anti-mitotic factor - used
```

Pr In the control of the G2/M phase of the cell cycle.

XX Claim 1: Page 4; 5pp; Japanese.

CC This is the amino acid sequence of the human MINI gene product. The
CC protein has a mol. wt. about 129 kD. The gene is expressed at the G2/M
CC border of the cell cycle and can inactivate the cell cycle progression
CC protein cdc2 kinase. The gene was isolated by functional complementation
CC of a yeast wee1/mki1 mutant strain. The gene and protein can be used in
CC the determination of cancer cell development and as an antimitotic
CC factor.

XX Sequence 1132 AA;

Query Match 19.0%; Score 68.5; DB 16; Length 1132;
Best Local Similarity 31.5%; Pred. No. 12;
Matches 23; Conservative 9; Mismatches 26; Indels 15; Gaps 3;

QY 1 QIREDEKESQALSSRDGAPVQHPLALLPSGSEYEDPQTILDDH-----LSRV 50

Db 976 qtleqlpkdhdhdfst---cpdqhrllpsfqgseddddlpmndknpptpsvlfpl 1032

QY 51 LKTPGCO--SPGV 61

Db 1033 vktpqgqhvspgm 1045

RESULT 9

W29659
ID W29659 standard; Protein; 397 AA.

XX W29659;

AC 18-FEB-1999 (first entry)

DE Homo sapiens BP202_3 clone secreted protein.

XX secreted protein; BP202_3.

XX Homo sapiens.

PN W09830695-A2.

PD 16-JUL-1998.

PF 09-JAN-1998; 98WO-US00543.

PR 08-JAN-1998; 98US-0004684.

PR 09-JAN-1997; 97US-0780814.

PA (GENE) GENETICS INST INC.

PI Agostino MJ, Jacobs K, Lavalije ER, McCoy JM, Merberg D;

PI Racie LA, Spaulding V, Treacy M;

DR WPI: 1998-413686/35.

DR N-PSDB; V40520.

XX New isolated nucleic acids and secreted proteins - obtained from
XX human adult ovary, human foetal kidney, human foetal brain and human
XX adult brain cDNA libraries

PS Disclosure; Page 67-68; 113pp; English.

XX The sequence is that of a novel, isolated secreted protein.

XX Sequence 397 AA;

Query Match 18.9%; Score 68; DB 19; Length 397;
Best Local Similarity 32.9%; Pred. No. 3.9;
Matches 25; Conservative 10; Mismatches 23; Indels 18; Gaps 4;

QY 1 QIREDE---KESQALSSRDGAPVQHPLALLPSGSEYEDPQTILDDH-----L 47

Db 238 qmrefleqlpkdhdhdfst---cpdqhrllpsfqgseddddlpmndknpptpsvlf 294

QY 48 SRVLTGPGCO--SPGV 61

Db 295 flvktpqgqhvspgm 310

RESULT 10

W44865
ID W44865 standard; Protein; 382 AA.

XX W44865;

DT 28-AUG-1998 (first entry)

DE Human TPC3 telomere length and telomerase regulatory protein.

KW TPC3; telomere length; telomerase; human; cancer; gene therapy;

KW diagnosis; vaccine.

XX Homo sapiens.

PN W09811204-A1.

PD 19-MAR-1998.

PF 13-SEP-1996; 96WO-US14679.

PR 13-SEP-1996; 96WO-US14679.

PA (GERO-) GERON CORP.

PI Adams RR, Andrews WH, Feng J, Villeponteau B;

DR WPI: 1998-207373/18.

DR N-PSDB; V19480.

XX Human TPC2, TPC3 and TR genes - regulate telomere length or modulate

XX telomerase activity

PS Disclosure; Fig 6A-C; 86pp; English.

XX This polypeptide comprises human TPC3, a protein that regulates
XX telomere length or modulates telomerase activity. Its amino acid
XX sequence was deduced from a cDNA clone (see V19480) obtained from a
XX human 293 cell library. TPC3 and TPC2 (see W44864) proteins can be
XX obtained by purification from natural sources, by in vitro
XX synthesis or by purification from recombinant host cells. They
XX have application in methods for reconstituting in vitro telomerase
XX or other enzymatic activities that maintain telomeres and regulate
XX telomere length. These methods have application in screens for
XX therapeutic agents, and for diagnostic tests. In addition,

XX peptides corresponding to TPC2 or TPC3 proteins can also be used to
XX regulate telomere length and telomerase activity in mammalian
XX cells. Immunogenic peptides and proteins of the invention can also
XX be used in therapeutic immunisation and vaccination procedures.
XX Antibodies that specifically bind to TPC2 or TPC3 proteins can
XX be used in screening, diagnosing and monitoring diseases and other
XX conditions, such as cancer, pregnancy or fertility.

XX Sequence 382 AA;

Query Match 17.6%; Score 63.5; DB 19; Length 382;
Best Local Similarity 35.0%; Pred. No. 13;
Matches 21; Conservative 9; Mismatches 17; Indels 13; Gaps 4;

QY 11 SEQALSSRDGAPVQHPLALLPSGSEYEDPQTILDDHLSRVLTGPGCO--SPGV 68
Db 184 seq--sasesapddqp-----dreedpragaed--pkexgpadsklgckrgspka 232

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RESULT 11
W73959
ID W73959 standard; Protein; 434 AA.
XX
XX AC W73959;
XX
XX DT 29-APR-1999 (first entry)
XX
XX DE Human TPC3 protein.
XX
XX TPC2; TPC3; human; telomere length regulation; cancer; pregnancy;
XX fertility; diagnosis; therapy.
XX
XX OS Homo sapiens.
XX
XX PN US5858777-A.
XX
XX PD 12-JAN-1999.
XX
XX PF 13-SEP-1996; 96US-0710249.
XX
XX PR 08-SEP-1995; 95US-0003492.
XX 05-JAN-1996; 96US-0583808.
XX 13-SEP-1996; 96US-0710249.
XX
XX PA (GERO-) GERON CORP.
XX
XX PI Adams RR, Andrews WH, Feng J, Villeponteau B;
XX
XX DR WPI: 1999-152104/13.
XX
XX DR N-PSDB: X01534.
XX
XX PT DNA encoding proteins TPC2 and TPC3 - useful for regulating telomere
XX length or modulating telomerase activity
XX
XX PS Disclosure; Fig 6; 59pp; English.
XX
XX CC This sequence is the human TPC3 protein, which is contained within
XX the recombinant mammalian host cell of the invention. The invention
XX provides methods and reagents for regulating telomere length and
XX modulating telomerase activity in mammalian cells as well as for
XX detecting, diagnosing, and treating related diseases and conditions such
XX as cancer, pregnancy, or fertility in humans and other mammals.
XX
XX SQ Sequence 434 AA;

Query Match 17.6%; Score 63.5; DB 20; Length 434;
Best Local Similarity 35.0%; Pred. No. 15;
Matches 21; Conservative 9; Mismatches 17; Indels 13; Gaps 4;

QY 11 SEQALSSRDGAPVQHPLALPSGSYEEDPQTILDHLSRYLKTGPCQSPGVG--RYSPRS 68
||| | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 236 seq--sasesapedgp-----dreedpragaed--pkaekspgadskgjgckrgspka 284

RESULT 12
Y57950
ID Y57950 standard; Protein; 605 AA.
XX
XX AC Y57950;
XX
XX DT 23-MAR-2000 (first entry)
XX
XX DE Human transmembrane protein HTPMN-74.
XX
XX KW Human; transmembrane protein; HTPMN; diagnosis; immunospecific;
XX antiproliferative; neuroprotective; immune disorder;
XX reproductive disorder; smooth muscle disorder; neurological disorder;
XX gastrointestinal disorder; developmental disorder;
XX cell proliferative disorder.

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XX
XX OS Homo sapiens.
XX
XX PN W09961471-A2.
XX
XX PD 02-DEC-1999.
XX
XX PF 28-MAY-1999; 99WO-US11904.
XX
XX PR 29-MAY-1998; 98US-0087260.
XX 02-JUL-1998; 98US-0091674.
XX 02-OCT-1998; 98US-0102954.
XX 24-NOV-1998; 98US-0109869.
XX
XX PA (INCY-) INCYTE PHARM INC.
XX
XX PI Tang YT, Lal P, Hillman JL, Yue H, Guegler KJ, Corley NC;
XX Bandman O, Patterson C, Gorgone GA, Kaser MR, Baughn MR;
XX Au-Young J;
XX
XX DR WPI: 2000-072605/06.
XX
XX DR N-PSDB: Z56771.
XX
XX PT Proteins, polynucleotides, vectors, host cells and antibodies used to
XX diagnose, treat or prevent immune, reproductive, smooth muscle,
XX neurological, gastrointestinal, developmental and cell proliferative
XX disorders -
XX
XX PS Claim 1; Page 172-174; 229pp; English.
XX
XX SQ Sequence 605 AA;

Query Match 17.6%; Score 63.5; DB 21; Length 605;
Best Local Similarity 33.9%; Pred. No. 23;
Matches 19; Conservative 10; Mismatches 24; Indels 3; Gaps 2;

QY 3 REDEKEGSEQALSSR--DGAPVQHPLALP-SGSYEEDPQTILDHLSRYLKTGP 55
||| | | : | : | : | | | | | | | | | | | | | | | | | | | | | |
Db 161 reeeeeeekemeekveekqdvveeeelipvngsgeakpqvdfststssqtpg 216

RESULT 13
B11732
ID B11732 standard; Protein; 1042 AA.
XX
XX AC B11732;
XX
XX DT 28-OCT-2000 (first entry)
XX
XX DE Cryptosporidium parvum Iowa isolate GP900, domain 5.
XX
XX KW GP900; Iowa isolate; glycoprotein; antibody; cryptosporidiosis;
XX competitive inhibition; attachment; invasion; ligand binding; sporozoite;
XX merozoite; diarrhoea; protozoacide; domain 5; transmembrane domain;
XX cytoplasmic domain.
XX
XX OS Cryptosporidium parvum.
XX
XX PN US6071518-A.
XX
XX DT 06-JUN-2000.

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XX 12-SEP-1997; 97US-0928361.
PF 13-SEP-1996; 96US-0026062.
XX 01-JUN-1993; 93US-0071880.
PR 29-MAY-1992; 92US-0891301.
PR 03-APR-1995; 95US-0415751.
PR 14-AUG-1996; 96US-0700651.
XX (RECC) UNIV CALIFORNIA.
PA
XX
PI Petersen C;
XX WPI: 2000-422065/36.
XX
XX New GP900 protein fragments and fusion proteins of Cryptosporidium
PT parvum, useful for detecting the presence of the parasite, and
PT diagnosing or treating Cryptosporidium infections by competitive
PT inhibition of the function of GP900 -
PS
XX Claim 3; Column 73-80; 59pp; English.
XX
XX The invention relates to the GP900 glycoprotein of the protozoan
CC Cryptosporidium parvum, DNA encoding it, GP900 fragments, and fusion
CC proteins comprising GP900 fragments. The invention also relates to the
CC administration of GP900 or fragments thereof to a host to elicit anti-
CC GP900 antibody production, and to a method of cryptosporidiosis treatment
CC or prophylaxis comprising administration of anti-GP900 antibodies to an
CC individual. Cryptosporidium parvum GP900 and GP900 fragments are able to
CC competitively inhibit sporozoite or merozoite attachment or invasion, and
CC are also useful for the generation of anti-GP900 antibodies. The
CC antibodies also inhibit sporozoite or merozoite attachment/invasion and
CC additionally inhibit the binding of GP900 ligands to GP900. GP900
CC proteins, fragments and antibodies may therefore be used to treat or
CC prevent cryptosporidiosis. Infection with Cryptosporidium is a common
CC cause of diarrhoea in humans and causes life-threatening diarrhoea in
CC immunocompromised persons. Cryptosporidiosis can be contracted from
CC contaminated municipal water supplies (e.g., public swimming pools). It
CC is also a cause of disease in animals, resulting in financial losses in
CC agriculture. GP900 fragments, fusion proteins and antibodies may also be
CC used for the diagnosis of Cryptosporidium parvum infections, and for the
CC detection of the parasite in the environment. Sequences B11728-B11732
CC represent the different domains of the Cryptosporidium parvum Iowa
CC isolate GP900 protein (B11726). The present sequence is that of domain 5
CC of GP900, which contains a putative transmembrane domain and a
CC cytoplasmic domain.
CC
XX
SQ Sequence 1042 AA;
Query Match 17.4%; Score 62.5; DB 21; Length 1042;
Best Local Similarity 29.2%; Pred. No. 59;
Matches 21; Conservative 8; Mismatches 26; Indels 17; Gaps 3;
OY 8 KEGSEALSSROGAPVQHLLALPSGSYEEDPOT-----ILDDHLRLVLT-PCG 56
DB 857 kagsgskdsdesgnpid-----pstrmpydkptkylidpesgiaidnsygvfatvpgt 910
OY 57 QSPGVGRYSPRS 68
DB 911 aapkgvgrvipes 922
RESULT 14
ID B11726
XX B11726 standard; Protein: 1837 AA.
AC B11726;
XX 28-OCT-2000 (first entry)
DT
XX Cryptosporidium parvum Iowa isolate GP900.
XX

KW GP900; Iowa isolate; glycoprotein; antibody; cryptosporidiosis;
KM competitive inhibition; attachment; invasion; ligand binding; sporozoite;
KW merozoite; diarrhoea; protozoacide.
XX
XX Cryptosporidium parvum.
OS
XX
XX Key location/Qualifiers
FH Misc-difference 1785 /note="Encoded by AAC in A61846"
FT
XX
XX US6071518-A.
XX
XX 06-JUN-2000.
PD
XX
XX 12-SEP-1997; 97US-0928361.
PF
XX 13-SEP-1996; 96US-0026062.
PR 01-JUN-1993; 93US-0071880.
PR 29-MAY-1992; 92US-0891301.
PR 03-APR-1995; 95US-0415751.
PR 14-AUG-1996; 96US-0700651.
XX
XX (RECC) UNIV CALIFORNIA.
XX
XX Petersen C;
PI
XX WPI: 2000-422065/36.
DR N-PSDB; A61846, A61847.
XX
XX New GP900 protein fragments and fusion proteins of Cryptosporidium
PT parvum, useful for detecting the presence of the parasite, and
PT diagnosing or treating Cryptosporidium infections by competitive
PT inhibition of the function of GP900 -
PS
XX Claim 2; Column 51-60; 59pp; English.
XX
XX The invention relates to the GP900 glycoprotein of the protozoan
CC Cryptosporidium parvum, DNA encoding it, GP900 fragments, and fusion
CC proteins comprising GP900 fragments. The invention also relates to the
CC administration of GP900 or fragments thereof to a host to elicit anti-
CC GP900 antibody production, and to a method of cryptosporidiosis treatment
CC or prophylaxis comprising administration of anti-GP900 antibodies to an
CC individual. Cryptosporidium parvum GP900 and GP900 fragments are able to
CC competitively inhibit sporozoite or merozoite attachment or invasion, and
CC are also useful for the generation of anti-GP900 antibodies. The
CC antibodies also inhibit sporozoite or merozoite attachment/invasion and
CC additionally inhibit the binding of GP900 ligands to GP900. GP900
CC proteins, fragments and antibodies may therefore be used to treat or
CC prevent cryptosporidiosis. Infection with Cryptosporidium is a common
CC cause of diarrhoea in humans and causes life-threatening diarrhoea in
CC immunocompromised persons. Cryptosporidiosis can be contracted from
CC contaminated municipal water supplies (e.g., public swimming pools). It
CC is also a cause of disease in animals, resulting in financial losses in
CC agriculture. GP900 fragments, fusion proteins and antibodies may also be
CC used for the diagnosis of Cryptosporidium parvum infections, and for the
CC detection of the parasite in the environment. The present sequence
CC represents the GP900 protein of the Iowa isolate of Cryptosporidium
CC parvum.
CC
XX
SQ Sequence 1837 AA;
Query Match 17.4%; Score 62.5; DB 21; Length 1837;
Best Local Similarity 29.2%; Pred. No. 1,2e+02;
Matches 21; Conservative 8; Mismatches 26; Indels 17; Gaps 3;
OY 8 KEGSEALSSROGAPVQHLLALPSGSYEEDPOT-----ILDDHLRLVLT-PCG 56
DB 1652 kagsgskdsdesgnpid-----pstrmpydkptkylidpesgiaidnsygvfatvpgt 1705
OY 57 QSPGVGRYSPRS 68
DB 1706 aapkgvgrvipes 1717

RESULT 15
ID G59725 standard; Protein; 303 AA.
XX G59725;
AC
XX
DT 18-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana protein fragment SEQ ID NO: 77283.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
XX Arabidopsis thaliana.
PN EP1033405-A2.
PD
XX 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123348.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 03-JUN-1999; 99US-0137529.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139452.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.

PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 18-JUN-1999; 99US-0139817.
PR 21-JUN-1999; 99US-0139899.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 26-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 06-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144335.
PR 19-JUL-1999; 99US-0144335.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 28-JUL-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147112.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.

PR	20-AUG-1999;	99US-0149722.
PR	20-AUG-1999;	99US-0149723.
PR	20-AUG-1999;	99US-0149929.
PR	23-AUG-1999;	99US-0149902.
PR	23-AUG-1999;	99US-0149930.
PR	25-AUG-1999;	99US-0150566.
PR	26-AUG-1999;	99US-0150884.
PR	27-AUG-1999;	99US-0151065.
PR	27-AUG-1999;	99US-0151066.
PR	27-AUG-1999;	99US-0151080.
PR	30-AUG-1999;	99US-0151303.
PR	31-AUG-1999;	99US-0151438.
PR	01-SEP-1999;	99US-0151930.
PR	07-SEP-1999;	99US-0152363.
PR	10-SEP-1999;	99US-0153070.
PR	13-SEP-1999;	99US-0153758.
PR	15-SEP-1999;	99US-0154018.
PR	16-SEP-1999;	99US-0154039.
PR	20-SEP-1999;	99US-0154779.
PR	22-SEP-1999;	99US-0155139.
PR	23-SEP-1999;	99US-0155486.
PR	24-SEP-1999;	99US-0155659.
PR	28-SEP-1999;	99US-0156458.
PR	29-SEP-1999;	99US-0156596.
PR	04-OCT-1999;	99US-0157117.
PR	05-OCT-1999;	99US-0157753.
PR	06-OCT-1999;	99US-0157865.
PR	07-OCT-1999;	99US-0158029.
PR	08-OCT-1999;	99US-0158232.
PR	12-OCT-1999;	99US-0158369.
PR	13-OCT-1999;	99US-0159293.
PR	13-OCT-1999;	99US-0159294.
PR	13-OCT-1999;	99US-0159285.
PR	14-OCT-1999;	99US-0159329.
PR	14-OCT-1999;	99US-0159330.
PR	14-OCT-1999;	99US-0159331.
PR	14-OCT-1999;	99US-0159637.
PR	14-OCT-1999;	99US-0159638.
PR	18-OCT-1999;	99US-0159584.
PR	21-OCT-1999;	99US-0160741.
PR	21-OCT-1999;	99US-0160767.
PR	21-OCT-1999;	99US-0160768.
PR	21-OCT-1999;	99US-0160770.
PR	21-OCT-1999;	99US-0160814.
PR	21-OCT-1999;	99US-0160815.
PR	22-OCT-1999;	99US-0160980.
PR	22-OCT-1999;	99US-0160981.
PR	22-OCT-1999;	99US-0160989.
PR	25-OCT-1999;	99US-0161404.
PR	25-OCT-1999;	99US-0161405.
PR	25-OCT-1999;	99US-0161406.
PR	26-OCT-1999;	99US-0161359.
PR	26-OCT-1999;	99US-0161360.
PR	26-OCT-1999;	99US-0161361.
PR	28-OCT-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161992.
PR	28-OCT-1999;	99US-0161993.
PR	29-OCT-1999;	99US-0162142.

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Query Match      17.2%  Score 62:  DB 21; Length 303;
Best Local Similarity 36.0%  Pred. No. 15;
Matches 18: Conservative 9; Mismatches 19; Indels 4; Gaps 2.

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      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Obb 71 elssseeeelssmearvgnqnsqg---seameddqsdlitlreler 117

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Search completed: June 7, 2001, 02:01:18
Job time: 5660 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2001, 02:02:10 ; Search time 40.76 Seconds

(without alignments)
32.521 Million cell updates/sec

Title: US-09-587-574-4

Perfect score: 360
Sequence: 1 QIREDEKRGSEGLASSRDC.....VLKTPCGSPGVGRVSPRR 69Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/2/1aa/5A-COMB.pep: *
2: /cgn2_6/ptodata/2/1aa/5B-COMB.pep: *
3: /cgn2_6/ptodata/2/1aa/6A-COMB.pep: *
4: /cgn2_6/ptodata/2/1aa/6B-COMB.pep: *
5: /cgn2_6/ptodata/2/1aa/6C-COMB.pep: *
6: /cgn2_6/ptodata/2/1aa/Backfile1.pep: *Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	63.5	17.6	434	2 US-08-710-249-4	Sequence 4, Appl1
2	62.5	17.4	1042	3 US-08-928-361B-11	Sequence 11, Appl1
3	62.5	17.4	1837	3 US-08-928-361B-5	Sequence 5, Appl1
4	62	17.2	348	3 US-08-415-655-5	Sequence 13, Appl1
5	62	17.2	348	3 US-08-415-655-13	Sequence 15, Appl1
6	62	17.2	348	3 US-08-415-655-15	Sequence 29, Appl1
7	59	16.4	1498	2 US-08-404-531B-29	Sequence 29, Appl1
8	59	16.4	1498	2 US-08-476-900A-29	Sequence 29, Appl1
9	59	16.4	1498	3 US-08-488-546A-29	Sequence 29, Appl1
10	59	16.4	1582	2 US-08-404-531B-9	Sequence 9, Appl1
11	59	16.4	1582	2 US-08-476-900A-9	Sequence 9, Appl1
12	59	16.4	1582	3 US-08-488-546A-9	Sequence 9, Appl1
13	59	16.4	1582	3 US-08-726-320-5	Sequence 5, Appl1
14	58	16.1	567	1 US-08-007-282B-8	Sequence 2, Appl1
15	58	16.1	1498	2 US-08-404-531B-28	Sequence 28, Appl1
16	58	16.1	1498	2 US-08-476-900A-28	Sequence 28, Appl1
17	58	16.1	1498	3 US-08-488-546A-28	Sequence 28, Appl1
18	58	16.1	1581	2 US-08-404-531B-6	Sequence 6, Appl1
19	58	16.1	1581	3 US-08-476-900A-6	Sequence 6, Appl1
20	58	16.1	1581	3 US-08-488-546A-6	Sequence 6, Appl1
21	58	16.1	1581	4 US-08-726-320-4	Sequence 4, Appl1
22	57.5	16.0	1043	3 US-08-928-361B-30	Sequence 30, Appl1
23	57.5	16.0	1721	3 US-08-700-651-5	Sequence 5, Appl1
24	57.5	16.0	1721	3 US-08-928-361B-6	Sequence 6, Appl1
25	57.5	16.0	352	4 US-09-102-204-1	Sequence 11, Appl1
26	57	15.8	416	2 US-09-211-930-11	Sequence 11, Appl1
27	57	15.8	416	3 US-09-340-993-11	Sequence 11, Appl1

28	56.5	15.7	449	2	US-08-657-392-2	Sequence 2, Appl1
29	56.5	15.7	449	5	PCT-US94-02539-2	Sequence 2, Appl1
30	56.5	15.7	459	2	US-08-673-312-2	Sequence 2, Appl1
31	56.5	15.7	471	2	US-08-657-392-31	Sequence 31, Appl1
32	56.5	15.7	471	5	PCT-US94-02539-31	Sequence 31, Appl1
33	56.5	15.7	711	1	US-08-235-838-7	Sequence 7, Appl1
34	56.5	15.7	711	2	US-08-465-473B-7	Sequence 8, Appl1
35	56	15.6	432	1	US-08-522-166-8	Sequence 8, Appl1
36	56	15.6	432	1	US-08-488-382A-8	Sequence 8, Appl1
37	56	15.6	432	2	US-08-480-912-8	Sequence 8, Appl1
38	56	15.6	1162	2	US-08-728-323A-2	Sequence 2, Appl1
39	56	15.6	1199	4	US-09-208-742-2	Sequence 2, Appl1
40	55.5	15.4	242	2	US-08-845-998-2	Sequence 2, Appl1
41	55.5	15.4	242	4	US-09-206-537-2	Sequence 2, Appl1
42	54.5	15.1	206	6	5185431-1	Patent No. 5185431
43	54.5	15.1	222	4	US-09-040-483-3	Sequence 3, Appl1
44	54.5	15.1	222	6	5185431-4	Patent No. 5185431
45	54	15.0	993	4	US-09-060-410-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-08-710-249-4
Sequence 4, Application US/08710249
Patent No. 5858777
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Andrews, William H.
APPLICANT: Adams, Robert R.
TITLE OF INVENTION: Methods and Reagents for Regulating
TITLE OF INVENTION: Telomere Length and Telomerase Activity
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/710,249
FILING DATE: 13-SEP-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/583,808
FILING DATE: 05-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/003,492
FILING DATE: 08-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-001220US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-710-249-4

Query Match 17.6%; Score 63.5; DB 2; Length 434;
Best Local Similarity 35.0%; Pred. No. 4.2;
Matches 21; Conservative 9; Mismatches 17; Indels 13; Gaps 4;

QY 11 SEQALSSDGAPOVHPLALPSGSTEEDPOTILDDHLSRVLT-PCG 56
Db 236 SEQ--SASESAPEDEP-----DREEDPRAGAED--PKAEKSPGADSKGICKKSGPKA 284

RESULT 2

US-08-928-361B-11
; Sequence 11, Application US/08928361B
; Patent No. 6071518
; GENERAL INFORMATION:
; APPLICANT: Petersen, Carolyn
; TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
; TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
; TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PETERS, VERNY, JONES & BIKSA
; STREET: 385 Sherman Avenue, Suite 6
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-1840
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,361B
; FILING DATE: 12-SEP-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,062
; FILING DATE: 13-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: VERNY, Hana
; REGISTRATION NUMBER: 30,518
; REFERENCE/DOCKET NUMBER: 480.76-1(HV)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-1677
; TELEFAX: 650-324-1678
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1042 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-928-361B-11

Query Match 17.4%; Score 62.5; DB 3; Length 1042;
Best Local Similarity 29.2%; Pred. No. 18;
Matches 21; Conservative 8; Mismatches 26; Indels 17; Gaps 3;

QY 8 KESSEQALSSRDGAPVOHPLALPSGSTEEDPOT-----ILDDHLSRVLT-PCG 56
Db 857 KAGSQSKSDSGNPID-----PSTNMPYDPKTKGLIDPSGIAIDNSVSGVATVPGT 910
QY 57 QSPGVGRYSPRS 68
Db 911 AAPKGGVPIES 922

RESULT 3
US-08-928-361B-5
; Sequence 5, Application US/08928361B
; Patent No. 6071518

; GENERAL INFORMATION:
; APPLICANT: Petersen, Carolyn
; TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
; TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
; TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PETERS, VERNY, JONES & BIKSA
; STREET: 385 Sherman Avenue, Suite 6
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-1840
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,361B
; FILING DATE: 12-SEP-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,062
; FILING DATE: 13-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: VERNY, Hana
; REGISTRATION NUMBER: 30,518
; REFERENCE/DOCKET NUMBER: 480.76-1(HV)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-1677
; TELEFAX: 650-324-1678
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1837 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-928-361B-5

Query Match 17.4%; Score 62.5; DB 3; Length 1837;
Best Local Similarity 29.2%; Pred. No. 40;
Matches 21; Conservative 8; Mismatches 26; Indels 17; Gaps 3;

QY 8 KESSEQALSSRDGAPVOHPLALPSGSTEEDPOT-----ILDDHLSRVLT-PCG 56
Db 1652 KAGSQSKSDSGNPID-----PSTNMPYDPKTKGLIDPSGIAIDNSVSGVATVPGT 1705
QY 57 QSPGVGRYSPRS 68
Db 1706 AAPKGGVPIES 1717

RESULT 4
US-08-415-655-5
; Sequence 5, Application US/08415655
; Patent No. 6025480
; GENERAL INFORMATION:
; APPLICANT: Massague, Joan
; APPLICANT: Lee, Mong-hong
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
; TITLE OF INVENTION: P75KIP2, A CYCLIN-DEPENDENT KINASE INHIBITOR AND USES OF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America

CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYLR-0026
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 1498 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-488-546A-29

Query Match 16.4%; Score 59; DB 3; Length 1498;
Best Local Similarity 36.7%; Pred. No. 84;
Matches 18; Conservative 7; Mismatches 18; Indels 6; Gaps 1;

QY 3 REDEKEGSEALSRDGAPOVHPLALPSGYEEDPOTILDHLSRVL 51
DB 948 KASEPSQGLPRAMSRDG-----LLDDEEEBEAEASEEDDNLSVL 990

RESULT 10
US-08-404-531B-9
Sequence 9, Application US/08404531B
Patent No. 5863724
GENERAL INFORMATION:
APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson, Pamela
APPLICANT: Thomas, Gilbert Cole, and Robert Gagel
TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonylurea Receptor
Patent No. 5863724
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESS: No. 58637241s
STREET: One Liberty Place 46th. Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,531B
FILING DATE: 15-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYLR-0003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1582 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-404-531B-9

Query Match 16.4%; Score 59; DB 2; Length 1582;
Best Local Similarity 36.7%; Pred. No. 91;
Matches 18; Conservative 7; Mismatches 18; Indels 6; Gaps 1;

QY 3 REDEKEGSEALSRDGAPOVHPLALPSGYEEDPOTILDHLSRVL 51
DB 948 KASEPSQGLPRAMSRDG-----LLDDEEEBEAEASEEDDNLSVL 990

RESULT 11
US-08-476-900A-9
Sequence 9, Application US/08476900A
Patent No. 6031150
GENERAL INFORMATION:
APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson
APPLICANT: Thomas, Gilbert Cole, and Robert Gagel
TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonylurea Receptor
Patent No. 6031150
TITLE OF INVENTION: and Method of detecting Persistent Hyperinsulinemic Hypogly
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESS: No. 60311501s
STREET: One Liberty Place 46th. Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,900A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYLR-0027
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1582 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-476-900A-9

Query Match 16.4%; Score 59; DB 3; Length 1582;
Best Local Similarity 36.7%; Pred. No. 91;
Matches 18; Conservative 7; Mismatches 18; Indels 6; Gaps 1;

QY 3 REDEKEGSEALSRDGAPOVHPLALPSGYEEDPOTILDHLSRVL 51
DB 948 KASEPSQGLPRAMSRDG-----LLDDEEEBEAEASEEDDNLSVL 990

RESULT 12
US-08-488-546A-9
Sequence 9, Application US/08488546A
Patent No. 6054313
GENERAL INFORMATION:
APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson, Pamela
APPLICANT: Thomas, Gilbert Cole, and Robert Gagel
TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonylurea Receptor
Patent No. 6054313
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESS: No. 60543131s
STREET: One Liberty Place 46th. Floor
CITY: Philadelphia

STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,546A
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/404,531
FILING DATE: 15-MARCH-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYLR-0026
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1582 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-488-546A-9

Query Match 16.4%; Score 59; DB 3; Length 1582;
Best Local Similarity 36.7%; Pred. No. 91;
Matches 18; Conservative 7; Mismatches 18; Indels 6; Gaps 1;
QY 3 REDEKESQALSRDQAPVQHPLALPPSGSYEDPQTITDHLRYL 51
DB 948 KASEPSQGLPRAMSSRDG-----LLDEEEFEPAESEEDDNLSVL 990

RESULT 13
US-08-726-320-5
Sequence 5, Application US/08726320
Patent No. 6171815
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Bandman, Olga
APPLICANT: Coleman, Roger
TITLE OF INVENTION: NOVEL HUMAN SULFONYLUREA RECEPTOR
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,320
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: AF-0001 US

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1582 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 784874
US-08-726-320-5

Query Match 16.4%; Score 59; DB 4; Length 1582;
Best Local Similarity 36.7%; Pred. No. 91;
Matches 18; Conservative 7; Mismatches 18; Indels 6; Gaps 1;
QY 3 REDEKESQALSRDQAPVQHPLALPPSGSYEDPQTITDHLRYL 51
DB 948 KASEPSQGLPRAMSSRDG-----LLDEEEFEPAESEEDDNLSVL 990

RESULT 14
US-08-007-282B-2
Sequence 2, Application US/08007282B
Patent No. 5403582
GENERAL INFORMATION:
APPLICANT: NAZERIAN, KEYVAN
APPLICANT: CALVERT, JAY G.
APPLICANT: WITTER, RICHARD L.
APPLICANT: YAMAGUCHI, NOBORU
TITLE OF INVENTION: VACCINE COMPRISING FOWLPOX VIRUS
TITLE OF INVENTION: RECOMBINANTS EXPRESSING THE ENVELOPE GLYCOPROTEIN OF AN
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatehouse Road Suite 500 East
CITY: Falls Church
STATE: VA
COUNTRY: USA
ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/007,282B
FILING DATE: 19930121
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR., GERALD M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1644-104P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 567 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOHETICAL: NO
ANTI-SENSE: NO
US-08-007-282B-2

Query Match 16.1%; Score 58; DB 1; Length 567;
Best Local Similarity 37.5%; Pred. No. 30;
Matches 15; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

OY 2 IREDEKESGQALSSRDGAPVOHPLALPSSGYEDDPOT 41
||| : | : : : ||||| : |||||
DB 194 IREESYRERLEIRHSYSYVOYHPLALPSSRGVDDLPOT 233

RESULT 15

US-08-404-531B-28
; Sequence 28, Application US/08404531B
; Patent No. 5863724
; GENERAL INFORMATION:
; APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson, Pamela
; APPLICANT: Thomas, Gilbert Cote, and Robert Gagel
; TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonyleurea Receptor
; Patent No. 5863724
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSER: No. 586372415
; STREET: One Liberty Place 46th. Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/404,531B
; FILING DATE: 15-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Beardell, Lori Y.
; REGISTRATION NUMBER: 34,293
; REFERENCE/DOCKET NUMBER: BYLR-0003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1498 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-404-531B-28

Query Match 16.1%; Score 58; DB 2; Length 1498;
Best Local Similarity 39.1%; Pred. No. 11+02;
Matches 18; Conservative 6; Mismatches 16; Indels 6; Gaps 1;
OY 6 EKEGSEQALSSRDGAPVOHPLALPSSGYEDDPOTILDDHLSRVL 51
| : | : ||||| : | : |||||
DB 951 EPSQGLPRAMSSRDG-----LLIDDEDEEEEAASEEDDNLSSVL 990

Search completed: June 7, 2001, 02:02:11
Job time: 5404 sec

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GenCore version 4.5
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OM protein - protein search, using SW model

Run on: June 7, 2001, 02:03:22 ; Search time 56.43 Seconds

(without alignments)
84.031 Million cell updates/sec

Title: US-09-587-574-4

Perfect score: 360
Sequence: 1 QIREDEKKGSEQALSSRDG.....VLKTPGQSPGVGRYSPRSR 69Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: PIR_67:*

1: pir1:*\n2: pir2:*\n3: pir3:*\n4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	360	100.0	838	2 T08423	Axin homolog Ax11
2	139.5	38.8	832	2 T08422	negative regulator
3	72	20.0	409	2 J70764	translational elonga
4	71	19.7	793	1 KXMSF	furin (EC 3.4.21.7
5	68.5	19.0	441	2 A45360	steroid hormone re
6	68	18.9	206	2 H64410	hypothetical prote
7	66	18.3	409	2 T38487	translational elonga
8	66	18.3	563	2 A69335	succinate dehydrog
9	65	18.1	793	1 KXRTF	furin (EC 3.4.21.7
10	64.5	17.9	262	2 C70648	probable nuclo prot
11	64.5	17.9	414	2 T49459	hypothetical prote
12	64	17.8	907	2 A45560	sporozoite surface
13	63	17.5	619	2 B71559	probable metallopr
14	62.5	17.4	1832	2 T31113	mucin-like glycopr
15	62	17.2	348	2 I49262	cyclin cdk inhibit
16	60.5	16.8	134	2 E57233	complexin II - hum
17	60.5	16.8	134	2 C57233	complexin II - rat
18	60.5	16.8	325	2 H70600	probable transfera
19	60.5	16.8	450	2 B71304	probable zinc prot
20	60	16.7	1544	2 T04464	hypothetical prote
21	59.5	16.5	349	2 T05857	hypothetical prote
22	59	16.4	223	2 D75515	hypothetical prote
23	59	16.4	291	2 C81943	probable integrase
24	59	16.4	291	2 F81163	integrase/recombin
25	59	16.4	970	2 C57282	ankyrin-related pr
26	59	16.4	1267	2 S53058	probable membrane
27	59	16.4	1582	2 A56248	sulfonylurea recep
28	59	16.4	1867	2 T15344	ankyrin-related un
29	59	16.4	2388	2 J60271	beta spectrin, bet

30	58.5	16.2	280	2 T50554	3-methyl-2-oxobuta
31	58.5	16.2	379	2 A45267	heterocyst pattern
32	58.5	16.2	513	2 T41011	hypothetical prote
33	58.5	16.2	595	1 EDBEMC	immediate-early ph
34	58.5	16.2	929	2 T52517	hypothetical prote
35	58.5	16.2	2219	2 T41547	hypothetical prote
36	58.5	16.2	2219	2 T27684	hypothetical prote
37	58.5	16.2	5105	2 T32650	hypothetical prote
38	58	16.1	226	2 S33024	hypothetical prote
39	58	16.1	300	2 S19560	proline-rich prote
40	58	16.1	413	4 F0H0E2	retrovirus-related
41	58	16.1	471	2 A53711	collagenase 3 (EC
42	58	16.1	567	1 VCEVAS	env polyprotein -
43	58	16.1	606	2 H71065	hypothetical prote
44	58	16.1	897	2 T21688	hypothetical prote
45	58	16.1	1209	2 T13153	bradma associated

ALIGNMENTS

RESULT 1
T08423
Axin homolog Ax11 - rat
N:Alternate names: Ax11
C:Species: Rattus norvegicus (Norway rat)
C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jul-2000
C:Accession: T08423
R:Yamamoto, H.; Kishida, S.; Uochi, T.; Ikeda, S.; Koyama, S.; Asashima, M.; Kikuchi, M.; Cell. Biol. 18, 2867-2875, 1998
A>Title: Ax11, a member of the Axin family, interacts with both glycogen synthase kin
A:Reference number: 216414; MUID:98226558
A:Accession: T08423
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-838 <YAM>
A:Cross-references: EMBL:AF017757; NID:g3080758; PIDN:AAC40089.1; PID:g3080759
A>Note: Interacts with GSK-3beta and beta-catenin
C:Keywords: phosphoprotein; signal transduction

Query Match 100.0%; Score 360; DB 2; Length 838;
Best Local Similarity 100.0%; Pred. No. 3.9e-32;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIREDEKKGSEQALSSRDGAPVQHPPLALPPSGTYEDPQTIIIDHLKRVLKTPGQSPG 60
|||||
DB 397 QIREDEKKGSEQALSSRDGAPVQHPPLALPPSGTYEDPQTIIIDHLKRVLKTPGQSPG 456
QY 61 VGRYSPRSR 69
|||||
DB 457 VGRYSPRSR 465

RESULT 2
T08422
negative regulator axin [imported] - rat
N:Alternate names: Axin
C:Species: Rattus norvegicus (Norway rat)
C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jul-2000
C:Accession: T08422
R:Ikeda, S.; Yamamoto, H.; Murai, H.; Kishida, S.; Kikuchi, A.
EMBO J. 17, 1371-1384, 1998
A>Title: Axin, a negative regulator of the Wnt signaling pathway, forms a complex wit
A:Reference number: 216413; MUID:98151361
A:Accession: T08422
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-832 <IKE>
A:Cross-references: EMBL:AF017756; NID:g2982197; PIDN:AAC40066.1; PID:g2982198
A>Note: GSK-3beta interacting protein
C:Keywords: phosphoprotein; signal transduction

Matches 26; Conservative 7; Mismatches 21; Indels 31; Gaps 4;

OY 3 REDEKESQALSRDAPVQH-----LALPSGYEDPQTILDD 45

Db 179 RERERKRTQRLSOERRPGCHPLPFGVYARNAVDVALLPDGYSY----- 230

OY 46 HLS--RVLT---PGQSPGVGRYS 65

Db 231 -LSVPRMLRTRGADSLQTRPSPGAVS 254

RESULT 11

T49459

hypothetical protein B14D6.110 [imported] - Neurospora crassa

C:Species: Neurospora crassa

C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000

C:Accession: T49459

R:Schulte, U.; Allyn, V.; Hohelsel, J.; Brandt, P.; Farimann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000

A:Reference number: 225022

A:Accession: T49459

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-414 <SCH>

A:Cross-references: EMBL:AL356173; GSPDB:GN00116; NCSP:B14D6.110

A:Experimental source: BAC clone B14D6; strain OR74A

A:Genetics:

A:Gene: NCSP:B14D6.110

A:Map position: 6

A:introns: 317/2

Query Match 17.9%; Score 64.5; DB 2; Length 414;

Best Local Similarity 34.0%; Pred. No. 14;

Matches 17; Conservative 7; Mismatches 25; Indels 1; Gaps 1;

OY 4 EDEKESQALSRDAPVQHPLALPSGYEDPQTILDDHLSRVLT 53

Db 54 EEEEEEEDDDDDGGEAHSLSSTRQESPT-SRDHYHLLVT 102

RESULT 12

A45560

sporozoite surface antigen SPAC-1 - Theileria annulata

C:Species: Theileria annulata

C>Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998

C:Accession: A45560

R:Hall, R.; Hunt, P.D.; Carrington, M.; Simmons, D.; Williamson, S.; Mechem, R.P.; Tait, M.; Blochem. Parasitol. 53, 105-112, 1992

A:Title: Mimicry of elastin repetitive motifs by Theileria annulata sporozoite surface

A:Reference number: A45560; MUID:92365719

A:Accession: A45560

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-907 <HAL>

A:Cross-references: GB:M63017; NID:g161884; PID:g161885

A:Note: sequence extracted from NCBI backbone (NCBIN:111148, NCBI:P.111150)

A:keywords: surface antigen

Query Match 17.8%; Score 64; DB 2; Length 907;

Best Local Similarity 26.5%; Pred. No. 39;

Matches 22; Conservative 12; Mismatches 15; Indels 34; Gaps 4;

OY 4 EDEKESQALSRD--GAPVQH-----LALPSGY-EDP 39

Db 120 DDEEEDDKSTSKNGSPKAPGVSSSTSSASPTTILSQGLGSPSGHAQDP 179

OY 40 QTILDDHLSRVLTGPGQSPGVG 62

Db 180 G-----VGVPGVGVGVG 192

RESULT 13

B71559

probable metalloproteinase - Chlamydia trachomatis (serotype D, strain UW3/Cx)

C:Species: Chlamydia trachomatis

C>Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999

C:Accession: B71559

R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitche Science 282, 754-759, 1998

A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia t

A:Reference number: A71570; MUID:9900809

A:Accession: B71559

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-619 <ARN>

A:Cross-references: GB:AE001282; GB:AE001273; NID:93328466; PID:MAC67663.1; PID:9332

A:Experimental source: serotype D, strain UW-3/Cx

C:Genetics:

A:Gene: yael

Query Match 17.5%; Score 63; DB 2; Length 619;

Best Local Similarity 28.4%; Pred. No. 33;

Matches 21; Conservative 19; Mismatches 18; Indels 16; Gaps 5;

OY 1 QIREDEK-----EGSEQALSRDAPVQHPLALPSGYEDPQTILDDHLSRVLT 53

Db 458 KFRDEQERRYTLERLEAKRISL--GIPLR-DLAV---QYNDPWTLMESVSLSIKT 510

OY 54 PGQSPGVGRYSR 67

Db 511 --VKALGMRVSPQ 522

RESULT 14

T31113

mucin-like glycoprotein 900 - Cryptosporidium parvum

C:Species: Cryptosporidium parvum

C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999

C:Accession: T31113

R:Barnes, D.A.; Bonnin, A.; Huang, J.X.; Gousset, L.; Wu, J.; Gut, J.; Doyle, P.; Dub Mol. Biochem. Parasitol. 96, 93-110, 1998

A:Title: A novel multi-domain mucin-like glycoprotein of Cryptosporidium parvum media

A:Reference number: 220989; MUID:99066935

A:Accession: T31113

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1832 <BAR>

A:Cross-references: EMBL:AF068065; NID:g4063041; PID:g4063042; PID:MAC98153.1

Query Match 17.4%; Score 62.5; DB 2; Length 1832;

Best Local Similarity 29.2%; Pred. No. 1.3e+02;

Matches 21; Conservative 8; Mismatches 26; Indels 17; Gaps 3;

OY 8 KEGSEQALSRDAPVQHPLALPSGYEDPQT-----ILDDHLSRVLT--PGC 56

Db 1647 KAGSQSKSSDSEGNPID-----PSTNMPYDPKTKGLIDPESGLAIDNSGVGATVPCT 1700

OY 57 QSPGVGRYSRPS 68

Db 1701 AAPKKGVIPEPS 1712

RESULT 15

I49262

cyclin cdk inhibitor p57 - mouse

N:Alternate names: CDI p57; cyclin-cyclin-dependent kinase inhibitor p57; p57-kip2

C:Species: Mus musculus (house mouse)

C>Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 05-Nov-1999

C:Accession: I49262

R:Lee, M.H.; Reynolds, I.; Massague, J. Genes Dev. 9, 639-649, 1995

A:Title: Cloning of p57KIP2, a cyclin-dependent kinase inhibitor with unique domain s

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OM protein - protein search, using sw model

Run on: June 7, 2001, 02:10:31 ; Search time 39.03 Seconds
(Without alignments)
60,559 Million cell updates/sec

Title: US-09-587-574-4
Perfect score: 360

Sequence: 1 QIREDEKRCSEGLASSRDC.....VLKTPCQSGRGVGRVSPRRR 69

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	360	100.0	838	1 AXN2_RAT	O70240 rattus norv
2	360	100.0	840	1 AXN2_MOUSE	O08566 mus musculu
3	332	92.2	843	1 AXN2_HUMAN	O99221 homo sapien
4	217.5	60.4	812	1 AXN2_BRARE	P57095 brachydanto
5	158	43.9	842	1 AXN_XENLA	O97950 xenopus lae
6	149	41.4	835	1 AXN1_BRARE	P57094 brachydanto
7	146	40.6	841	1 AXN_CHICK	O42400 gallus gall
8	139.5	38.8	893	1 AXN1_RAT	O70239 rattus norv
9	139.5	38.8	992	1 AXN1_MOUSE	O35625 mus musculu
10	113.5	31.5	900	1 AXN1_HUMAN	O13169 homo sapien
11	72	20.0	409	1 EF1G_SCHPO	P40921 schizosach
12	71	19.7	793	1 FUR1_MOUSE	P23188 mus musculu
13	68.5	19.0	441	1 PRAS_HUMAN	O03181 homo sapien
14	68	18.9	206	1 P688_METJA	O58298 methanococ
15	65	18.1	793	1 FUR1_RAT	P23377 rattus norv
16	62.5	17.4	134	1 CLX2_NAKJA	O42105 natke japon
17	62.5	17.4	708	1 ABB1_MOUSE	O49xj1 mus musculu
18	62	17.2	348	1 CDNC_MOUSE	P49919 mus musculu
19	62	17.2	471	1 MM13_BOVIN	O77656 bos taurus
20	61.5	17.1	745	1 AXN_DROME	O97407 drosophila
21	61	16.9	1490	1 CRK7_HUMAN	O99y44 homo sapien
22	60.5	16.8	593	1 DR11_HUMAN	O99856 homo sapien
23	59	16.4	1267	1 DHR1_YEAST	O04217 saccharomyc
24	59	16.4	1581	1 ACC8_CRICR	O09427 cricetus cr
25	58.5	16.2	379	1 PAT4_ANASP	P33048 anabaena sp
26	58.5	16.2	595	1 VIE1_MCMVS	P11210 murine cyto
27	58	16.1	217	1 YKR4_EBV	P30117 Epstein-Bar
28	58	16.1	413	1 GAG2_HUMAN	P10264 homo sapien
29	58	16.1	471	1 MM13_HUMAN	P45452 homo sapien
30	58	16.1	471	1 MM13_RABIT	O62806 oryctolagus
31	58	16.1	567	1 ENY_AVIS	P31796 avian splee
32	58	16.1	1320	1 PURL_NEIMA	O91wcs neisseria m
33	58	16.1	1320	1 PURL_NEIMA	O91xks neisseria m

34	58	16.1	1580	1 ACC8_RAT	O09429 rattus norv
35	58	16.1	3924	1 ANK2_HUMAN	O01484 homo sapien
36	57.5	16.0	730	1 MM02_MOUSE	P41245 mus musculu
37	57	15.8	237	1 CAS1_MACOU	P28549 macropus eu
38	57	15.8	449	1 CMGA_BOVIN	P05059 bos taurus
39	57	15.8	472	1 MM13_HORSE	O18927 equus caball
40	57	15.8	913	1 UBPK_HUMAN	O99266 homo sapien
41	56.5	15.7	243	1 AX28_SOYBN	P13089 glycine max
42	56.5	15.7	330	1 NDPM_CHICK	P79766 gallus gall
43	56.5	15.7	348	1 P2C2_CAEBL	P43596 caenorhabdi
44	56.5	15.7	423	1 TIG_BACSU	P80698 bacillus su
45	56.5	15.7	457	1 CMGA_HUMAN	P10645 homo sapien

ALIGNMENTS

RESULT 1	ID	AXN2_RAT	STANDARD	PRT	838 AA.
AC	O70240				
DR	01-OCT-2000 (rel. 40, Created)				
DR	01-OCT-2000 (rel. 40, Last sequence update)				
DR	01-OCT-2000 (rel. 40, Last annotation update)				
DE	AXIN 2 (AXIS INHIBITION PROTEIN 2) (CONDUCTIN) (AXIN-LIKE PROTEIN)				
DE	(AXIL)				
GN	AXIN2				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.				
OX	NCBI_TaxID=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Brain;				
RX	MEDLINE=9826558; PubMed=9566905;				
RA	Yamamoto H., Kishida S., Uochi T., Ikeda S., Koyama S., Asashima M.,				
RA	Kikuchi A.;				
RT	"Axil", a member of the Axin family, interacts with both glycogen				
RT	synthase Kinase 3beta and beta-catenin and inhibits axis formation of				
RT	Xenopus embryos."				
RL	Mol. Cell. Biol. 18:2867-2875(1998).				
CC	- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES				
CC	BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-				
CC	CATENIN AND APC BY GSK-3B (BY SIMILARITY).				
CC	- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)				
CC	AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN				
CC	OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN.				
CC	TERNARY COMPLEX.				
CC	- SUBCELLULAR LOCATION: CYTOPLASMIC.				
CC	- TISSUE SPECIFICITY: EXPRESSED IN LUNG AND THYMUS.				
CC	- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY				
CC	PP2A.				
CC	- SIMILARITY: CONTAINS 1 RGS DOMAIN.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sdb.ch/announce/				
CC	or send an email to license@sdb.ch).				
CC	-----				
CC	EMBL; AF017757; AAC40089.1; -				
DR	HSSP; P49799; IACR.				
DR	InterPro: IPR000342; -				
DR	InterPro: IPR001158; -				
DR	Pfam; PR00615; RGS; 1.				
DR	Pfam; PR00778; DIX; 1.				
DR	PROSITE; PSS0132; RGS; 1.				
KW	Developmental protein; Phosphorylation.				
FT	DOMAIN 81 200				
FT	DOMAIN 327 413				
FT	GSK-3B BINDING SITE (BY SIMILARITY).				

```

FT DOMAIN 413 476 BETA-CATENIN BINDING SITE (BY
FT DOMAIN 469 474 SIMILARITY).
FT DOMAIN 756 838 POLY-HIS.
SQ SEQUENCE 838 AA; 92947 MW; 45B825C13BA07F37 CRC64;

Query Match 100.0%; Score 360; DB 1; Length 838;
Best Local Similarity 100.0%; Pred. No. 8.3e-32;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QIREDEKEGSEQALSSDGAPOVQHPLALLPSGYEEDPOTILDDHLSRVLTGCGSPG 60
DB 397 QIREDEKEGSEQALSSDGAPOVQHPLALLPSGYEEDPOTILDDHLSRVLTGCGSPG 456

OY 61 VGRYSPRSR 69
DB 457 VGRYSPRSR 465

RESULT 2
AXN2_MOUSE STANDARD; PRT; 840 AA.
ID AXN2_MOUSE
AC 088566; 090XJ6;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DE AXIN 2 (AXIS INHIBITION PROTEIN 2) (CONDUCTIN) (AXIN-LIKE PROTEIN)
DE (AXIL).
GN AXIN2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=98221239; PubMed=9554852;
RX Behrens J., Jerchow B.-A., Muerle M., Grimm J., Asbrand C.,
RA Witz R., Kuehl M., Wedlich D., Birchmeier W.,
RT "Functional interaction of an axin homolog, conductin, with beta-
RT catenin, APC, and GSK3beta."
RL Science 280:596-599(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G.,
RA Jenkins N.A., Warburton D., Costantini F.;
RT "Properties of mouse Axin2 and human AXIN2: chromosomal location,
RT expression pattern, interaction with Axin and effects on embryonic
RT axis formation."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
CC -I- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)
CC AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN
CC OCCURS VIA THE ARMD/DILLO REPEATS CONTAINED IN BETA-CATENIN.
CC TERNARY COMPLEX (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -I- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC PP2A (BY SIMILARITY).
CC -I- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -I- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -----
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CC -----
CC DR EMBL; AF073788; AAC26047.1; -
CC EMBL; AF205889; AAF22800.1; -

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DR MGD: MGI:1270862; Axin2.
DR HSSP: P49799; IAGR.
DR InterPro: IPR000342; -
DR InterPro: IPR001158; -
DR Pfam: PF00615; RGS; 1.
DR Pfam: PF00778; DIX; 1.
DR PRINTS: PR01301; RGS-PROTEIN.
DR PROSITE: PS01332; RGS; 1.
KW Anti-oncogene; Phosphorylation.
FT DOMAIN 81 200 RGS.
FT DOMAIN 327 413 GSK-3B BINDING SITE (BY SIMILARITY).
FT DOMAIN 413 478 BETA-CATENIN BINDING SITE (BY
FT DOMAIN 469 476 SIMILARITY).
FT DOMAIN 758 840 POLY-HIS.
FT DOMAIN 101 101 DIX.
FT CONFLICT 101 101 R -> K (IN REF. 2).
FT CONFLICT 474 474 H -> Y (IN REF. 2).
FT CONFLICT 484 484 S -> P (IN REF. 2).
FT CONFLICT 503 503 F -> S (IN REF. 2).
FT CONFLICT 603 603 G -> A (IN REF. 2).
SQ SEQUENCE 840 AA; 92934 MW; A07D5EFB25DE7277 CRC64;

Query Match 100.0%; Score 360; DB 1; Length 840;
Best Local Similarity 100.0%; Pred. No. 8.3e-32;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QIREDEKEGSEQALSSDGAPOVQHPLALLPSGYEEDPOTILDDHLSRVLTGCGSPG 60
DB 397 QIREDEKEGSEQALSSDGAPOVQHPLALLPSGYEEDPOTILDDHLSRVLTGCGSPG 456

OY 61 VGRYSPRSR 69
DB 457 VGRYSPRSR 465

RESULT 3
AXN2_HUMAN STANDARD; PRT; 843 AA.
ID AXN2_HUMAN
AC Q9Y2T1; Q9UH84;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN 2 (AXIS INHIBITION PROTEIN 2) (CONDUCTIN) (AXIN-LIKE PROTEIN)
DE (AXIL).
GN AXIN2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99168905; PubMed=10049590;
RA Mai M., Qian C., Yokomizo A., Smith D.I., Liu W.;
RT "Cloning of the human homolog of conductin (AXIN2), a gene mapping to
RT chromosome 17q23-q24."
RL Genomics 55:341-344(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Tissue-Brain, and Lymphoblast;
RC Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G.,
RA Jenkins N.A., Warburton D., Costantini F.;
RT "Properties of mouse Axin2 and human AXIN2: chromosomal location,
RT expression pattern, interaction with Axin and effects on embryonic
RT axis formation."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
CC -I- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)
CC AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN
CC OCCURS VIA THE ARMD/DILLO REPEATS CONTAINED IN BETA-CATENIN.
CC TERNARY COMPLEX (BY SIMILARITY).
CC -----

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CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN AND LYMPHOBLAST.
CC -1- PFM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC P2A (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -----
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CC -----
CC EMBL: AF078165; AAD20976.1; -.
CC EMBL: AF205888; AAF22799.1; -.
CC MIM: 604025; -.
CC InterPro: IPR000342; -.
CC InterPro: IPR001158; -.
CC Pfam: PF00615; RGS: 1.
CC Pfam: PF00778; DIX: 1.
CC PRINTS: PR01301; RGS-PROTEIN.
CC PROSITE: PS50132; RGS: 1.
CC KW Developmental protein; Phosphorylation.
CC FT DOMAIN 81 200 RGS.
CC FT DOMAIN 327 413 GSK-3B BINDING SITE (BY SIMILARITY).
CC FT DOMAIN 413 476 BETA-CATENIN BINDING SITE (BY
CC SIMILARITY).
CC FT DOMAIN 469 474 DIX.
CC FT DOMAIN 761 843 POLY-HIS.
CC FT CONFLICT 37 62 ORCVKGVTKPMYSVSNTRRDEGL -> HHGGGPGHQT
CC CONFLICT 346 346 Q -> R (IN REF. 2).
CC FT CONFLICT 572 636 MISSING (IN REF. 2).
CC FT CONFLICT 687 687 P -> S (IN REF. 2).
CC FT CONFLICT 696 696 O -> H (IN REF. 2).
CC FT SEQUENCE 843 AA: 93557 MW: 17862BED6A84664D CRC64;
SQ
Query Match 92.2%; Score 332; DB 1; Length 843;
Best Local Similarity 89.9%; Pred. No. 9.7e-29;
Matches 62; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 1 QIREDEKESQALSSRDGAPVQHPLALPSGSYEDPQTIIIDHLRYLTKPGQSPG 60
DB 397 QIREDEKESQALSSRDGAPVQHPLALPSGSYEDPQTIIIDHLRYLTKPGQSPG 456
QY 61 VGRYSPRSR 69
DB 457 VGRYSPRSR 465
RESULT 4
AXN2_BRARE STANDARD: PRT: 812 AA.
ID AXN2_BRARE
AC P37095;
DT 01-OCT-2000 (Rel. 40; Created)
DT 01-OCT-2000 (Rel. 40; Last sequence update)
DT 01-OCT-2000 (Rel. 40; Last annotation update)
DE AXIN 2 (AXIS INHIBITION PROTEIN 2).
CN AXIN2.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20171051; PubMed=10704853;
RX Shintzu T., Yamana Y., Ryu S.-L., Hashimoto H., Yabe T., Hirata T.,
RA Bae Y.-K., Hibi M., Hirano T.;
RT "Cooperative roles of Bozozok/Dharma and Nodal-related proteins in the

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RT formation of the dorsal organizer in zebrafish.";
RL Mech. Dev. 91:293-303(2000)
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATENIN AND APC BY GSK-3B (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- PFM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC P2A (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -----
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CC -----
CC EMBL: AB032263; BAA92440.1; -.
CC HSP: P49799; IAGR.
CC InterPro: IPR000342; -.
CC InterPro: IPR001158; -.
CC Pfam: PF00615; RGS: 1.
CC Pfam: PF00778; DIX: 1.
CC PROSITE: PS50132; RGS: 1.
CC KW Developmental protein; Phosphorylation.
CC FT DOMAIN 84 203 RGS.
CC FT DOMAIN 329 415 GSK-3B BINDING SITE (BY SIMILARITY).
CC FT DOMAIN 415 467 BETA-CATENIN BINDING SITE (BY
CC SIMILARITY).
CC FT DOMAIN 412 419 POLY-SER.
CC FT DOMAIN 730 812 DIX.
CC FT SEQUENCE 812 AA: 91496 MW: 46550A8DE2240CC CRC64;
SQ
Query Match 60.4%; Score 217.5; DB 1; Length 812;
Best Local Similarity 63.8%; Pred. No. 3.1e-16;
Matches 44; Conservative 9; Mismatches 11; Indels 5; Gaps 1;
QY 1 QIREDEKESQALSSRDGAPVQHPLALPSGSYEDPQTIIIDHLRYLTKPGQSPG 60
DB 399 QIREDEKESQALSSRDGAPVQHPLALPSGSYEDPQTIIIDHLRYLTKPGQSPG 453
QY 61 VGRYSPRSR 69
DB 454 LTRHSPRSR 462
RESULT 5
AXN_XENLA STANDARD: PRT: 842 AA.
ID AXN_XENLA
AC Q9YGYO;
DT 01-OCT-2000 (Rel. 40; Created)
DT 01-OCT-2000 (Rel. 40; Last sequence update)
DT 01-OCT-2000 (Rel. 40; Last annotation update)
DE AXIN OR AXIN.
CN AXIN OR AXIN.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae.
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99173782; PubMed=10072781;
RX Hedgepeth C.M., Deardorff M.A., Klein P.S.;
RT "Xenopus axin interacts with glycogen synthase kinase-3 beta and is
RT expressed in the anterior midbrain.";
RL Mech. Dev. 80:147-151(1999).
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATENIN AND APC BY GSK-3B (BY SIMILARITY).

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DR EMBL: AF09012; AAC60245.1; -
DR HSSP: P49799; IAGR.
DR InterPro: IPR000342; -
DR InterPro: IPR001158; -
DR Pfam: PF00615; RGS; 1.
DR Pfam: PF00778; DIX; 1.
DR PROSITE: PSS0132; RGS; 1.
DR Developmental protein: Phosphorylation.
FT DOMAIN 88 211
FT 348 433 RGS.
FT 434 508 BETA-CATENIN BINDING SITE (BY
FT SIMILARITY).
FT DOMAIN
FT 759 841
FT 841 94931 MW: 400D0C90E72506FE CRC64;
SQ SEQUENCE 841 AA: 94931 MW: 400D0C90E72506FE CRC64;

Query Match 40.6%; Score 146; DB 1; Length 841;
Best Local Similarity 34.7%; Pred. No. 2, 2e-08;
Matches 35; Conservative 14; Mismatches 14; Indels 38; Gaps 4;

OY 3 REDEER-----ECSEQALSSRDGAPVQHPLALLPS----- 33
DB 403 REAELEERLKRVAEEEDADISSGFSV-ISHK---MPSAQPHHFAPRYSEMGAC 458
OY 34 -----SYEDPOTILDDHLSRYLKTGCGSPGVGRYSPRS 69
DB 459 MQRDAHEHPESILDEHVQRVKTGCGSPGGRHSPKR 499

RESULT 8
AXNL_RAT
ID AXNL_RAT STANDARD: PRT: 893 AA.
AC 070239;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN 1 PROTEIN (AXIS INHIBITION PROTEIN 1) (RAXIN) (FRAGMENT).
GN AXIN1 OR AXIN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain;
RX MEDLINE=98151161; PubMed=9482734;
RA Ikeda S., Kishida S., Yamamoto H., Mural H., Koyama S., Kikuchi A.;
RT Axin, a negative regulator of the Wnt signaling pathway, forms a
RT complex with GSK-3beta and beta-catenin and promotes GSK-3beta-
RT dependent phosphorylation of beta-catenin.";
RL EMBL J. 171371-1384(1998).
RL
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
CC -1- SUBUNIT: INTERACTS WITH GSK-3B AND BETA-CATENIN. THE INTERACTION
CC BETWEEN AXIN AND BETA-CATENIN OCCURS VIA THE ARADILLO REPEATS
CC CONTAINED IN BETA-CATENIN. TERNARY COMPLEX. ALSO BINDS TO
CC PLAKGLOBIN (GAMA-CATENIN), APC, DVL AND PP2A (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS, THYMUS AND LUNG
CC FOLLOWED BY CEREBRUM, CEREBELLUM, HEART, KIDNEY, SKELETAL MUSCLE,
CC SPLEEN AND LIVER.
CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC PP2A (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -----
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DR EMBL: AF017756; AAC40066.1; ALT_INIT.
DR HSSP: P49799; IAGR.
DR InterPro: IPR000342; -
DR InterPro: IPR001158; -
DR Pfam: PF00615; RGS; 1.
DR Pfam: PF00778; DIX; 1.
DR PROSITE: PSS0132; RGS; 1.
DR Developmental protein: Phosphorylation.
FT NON_TER 1 1
FT DOMAIN 154 277 RGS.
FT 414 498 GSK-3B BINDING SITE.
FT 499 567 BETA-CATENIN BINDING SITE.
FT DOMAIN 811 893
FT 811 893 DIX.
SQ SEQUENCE 893 AA: 99188 MW: 3C8BD2224EDD384C CRC64;

Query Match 38.8%; Score 139.5; DB 1; Length 893;
Best Local Similarity 35.3%; Pred. No. 1, 2e-07;
Matches 30; Conservative 14; Mismatches 20; Indels 21; Gaps 2;

OY 1 QIREDEKEGSEQALSSRDGAPVQHPLALLPS-----GSYEDPOTIL 43
DB 481 RVMEEGEGDEGMP---SCPMSHKLPSVPAWHFPPRYVDMCGSLRDAHEHPESIL 536
OY 44 DDHLSRYLKTGCGSPGVGRYSPRS 68
DB 537 DEHVQRVMTGCGSPGGRHSPDS 561

RESULT 9
AXNL_MOUSE
ID AXNL_MOUSE STANDARD: PRT: 992 AA.
AC 035625;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN 1 (AXIS INHIBITION PROTEIN 1) (FUSED PROTEIN) (FRAGMENT).
GN AXIN1 OR AXIN OR FU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=97373830; PubMed=9230313;
RA Zeng L., Fagotto F., Zhang T., Hsu W., Vasicsek T.J., Perry W.L. III,
RA Lee J.J., Tilgman S.M., Gunhiner B.M., Costantini F.;
RT "The mouse fused locus encodes Axin, an inhibitor of the Wnt signaling
RT pathway that regulates embryonic axis formation.";
RL Cell 90:181-192(1997).
RL
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
CC -1- SUBUNIT: INTERACTS WITH GSK-3B AND BETA-CATENIN. THE INTERACTION
CC BETWEEN AXIN AND BETA-CATENIN OCCURS VIA THE ARADILLO REPEATS
CC CONTAINED IN BETA-CATENIN. TERNARY COMPLEX. ALSO BINDS TO
CC PLAKGLOBIN (GAMA-CATENIN), APC, DVL AND PP2A (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1 (SHOWN HERE) AND 2; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN EMBRYONIC STEM CELLS.
CC -1- DEVELOPMENTAL STAGE: WIDELY EXPRESSED AT E10.5 TO E16.5 DAY.
CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC PP2A.
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -----

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CC EMBL; AF009011; AAC53285.1; -
 CC HSSP; P49799; IAGR.
 CC MGD; MGI:1096327; Axin.
 CC InterPro; IPR000342; -
 CC InterPro; IPR001158; -
 CC Pfam; PF00615; RGS; 1.
 CC Pfam; PF00778; DIX; 1.
 CC PROSITE; PS50132; RGS; 1.
 CC Developmental protein; Phosphorylation; Alternative splicing.
 CC NON_TER 1 18
 CC DOMAIN 10 18 POLY-ALA.
 CC FT 217 340 RGS-3B BINDING SITE (BY SIMILARITY).
 CC FT 477 561 BETA-CATENIN BINDING SITE (BY
 CC FT DOMAIN 562 630 SIMILARITY).
 CC FT DOMAIN 910 992 DIX.
 CC FT VARSPLIC 860 895 MISSING (IN ISOPFORM 2).
 CC FT SEQUENCE 992 AA; 109917 MW; 70EBB53D87BD26F CRC64;

Query Match 38.88; Score 139.5; DB 1; Length 992;
 Best Local Similarity 35.38; Pred. No. 1.3e-07;
 Matches 30; Conservative 14; Mismatches 20; Indels 21; Gaps 2;

QY 1 QIREDEKESGQALSSRDGAPVQHPALPLPS-----GSVEEDPQITL 43
 DB 544 RYRMEEGEDGEMP-----SGPMASHKLPSPVAMHPPRYVDMGCSGLRDAAENPESIL 599
 DB 44 DDHLSRYLKTPTGCSGPGVGRYSPRS 68
 DB 600 DEHYORVMKTPGCSGPGHRSPTS 624

RESULT 10
 AXIN1_HUMAN STANDARD; PRT; 900 AA.
 ID AXIN1_HUMAN
 AC 015169;
 DT 01-OCT-2000 (Rel. 40; Created)
 DT 01-OCT-2000 (Rel. 40; Last sequence update)
 DT 01-OCT-2000 (Rel. 40; Last annotation update)
 DE AXIN1 (AXIN INHIBITION PROTEIN 1) (HAXIN) (FRAGMENT).
 GN AXIN1 OR AXIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eultheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=97373830; PubMed=9230313;
 RA Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perry W.L. III,
 RA Lee J.D., Tildeman S.M., Gumbiner B.M., Costantini F.,
 RA "The mouse fused locus encodes Axin, an inhibitor of the Wnt signaling
 RA pathway that regulates embryonic axis formation.";
 RL Cell 90:181-192(1997).
 RL -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
 CC CATEININ AND APC BY GSK-3B.
 CC -1- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)
 CC AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN
 CC OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN.
 CC TERNARY COMPLEX MAY ALSO BINDS TO PLAKOGLOBIN (GAMMA-CATENIN),
 CC APC, DVL AND PP2A.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- TISSUE SPECIFICITY: UBICITOUSLY EXPRESSED.

CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
 CC PP2A.
 CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.

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CC EMBL; AF009674; AAC51624.1; -
 CC HSSP; P49799; IAGR.
 CC MIM; 603816; -
 CC InterPro; IPR000342; -
 CC InterPro; IPR001158; -
 CC Pfam; PF00615; RGS; 1.
 CC Pfam; PF00778; DIX; 1.
 CC PROSITE; PS50132; RGS; 1.
 CC Developmental protein; Phosphorylation.
 CC NON_TER 1 248
 CC DOMAIN 125 248 RGS.
 CC FT 385 470 GSK-3B BINDING SITE (BY SIMILARITY).
 CC FT DOMAIN 471 540 BETA-CATENIN BINDING SITE (BY
 CC FT DOMAIN 818 900 SIMILARITY).
 CC FT SEQUENCE 900 AA; 99803 MW; EE5F90B1FC7B3B CRC64;

Query Match 31.58; Score 113.5; DB 1; Length 900;
 Best Local Similarity 34.48; Pred. No. 8.4e-05;
 Matches 33; Conservative 10; Mismatches 22; Indels 31; Gaps 3;

QY 3 RDEDEK-----EGSEQALSSRDGAPVQHPALPLPS-----GSVEEDPQITL 43
 DB 440 REAEKLEERLRYRMEEGEDGDPSSGPRPC-HKLPRAVAMHPPRLCWTACAGLR 498
 QY 33 GSVEEDPQITLDDHLSRYLKTPTGCSGPGVGRYSPRS 68
 DB 499 DAHEENPESILDEHYORVLRRTGROSPGGRHSPTS 534

RESULT 11
 EPLG_SCHPO STANDARD; PRT; 409 AA.
 ID EPLG_SCHPO
 AC P40921; O14005;
 DT 01-FEB-1995 (Rel. 31; Created)
 DT 01-FEB-1995 (Rel. 31; Last sequence update)
 DT 15-JUL-1998 (Rel. 36; Last annotation update)
 DE ELONGATION FACTOR 1-GAMMA (EF-1-GAMMA).
 GN TEF3 OR SPAC29A4.02C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 226-244.
 RA STRAIN=972;
 RA MEDLINE=94063505; PubMed=8244022;
 RA Momoi H., Yamada H., Ueguchi C., Mizuno T.,
 RA "Sequence of a fission yeast gene encoding a protein with extensive
 RA homology to eukaryotic elongation factor-1 gamma.";
 RL gene 134:119-122(1993).
 RL [2]
 RP SEQUENCE FROM N.A.
 RA STRAIN=972;
 RA Brown D., Churcher C.M., Wood V., Barrell B.G., Rajandream M.A.,
 RA Submitted (JUN-1997) to the EMBL/Genbank/DBJ databases.
 RL -1- FUNCTION: PROBABLY PLAYS A ROLE IN ANCHORING THE COMPLEX TO OTHER
 CC CELLULAR COMPONENTS.

CC -1 SUBUNIT: EF-1 IS COMPOSED OF FOUR SUBUNITS: ALPHA, BETA,
CC DELTA, AND GAMMA.
CC -1 SIMILARITY: TO OTHER SPECIES; GAMMA SUBUNIT AS WELL AS TO THE
CC N-TERMINAL OF SOME EUKARYOTIC AMINO ACID-TRNA SYNTHETASES.
CC -----
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CC -----
DR EMBL: D14606; BAA03456.1; -
DR EMBL: Z97210; CAB10129.1; -
DR PIR: J70764; J70764.
DR InterPro: IPR000521; -
DR InterPro: IPR001662; -
DR Pfam: PF00647; EF1G_domain; 1.
DR Pfam: PF00643; GST; 1.
DR PROSITE: PS50040; EF1G; 1.
DR Elongation factor; Protein biosynthesis.
KW CONFLICT 246 R->A (IN REF. 2).
FT SEQUENCE 409 AA; 45786 MW; A49CB947A9F66DF0 CRC64;
SQ
Query Match 20.0%; Score 72; DB 1; Length 409;
Best Local Similarity 35.3%; Pred. No. 1.2;
Matches 12; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

3 REDEKESQALSSRDGAPVQHPLALPSCSYE 36
DB 231 KDKKKKNAKPKPAERKPRKHPPLASAPNGSFD 264

RESULT 12
ID FURL_MOUSE STANDARD: PRT: 793 AA.
AC P23188;
DT 01-NOV-1991 (Rel. 20, Created)
DT 30-NOV-1991 (Rel. 20, Last sequence update)
DT 30-NOV-2000 (Rel. 39, Last annotation update)
DE FURLIN PRECURSOR (EC 3.4.21.75) (PAIRED BASIC AMINO ACID RESIDUE
DE CLEAVING ENZYME) (PACE) (DIBASIC PROCESSING ENZYME).
GN FUR OR PCSK3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
CY [1]
RN SEQUENCE FROM N.A.
RP MEDLINE-91093035; PubMed-2266110;
RA Hatawaza K., Hosaka M., Nakagawa T., Nagase M., Shoda A.,
RA Murakami K., Nakayama K.;
RT "Structure and expression of mouse furin, a yeast Kex2-related
RT protease. Lack of processing of coexpressed prorenin in GH4C1
RT cells.";
RT J. Biol. Chem. 265:22075-22078(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Liver;
RA Creemers J.W.M., Roebroek A.J.M., van den Ouweland A.M.W.,
RA van Duijnhoven H.L.P., van de Ven W.J.M.;
RT "Cloning and functional expression of a 4.3 kbp mouse fur cDNA:
RT evidence for differential expression.";
RT Life Sci. Adv. (Mol. Biol.) 11:127-138(1992).
CC -1 FUNCTION: FURLIN IS LIKELY TO REPRESENT THE UBIQUITOUS ENDOPEPTASE
CC ACTIVITY WITHIN CONSTITUTIVE SECRETORY PATHWAYS AND CAPABLE OF
CC CLEAVAGE AT THE RX(R/R)R CONSENSUS MOTIF.
CC -1 CATALYTIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR
CC PROPEPTIDES BY CLEAVAGE OF ARG-XAA-YAA-ARG-1-ZAA BONDS, WHERE XAA
CC CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS. RELEASES ALBUMIN,
CC COMPLEMENT COMPONENT C3 AND VON WILLEBRAND FACTOR FROM THEIR

CC RESPECTIVE PRECURSORS.
CC -1 COPACITOR: CALCIUM-DEPENDENT (BY SIMILARITY).
CC -1 ENZYME REGULATION: COULD BE INHIBITED BY THE NOT SECONDLY CLEAVED
CC PROPEPTIDE.
CC -1 SUBCELLULAR LOCATION: SEEMS TO BE LOCALIZED INTRACELLULARLY TO THE
CC TRANS GOLGI NETWORK. PROPEPTIDE CLEAVAGE IS A PREREQUISITE FOR
CC EXIT OF FURLIN MOLECULES OUT OF THE ENDOPLASMIC RETICULUM (ER).
CC SECOND CLEAVAGE IN THE PROPEPTIDE OCCUR IN THE TRANS GOLGI NETWORK
CC (TGN), WHICH IS FOLLOWED BY THE RELEASE OF THE PROPEPTIDE BOUND TO
CC FURLIN AND THE ACTIVATION OF FURLIN.
CC -1 TISSUE SPECIFICITY: SEEMS TO BE EXPRESSED UBIQUITOUSLY.
CC -1 DOMAIN: CONTAINS A HOMO B DOMAIN, ALSO KNOWN AS P OR MIDDLE DOMAIN
CC AND A SUBTILISIN-LIKE CATALYTIC DOMAIN. ESSENTIAL DOMAINS FOR
CC CATALYTIC ACTIVITY.
CC -1 DOMAIN: CONTAINS A CYTOPLASMIC DOMAIN RESPONSIBLE FOR ITS TGN
CC LOCALIZATION AND RECYCLING FROM THE CELL SURFACE.
CC -1 PTM: THE PROPEPTIDE IS AUTOCATALYTICALLY REMOVED THROUGH AN
CC INTRAMOLECULAR CLEAVAGE PROBABLY IN THE ENDOPLASMIC RETICULUM
CC (ER). IN THE TGN THE SECOND CLEAVAGE IN THE PROPEPTIDE COULD LEAD
CC TO THE ACTIVATION OF FURLIN.
CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE
CC SUBTILASE FAMILY. HIGH SIMILARITY WITH OTHER FURLIN-LIKE ENZYMES.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: X54056; CAA37988.1; -
DR EMBL: U26489; AAA37643.1; -
DR PIR: A23679; KXMF.
DR HSP: O99405; IMPF.
DR MEROPS: S08_071; -
DR MGD: MGI:97513; PCSK3.
DR InterPro: IPR002029; -
DR InterPro: IPR002884; -
DR Pfam: PF01483; P; 1.
DR Pfam: PF00082; Peptidase_S8; 1.
DR PRINTS: PR00723; SUBTILISIN.
DR PROSITE: PS00136; SUBTILASE_ASP; 1.
DR PROSITE: PS00137; SUBTILASE_HIS; 1.
DR PROSITE: PS00138; SUBTILASE_SER; 1.
KW Hydrolyase; Serine protease; Transmembrane; Glycoprotein; Signal;
KW Zymogen; Calcium.
FT SIGNAL 1 24
FT PROPEP 25 107
FT CHAIN 108 793
FT DOMAIN 356 705
FT TRANSMEM 715 735
FT ACT_SITE 153 153
FT ACT_SITE 194 194
FT ACT_SITE 368 368
FT DISULFID 211 360
FT DISULFID 303 333
FT CARBOHYD 387 387
FT CARBOHYD 440 440
FT CARBOHYD 553 553
FT SITE 70 75
FT SITE 104 107
FT SITE 758 761
FT SITE 772 778
FT SITE 498 500
FT SITE 746 746
FT CONFLICT 746 746
FT SEQUENCE 793 AA; 86804 MW; 5F121C3DE2E1A42D CRC64;
SQ
Query Match 19.7%; Score 71; DB 1; Length 793;
Best Local Similarity 40.0%; Pred. No. 3.2;
Matches 20; Conservative 3; Mismatches 27; Indels 0; Gaps 0;

OY 7 EKEGSEALSSRGAPVQHPLALPPSGSYEEEDPQTILDDHLSRYLTKPG 56
 Db 672 EQGCSROSOSRESRPOQAPPALPEVEMERLQAGLASHLEPVLAGLSC 721

RESULT 13
 ID PPAS_HUMAN STANDARD; PRT; 441 AA.

AC 003181;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR BETA (PPAR-BETA)
 DE (PPAR-DELTA) (NUCLEAR HORMONE RECEPTOR 1) (NRC1) (NRC1)
 GN PPARB OR NR1C2 OR PPARB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC NBL_TaxID=9606;

CC [1]
 CC SEQUENCE FROM N.A.
 CC MEDLINE=93078797; Pubmed=1333051;
 CC Schmidt A., Endo N., Rutledge S.J., Vogel R., Shinar D.,
 CC Rodan G.A.;
 CC "Identification of a new member of the steroid hormone receptor
 CC superfamily that is activated by a peroxisome proliferator and fatty
 CC acids";
 CC Mol. Endocrinol. 6:1634-1641(1992).
 CC -1- FUNCTION: RECEPTOR THAT BIND PEROXISOME PROLIFERATORS SUCH AS
 CC HYPOLIPIDEMIC DRUGS AND FATTY ACIDS. ONCE ACTIVATED BY A LIGAND,
 CC THE RECEPTOR BINDS TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-COA
 CC OXIDASE AND ACTIVATES ITS TRANSCRIPTION. IT THEREFORE CONTROLS THE
 CC PEROXISOMAL BETA-OXIDATION PATHWAY OF FATTY ACIDS.
 CC -1- SUBUNIT: HETERODIMER WITH THE RETINOID X RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
 CC NRI SUBFAMILY.

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CC EMBL; L07592; AAA36469.1; -
 CC PIR; A45360; A45360.
 CC HSSP; P03372; IHCO.
 CC MIM; 600409; -
 CC InterPro; IPR000536; -
 CC InterPro; IPR001628; -
 CC InterPro; IPR001723; -
 CC InterPro; IPR003074; -
 CC InterPro; IPR003075; -
 CC Pfam; PF00104; hormone_rec.1.
 CC Pfam; PF00105; zf-C4.1
 CC PRINTS; PR00067; STEROIDINGER.
 CC PRINTS; PR00398; STRDHOMONER.
 CC PRINTS; PR01288; PROXISOMPAR.
 CC PRINTS; PR01290; PROXISOMPAR.
 CC PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
 CC Receptor; Transcription regulation; Activator; DNA-binding;
 CC Nuclear protein; Zinc-finger; Multigene family
 CC DNA_BIND 74 138 NUCLEAR RECEPTOR-TYPE.
 CC ZN_FING 74 94 C4-TYPE.
 CC ZN_FING 111 133 C4-TYPE.
 CC DOMAIN 254 441 LIGAND-BINDING (BY SIMILARITY).
 CC SEQUENCE 441 AA; 49903 MW; 94FBB2A4B46521E8 CRC64;

Query Match 19.0%; Score 68.5; DB 1; Length 441;
 Best Local Similarity 30.3%; Pred. No. 3.1;

Matches 23; Conservative 10; Mismatches 26; Indels 17; Gaps 4;

OY 1 QIREDEKESGALSSRGAPVQH--PLALPPSGSYEE-----DPQTILDDHLSRYLTKT 53
 Db 10 EVREDEKEEVAER-----EGAPELNGPQHALLPSSSYTDLSSRSPSLDDQ-----LQ 59

OY 54 PGCSPGCVGRYSPRSR 69
 Db 60 MCGDGCAGCSGLNMECR 75

RESULT 14
 ID Y888_METJA STANDARD; PRT; 206 AA.

AC 058298;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HYPOTHETICAL PROTEIN MJ0888.
 GN MJ0888.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
 OC Methanococcus.

CC [1]
 CC SEQUENCE FROM N.A.
 CC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 CC MEDLINE=96337999; Pubmed=8688087;
 CC Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 CC Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 CC Kellavag A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.J.,
 CC Kierulff R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 CC Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 CC Uterback T.R., Kelley J.R., Peterson J.D., Sadow P.W., Hanna M.C.,
 CC Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 CC Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 CC "Complete genome sequence of the methanogenic archaeon, Methanococcus
 CC jannaschii";
 CC Science 273:1058-1073(1996).
 CC -1- SIMILARITY: WEAK, TO B.SUBTILIS Y0GX AND TO M.JANNASCHII MJ0296.
 CC -----
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CC EMBL; U67532; AAB98892.1; -
 CC TIGR; MJ0888; -
 CC InterPro; IPR001279; -
 CC Pfam; PF00753; lactamase_B.1.
 CC Hypothetical protein.
 CC SEQUENCE 206 AA; 23229 MW; AC2C59F1E80840E CRC64;

Query Match 18.9%; Score 68; DB 1; Length 206;
 Best Local Similarity 32.8%; Pred. No. 1.4;
 Matches 19; Conservative 10; Mismatches 21; Indels 8; Gaps 2;

OY 2 IREDEE-----KEGSEALSSRGAPVQHPLALPPSGSYEEEDPQTILDDHLSRYLTKPG 55
 Db 76 IREDEEVLKNGDEVTVSSLGAKLNPKKELIPLSEIEE---LKSIGLEIRTPG 129

RESULT 15
 ID FURL_RAT STANDARD; PRT; 793 AA.

AC P23377;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE FURIN PRECURSOR (EC 3.4.21.75) (PAIRED BASIC AMINO ACID RESIDUE
DE CLEAVING ENZYME) (PAGE) (DIBASIC PROCESSING ENZYME).
GN FUR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MISTAR; TISSUE=Liver;
RA MEDLINE=91067492; PubMed=2251148;
RA Mitsuami Y., Sohoda M., Ikehara Y.;
RT *Sequence of the cDNA encoding rat furin, a possible propeptide-
RT processing endoprotease.*;
RT Nucleic Acids Res. 18:6719-6719(1990).
CC -1- FUNCTION: FURIN IS LIKELY TO REPRESENT THE UBIQUITOUS ENDOPEPTASE
CC ACTIVITY WITHIN CONSTITUTIVE SECRETORY PATHWAYS AND CAPABLE OF
CC CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF.
CC -1- CATALYTIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR
CC PROPEPTIDES BY CLEAVAGE OF ARG-XAA-YAA-ARG-1-ZAA BONDS, WHERE XAA
CC CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS. RELEASES ALBUMIN,
CC COMPLEMENT COMPONENT C3 AND VON WILLEBRAND FACTOR FROM THEIR
CC RESPECTIVE PRECURSORS.
CC -1- CORRELATION: CALCIUM-DEPENDENT (BY SIMILARITY).
CC -1- ENZYME REGULATION: COULD BE INHIBITED BY THE NOT SECONDLY CLEAVED
CC PROPEPTIDE.
CC -1- SUBCELLULAR LOCATION: SEEMS TO BE LOCALIZED INTRACELLULARLY TO THE
CC TRANS GOLGI NETWORK. PROPEPTIDE CLEAVAGE IS A PREREQUISITE FOR
CC EXIT OF FURIN MOLECULES OUT OF THE ENDOPLASMIC RETICULUM (ER).
CC SECOND CLEAVAGE IN THE PROPEPTIDE OCCUR IN THE TRANS GOLGI NETWORK
CC (TGN), WHICH IS FOLLOWED BY THE RELEASE OF THE PROPEPTIDE BOUND TO
CC FURIN AND THE ACTIVATION OF FURIN.
CC -1- TISSUE SPECIFICITY: SEEMS TO BE EXPRESSED UBIQUITOUSLY.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT E7 DAY IN EMBRYO AND MESODERM,
CC UNIFORMLY EXPRESSED UNTIL E10, WHEN EXPRESSION IS HIGHER IN HEART
CC AND LIVER PRIMORDIA. IN MID- AND LATE- GESTATIONAL STAGES, WIDELY
CC EXPRESSED.
CC -1- DOMAIN: CONTAINS A HOMO B DOMAIN, ALSO KNOWN AS P OR MIDDLE DOMAIN
CC AND A SUBTILISIN-LIKE CATALYTIC DOMAIN. ESSENTIAL DOMAINS FOR
CC CATALYTIC ACTIVITY.
CC -1- DOMAIN: CONTAINS A CYTOPLASMIC DOMAIN RESPONSIBLE FOR ITS TGN
CC LOCALIZATION AND RECYCLING FROM THE CELL SURFACE.
CC -1- PTM: THE PROPEPTIDE IS AUTOCATALYTICALLY REMOVED THROUGH AN
CC INTRAMOLECULAR CLEAVAGE PROBABLY IN THE ENDOPLASMIC RETICULUM
CC (ER). IN THE TGN THE SECOND CLEAVAGE IN THE PROPEPTIDE COULD LEAD
CC TO THE ACTIVATION OF FURIN.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE
CC SUBTILASE FAMILY. HIGH SIMILARITY WITH OTHER FURIN-LIKE ENZYMES.
CC -----
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CC -----
CC EMBL: X55660; CAA39193.1; -.
DR EMBL: X55660; CAA39193.1; -.
DR PIR: S13106; KXRTF.
DR HSSP: G99405; IMPT.
DR MEROPS: S08.071; -.
DR InterPro: IPR000209; -.
DR InterPro: IPR002884; -.
DR Pfam: PF01483; P; 1.
DR Pfam: PF00082; Peptide_S8; 1.
DR PRINTS: PR00723; SUBTILISIN.
DR PROSITE: PS00136; SUBTILASE_ASP; 1.
DR PROSITE: PS00137; SUBTILASE_HIS; 1.
DR PROSITE: PS00138; SUBTILASE_SER; 1.
DR PROSITE: PS00139; Serine protease; Transmembrane; Glycoprotein; Signal;
KW Hydroxylase; Calcium; Transmembrane; Glycoprotein; Signal;
KW Zymogen; Calcium.
FT SIGNAL 1 24 POTENTIAL.
FT PROPEPT 25 107 BY SIMILARITY.

FT	CHAIN	108	793	FURIN.
FT	DOMAIN	556	705	CYS-RICH.
FT	TRANSMEM	715	735	POTENTIAL.
FT	ACT_SITE	153	153	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	ACT_SITE	194	194	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	ACT_SITE	368	368	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	DISULFID	211	360	POTENTIAL.
FT	DISULFID	303	333	POTENTIAL.
FT	CARBOHYD	387	387	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	440	440	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	553	553	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	SITE	70	75	CLEAVAGE (SECOND AUTO-).
FT	SITE	104	107	CLEAVAGE (FIRST AUTO-).
FT	SITE	498	500	CELL ATTACHMENT SITE (POTENTIAL).
FT	SITE	758	761	CELL SURFACE SIGNAL.
FT	SITE	772	778	TRANS GOLGI NETWORK SIGNAL.
SO	SEQUENCE	793 AA;	86653 MW;	87C22C345AE0A25C CRC64;

Query Match: 18.1%; Score 65; DB 1; Length 793;
Best Local Similarity 38.0%; Pred. No. 15;
Matches 19; Conservative 4; Mismatches 27; Indels 0; Gaps 0;

OY 7 EKEGSEQALSSRDGAPVQHPPLALLPSGSEDEPQTILDDHLSRYLKTGPG 56
DB 672 EOTCSROSOSRESRPOQPPALRPEVEPRRLRAGLASHLPEVYGLSC 721

Search completed: June 7, 2001, 02:10:32
Job time: 420 sec

DB 457 VGRYSPRSR 465

RESULT 2

ID 088566 PRELIMINARY; PRT: 840 AA.

AC 088566;

DT 01-NOV-1998 (TREMBlrel. 08, Created)

DT 01-NOV-1998 (TREMBlrel. 08, last sequence update)

DT 01-OCT-2000 (TREMBlrel. 15, last annotation update)

DE CONDUCTIN.

GN AXIN2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RL MEDLINE=98221239; PubMed=9554852;

RA Behrens J., Jerchow B.-A., Wurttele M., Grimm J., Asbrand C., Wirtz R., Kuhl M., Wedlich D., Birchmeier W.;

RT "Functional interaction of an axin homolog, conductin, with beta-catenin, APC, and GSK3beta.";

RT Science 280:596-599(1998).

RI EMBL; AF073378; AAC26047.1; -

DR HSSP; P49799; IAGR.

DR MGD; MGI:1270862; Axin2.

DR INTERPRO; IPR000342; -

DR INTERPRO; IPR001158; -

DR PFAM; PF00615; RGS; 1.

DR PFAM; PF00778; DIX; 1.

DR PRODOM; PD001580; -; 1.

DR PRODOM; PD003639; -; 1.

SO SEQUENCE 840 AA; 92934 MW; A07DEEB25DE7277 CRC64;

Query Match 100.0%; Score 360; DB 11; Length 840;

Best Local Similarity 100.0%; Pred. No. 5,5e-34;

Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIREDEKESGQALSSRDGAPVQHPHLLPSSGYEDPQTIIIDHLSRVLTPTGCGSPG 60

DB 397 QIREDEKESGQALSSRDGAPVQHPHLLPSSGYEDPQTIIIDHLSRVLTPTGCGSPG 456

QY 61 VGRYSPRSR 69

DB 457 VGRYSPRSR 465

RESULT 3

ID 090XJ6 PRELIMINARY; PRT: 840 AA.

AC 090XJ6;

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)

DT 01-OCT-2000 (TREMBlrel. 15, last annotation update)

DE AXIN2.

GN Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RL Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G., Jenkins N.A., Warburton D., Costantini F.;

RT "Properties of mouse Axin2 and human AXIN2: chromosomal location, expression pattern, interaction with Axin and effects on embryonic axis formation.";

RT Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

RI EMBL; AF205888; AAF22799.1; -

DR HSSP; P49799; IAGR.

DR INTERPRO; IPR000342; -

DR INTERPRO; IPR001158; -

DR PFAM; PF00615; RGS; 1.

DR PFAM; PF00778; DIX; 1.

DR PRINTS; PRO1301; RGSPTOTEN.

SO SEQUENCE 777 AA; 86857 MW; 3A4943ABF430BBD3 CRC64;

DR INTERPRO; IPR001158; -

DR PFAM; PF00615; RGS; 1.

DR PFAM; PF00778; DIX; 1.

DR PRINTS; PRO1301; RGSPTOTEN.

SO SEQUENCE 840 AA; 92896 MW; 767D546B43C921C5 CRC64;

Query Match 100.0%; Score 360; DB 11; Length 840;

Best Local Similarity 100.0%; Pred. No. 5,5e-34;

Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIREDEKESGQALSSRDGAPVQHPHLLPSSGYEDPQTIIIDHLSRVLTPTGCGSPG 60

DB 397 QIREDEKESGQALSSRDGAPVQHPHLLPSSGYEDPQTIIIDHLSRVLTPTGCGSPG 456

QY 61 VGRYSPRSR 69

DB 457 VGRYSPRSR 465

RESULT 4

ID 090H84 PRELIMINARY; PRT: 777 AA.

AC 090H84;

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)

DT 01-OCT-2000 (TREMBlrel. 15, last annotation update)

DE AXIN2.

GN Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=BRAIN; LYMPHOBLAST;

RA Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G., Jenkins N.A., Warburton D., Costantini F.;

RT "Properties of mouse Axin2 and human AXIN2: chromosomal location, expression pattern, interaction with Axin and effects on embryonic axis formation.";

RT Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

RI EMBL; AF205888; AAF22799.1; -

DR HSSP; P49799; IAGR.

DR INTERPRO; IPR000342; -

DR INTERPRO; IPR001158; -

DR PFAM; PF00615; RGS; 1.

DR PFAM; PF00778; DIX; 1.

DR PRINTS; PRO1301; RGSPTOTEN.

SO SEQUENCE 777 AA; 86857 MW; 3A4943ABF430BBD3 CRC64;

Query Match 92.2%; Score 332; DB 4; Length 777;

Best Local Similarity 89.9%; Pred. No. 9,8e-31;

Matches 62; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 QIREDEKESGQALSSRDGAPVQHPHLLPSSGYEDPQTIIIDHLSRVLTPTGCGSPG 60

DB 396 QIREDEKESGQALSSRDGAPVQHPHLLPSSGYEDPQTIIIDHLSRVLTPTGCGSPG 455

QY 61 VGRYSPRSR 69

DB 456 VGRYSPRSR 464

RESULT 5

ID 09Y2T1 PRELIMINARY; PRT: 843 AA.

AC 09Y2T1;

DT 01-NOV-1999 (TREMBlrel. 12, Created)

DT 01-NOV-1999 (TREMBlrel. 12, last sequence update)

DT 01-OCT-2000 (TREMBlrel. 15, last annotation update)

DE CONDUCTIN.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99168905; PubMed=10049590;
 RA Mei M., Qian C., Yokomizo A., Smith D.I., Liu W.;
 RT "Cloning of the human homolog of conductin (AXIN2), a gene mapping to
 chromosome 17q23-q24."
 RL Genomics 55:341-344(1999).
 DR EMBL: AF078165; AAD20976.1; -
 DR HSSP: P49799; IAGR.
 DR INTERPRO: IPR000342; -
 DR INTERPRO: IPR001158; -
 DR PFAM: PF00615; RGS; 1.
 DR PFAM: PF00778; DIX; 1.
 SQ SEQUENCE 843 AA; 93557 MW; F7B62BBD6A84664D CRC64;

Query Match 92.2%; Score 332; DB 4; Length 843;
 Best Local Similarity 89.9%; Pred. No. 1.1e-30;

Matches 62; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 QREDEKESGSEALSRDCAVQHPALPLPSGSEYEDPQTILDDHLSRVLTGCGSPG 60
 DB 397 QREDEKESGSEALSRDCAVQHPALPLPSGSEYEDPQTILDDHLSRVLTGCGSPG 456
 OY 61 VGRYSPRSR 69
 DB 457 VGRYSPRSR 465

RESULT 6
 OYGYO PRELIMINARY; PRT; 842 AA.

AC OYGYO;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE AXIN.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
 OC Xenopodidae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99173782; PubMed=10072781;
 RA Hedgepeth C.M., Deardorff M.A., Klein P.S.;
 RT "Xenopus axin interacts with glycogen synthase kinase-3 beta and is
 expressed in the anterior midbrain."
 RL Mech. Dev. 80:147-151(1999).
 DR EMBL: AF097313; AAC71036.1; -
 DR HSSP: P49799; IAGR.
 DR INTERPRO: IPR000342; -
 DR INTERPRO: IPR001158; -
 DR PFAM: PF00615; RGS; 1.
 DR PFAM: PF00778; DIX; 1.
 DR PRODOM: PD001580; -; 1.
 DR PRODOM: PD003639; -; 1.
 SQ SEQUENCE 842 AA; 94459 MW; BDA152734C97191E CRC64;

Query Match 43.9%; Score 158; DB 13; Length 842;
 Best Local Similarity 40.0%; Pred. No. 3e-10;

Matches 34; Conservative 14; Mismatches 11; Indels 26; Gaps 3;

OY 7 EKSGSEALSRDCAVQHPALPLPSG-----SYEDDPQTILDDHLSRVLTGCGSPG 44
 DB 419 EEDGDDGDVSSGSPV-ISHK---LPSGPMHNFNSRYSETGCGVMOIRDAHEENPESILD 474
 OY 45 DHSRLVLTGCGSPGVRSPRSR 69

DB 475 EHYGRVMTKTPGCGSPGGRHSPRSR 499

RESULT 7
 ID 042400 PRELIMINARY; PRT; 841 AA.
 AC 042400;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE AXIN.
 GN AXIN.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97373830; PubMed=9230313;
 RA Zeng L., Foglio F., Zhang T., Hsu W., Vasicek T.J., Perry W.L.,
 RA III Lee J.J., Tilghman S.M., Gumbiner B.M., Constantini F.;
 RT "The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling
 pathway that regulates embryonic axis formation."
 RL Cell 90:181-192(1997).
 DR EMBL: AF009012; AAC60245.1; -
 DR HSSP: P49799; IAGR.
 DR INTERPRO: IPR000342; -
 DR INTERPRO: IPR001158; -
 DR PFAM: PF00615; RGS; 1.
 DR PFAM: PF00778; DIX; 1.
 DR PRODOM: PD001580; -; 1.
 DR PRODOM: PD003639; -; 1.
 SQ SEQUENCE 841 AA; 94931 MW; 40DDC90E72506FE CRC64;

Query Match 40.6%; Score 146; DB 13; Length 841;
 Best Local Similarity 34.7%; Pred. No. 7.7e-09;

Matches 35; Conservative 14; Mismatches 14; Indels 38; Gaps 4;

OY 3 REDEK-----EGSEALSRDCAVQHPALPLPSG----- 33
 DB 403 REDEKLEKRVRAEEEDADISSGSPV-ISHK---MPSQPFHNFARYSKMGACG 458
 OY 34 -----SYEDDPQTILDDHLSRVLTGCGSPGVRSPRSR 69
 DB 459 MQRDAHEENPESILDEHYGRVMTKTPGCGSPGGRHSPRSR 499

RESULT 8
 ID 070239 PRELIMINARY; PRT; 832 AA.
 AC 070239;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE RAXIN.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98151361; PubMed=9482734;
 RA Ikeda S., Yamamoto H., Murali H., Kishida S., Kikuchi A.;
 RT "Axin, a negative regulator of the Wnt signaling pathway, forms a
 complex with GSK-3beta and beta-catenin and promotes GSK-3beta-
 dependent phosphorylation of beta-catenin."
 RL EMBL: AF017756; AAC40066.1; -
 DR HSSP: P49799; IAGR.
 DR INTERPRO: IPR000342; -

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DR INTERPRO: IPR001158; -.
DR PFAM: PF00615; RGS; 1.
DR PFAM: PF00778; DIX; 1.
DR PRODOM: PD001360; -. 1.
DR PRODOM: PD003639; -. 1.
SQ SEQUENCE 832 AA; 92856 MW; B489504C7E594347 CRC64;

Query Match 38.8%; Score 139.5; DB 11; Length 832;
Best Local Similarity 35.3%; Pred. No. 4,4e-08;
Matches 30; Conservative 14; Mismatches 20; Indels 21; Gaps 2;

OY 1 QIRDEKEGSEQALSSRDGAPVOHPALPLPS-----GSYEEDPOTIL 43
DB 420 RVRMEEGEDDEMP-----SGPMASHKLPSPVAMHPPRYVMGCSGLRDHAHEENPESIL 475
OY 44 DDHLSRYLKTGPGCSPGVGRYSPRS 68
DB 476 DEHVORVARTPGCSPGPHRSPDS 500

RESULT 9
ID 035625 PRELIMINARY; PRT; 992 AA.
AC 035625;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE AXIN (FRAGMENT).
GN AXIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OY NCBI_TaxId=10090;
RX [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-97373830; PubMed-9230313;
RA Zeng L., Fagotto F., Zhang T., Hsu W., Vasilek T.J., Perry W.L.,
RA Ili Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F.;
RT "The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling
RT pathway that regulates embryonic axis formation."
RL Cell 90:181-192(1997).
DR EMBL: AF009011; AAC53285.1; -.
DR HSSP: P49799; IAGR.
DR MGD: MGI:1096327; Axin.
DR INTERPRO: IPR000342; -.
DR INTERPRO: IPR001158; -.
DR PFAM: PF00615; RGS; 1.
DR PFAM: PF00778; DIX; 1.
DR PRINTS: PRO1301; RGSPROTEIN.
FT NON_TER 1
SQ SEQUENCE 992 AA; 109917 MW; 70EBB53D387BD26F CRC64;

Query Match 38.8%; Score 139.5; DB 11; Length 992;
Best Local Similarity 35.3%; Pred. No. 5,4e-08;
Matches 30; Conservative 14; Mismatches 20; Indels 21; Gaps 2;

OY 1 QIRDEKEGSEQALSSRDGAPVOHPALPLPS-----GSYEEDPOTIL 43
DB 544 RVRMEEGEDDEMP-----SGPMASHKLPSPVAMHPPRYVMGCSGLRDHAHEENPESIL 599
OY 44 DDHLSRYLKTGPGCSPGVGRYSPRS 68
DB 600 DEHVORVARTPGCSPGPHRSPDS 624

RESULT 10
ID 015169 PRELIMINARY; PRT; 900 AA.
AC 015169;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)

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DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE AXIN (FRAGMENT).
GN AXIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OY NCBI_TaxId=9606;
RX [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-97373830; PubMed-9230313;
RA Zeng L., Fagotto F., Zhang T., Hsu W., Vasilek T.J., Perry W.L.,
RA Ili Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F.;
RT "The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling
RT pathway that regulates embryonic axis formation."
RL Cell 90:181-192(1997).
DR EMBL: AF009674; AAC51624.1; -.
DR HSSP: P49799; IAGR.
DR INTERPRO: IPR000342; -.
DR INTERPRO: IPR001158; -.
DR PFAM: PF00615; RGS; 1.
DR PFAM: PF00778; DIX; 1.
DR PRINTS: PRO1301; RGSPROTEIN.
FT NON_TER 1
SQ SEQUENCE 900 AA; 99803 MW; EE5F90B11FC7B3B CRC64;

Query Match 31.5%; Score 113.5; DB 4; Length 900;
Best Local Similarity 34.4%; Pred. No. 5,5e-05;
Matches 33; Conservative 10; Mismatches 22; Indels 31; Gaps 3;

OY 3 REDEEK-----EGSEQALSSRDGAPVOHPALPLPS----- 32
DB 440 REAEKLEERLKRVRMEEGEDGDPSSGPPGFC-HKLRPRAMHPPRLCWTACAGLR 498
OY 33 GSYEDPOTILDDHLSRYLKTGPGCSPGVGRYSPRS 68
DB 499 DAHEENPESILDEHVORVARTPGCSPGPHRSPDS 534

RESULT 11
ID 09PTP2 PRELIMINARY; PRT; 706 AA.
AC 09PTP2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE AXIN-RELATED PROTEIN.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OY NCBI_TaxId=8355;
RX [1]
RP SEQUENCE FROM N.A.
RA Tissue-Ovary;
RA Itoh K., Antipova A., Ratcliffe M., Sokol S.;
RT "Dishevelled transduces a signal by displacing GSK3 from axin-GSK3
RT complex."
RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF140243; AF22574.1; -.
DR INTERPRO: IPR000342; -.
DR INTERPRO: IPR001158; -.
DR PFAM: PF00778; DIX; 1.
DR PRINTS: PRO1301; RGSPROTEIN.
SQ SEQUENCE 706 AA; 79196 MW; C3D0AF0D9540F162 CRC64;

Query Match 31.2%; Score 112.5; DB 13; Length 706;
Best Local Similarity 37.8%; Pred. No. 5,5e-05;
Matches 28; Conservative 13; Mismatches 16; Indels 17; Gaps 3;

OY 1 QIRDEKEGSEQALSSRDGAPVOHPALPLPSGSYEEDPOTILDDHLSRYLKTGPG----- 55

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DB 357 RUKKEEELADVDIPSSHE-----TVPGALEDDPOSILDDHVSRLKTPANLSPR 407
 OY 56 COSPGV---GRYSP 66
 DB 408 SOSPFVORKKFP 421

RESULT 12

0918W3

ID 0918W3 PRELIMINARY; PRT: 443 AA.

AC 0918W3;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE PEROXISOME PROLIFERATOR-ACTIVATED RECEPTOR BETA.
 GN PPARBETA.

OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Archosauiria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus
 NC NCB1_TaxID=9031;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=20267232; PubMed=10809235;
 RA Takada I., Yu R.T., Xu H.E., Lambert M.H., Montana V.G., Klierer S.A.,
 RA Evans R.M., Umesono K.;
 RT "Alteration of a single amino acid in peroxisome proliferator-
 activated receptor-alpha (PPAR alpha) generates a PPAR delta
 phenotype.";
 RT Mol. Endocrinol. 14:733-740(2000).
 DR EMBL: AF163810; AAF80480.1; .

DR EMBL: AF163810; AAF80480.1; .
 KW Receptor.
 SQ SEQUENCE 443 AA; 50108 MW; EB6E0C39554C76CD CRC64;

Query Match 19.4%; Score 70; DB 13; Length 443;
 Best Local Similarity 32.4%; Pred. No. 3.2;
 Matches 24; Conservative 12; Mismatches 26; Indels 12; Gaps 4;

OY 1 QIREDEKESQALSSRDG--PVQHPALLPSSGYEDPQT---LDDHLSRVLKTPG 55
 DB 10 EYREEEEEE--EAVTVSGASDPSSGSLPSSSYTDLSSSSPSLSLQIQM-----G 62

OY 56 COSPGVGRYSPRSR 69
 DB 63 CEETASGALNVECR 76

RESULT 13

09JL71

ID 09JL71 PRELIMINARY; PRT: 1098 AA.

AC 09JL71;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE TEASHIRT 2 (FRAGMENT).
 GN TSH2.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCB1_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Caudit X., Core N., Boned A., Kerridge S., Djabali M., Fasano L.;
 RT "Vertebrate orthologues of the Drosophila region-specific patterning
 gene teashirt.";
 RT Mech. Dev. 91:445-448(2000).
 RL EMBL: AF207880; AAF64095.1; .

DR EMBL: AF207880; AAF64095.1; .
 FT NON_TER 1
 FT NON_TER 1098 1098
 SQ SEQUENCE 1098 AA; 121367 MW; 42BA01C7DB2BAFEB CRC64;

Query Match 18.8%; Score 67.5; DB 11; Length 1098;
 Best Local Similarity 35.0%; Pred. No. 17;
 Matches 21; Conservative 11; Mismatches 23; Indels 5; Gaps 3;

OY 4 EDEKEGSEQALSSRDG-APVQHPALLPSSGYEDPQTILDDHLSRV---LKTPEGCOSP 59
 DB 726 OKEKEPELEPVSLTNGCAPANHTPA-LPSINPLSALQSVLNNHIGKATPELRSPSCSSP 784

RESULT 14

029576

ID 029576 PRELIMINARY; PRT: 563 AA.

AC 029576;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE SUCCINATE DEHYDROGENASE, FLAVOPROTEIN SUBUNIT A (SDHA).
 GN AF0681.

OS Archaeoglobus fulgidus.
 OC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
 OC Archaeoglobus.
 NC NCB1_TaxID=2234;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
 RX MEDLINE=98049343; PubMed=9389475;
 RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
 RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
 RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrtides N.C.,
 RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
 RA Kirschner E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
 RA Peterson S., Reich C.I., McNeill L.K., Badger J.H., Glodek A., Zhou L.,
 RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
 RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
 RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
 RA Venter J.C.;

RA "The complete genome sequence of the hyperthermophilic, sulphate-
 reducing archaeon Archaeoglobus fulgidus.";
 RT Nature 390:364-370(1997).
 RL EMBL: AE001057; AAB90557.1; .

DR HSSP: P00363; 1FUM.
 DR TIGR: AF0681; .
 DR INTERPRO: IPR000464; .
 DR INTERPRO: IPR001005; .
 DR PFAM: PF00890; FAD_binding_2; 1.
 DR PROSITE: PS00037; MYB_1; UNKNOMN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 563 AA; 63189 MW; 7F2B92DFD242311 CRC64;

Query Match 18.3%; Score 66; DB 1; Length 563;
 Best Local Similarity 25.3%; Pred. No. 12;
 Matches 19; Conservative 10; Mismatches 12; Indels 34; Gaps 3;

OY 10 GSEQALSSRDGAPVQ-----HPLALLPSSGYEDPQTILDDHLSRVLKTPGCGOSP-- 60
 DB 208 GGLAIAYRNGIPLKDMFEQFHPGLVPSG-----ILMTSCRGEGGY 251

OY 61 -----VGRYSP 66
 DB 252 LUNKGERFMKRYAP 266

RESULT 15

09JUV8

ID 09JUV8 PRELIMINARY; PRT: 679 AA.

AC 09JUV8;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE HYPOTHETICAL 73.8 KDA PROTEIN.
 GN L7836.04.

OS Leishmania major.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-FRIEDLIN;
 RA Oliver K., Harris D., Ivens A.C., Lawson D., Quail M.,
 RA Rajandream M.A., Barrell B.G.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-FRIEDLIN;
 RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
 RA Smith D.F.;
 RT "A physical map of the Leishmania major Friedlin genome.";
 RL Genome Res. 8:135-143(1998).
 DR EMBL; AL117263; CAB55379.1; -.
 KM Hypothetical protein.
 SQ SEQUENCE 679 AA; 73834 MW; 1FCDF361BD81243E CRC64;

Query Match 18.28; Score 65.5; DB 5; Length 679;
 Best Local Similarity 39.38; Pred. No. 18;
 Matches 17; Conservative 6; Mismatches 13; Indels 7; Gaps 2;
 QY 11 SFOALSRDGA-PVOHPLAL-----PSGSYEEDPQTILDDH 46
 DB 129 SEPAPAAATGAQPRPRGLAMLNIAIRKHPEGSTIEQGPVVTEKH 171

Search completed: June 7, 2001, 02:09:43
 Job time: 446 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 7, 2001, 02:01:18 ; Search time 80.96 Seconds
(without alignments)
36.009 Million cell updates/sec

Title: US-09-587-574-5
Perfect score: 276
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Scoring table:
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Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues
Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :
1: A_Geneseq_0401.*
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12: /SIDS2/gcgdata/geneseq/geneseq/AA1990.DAT.*
13: /SIDS2/gcgdata/geneseq/geneseq/AA1991.DAT.*
14: /SIDS2/gcgdata/geneseq/geneseq/AA1992.DAT.*
15: /SIDS2/gcgdata/geneseq/geneseq/AA1993.DAT.*
16: /SIDS2/gcgdata/geneseq/geneseq/AA1994.DAT.*
17: /SIDS2/gcgdata/geneseq/geneseq/AA1995.DAT.*
18: /SIDS2/gcgdata/geneseq/geneseq/AA1996.DAT.*
19: /SIDS2/gcgdata/geneseq/geneseq/AA1997.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseq/AA1998.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseq/AA1999.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq/AA2000.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	276	100.0	840	20	W93570 Human conductin pr
2	276	100.0	840	20	W93569 Human conductin pr
3	191	69.2	900	20	W96264 Human axin. Homo
4	190	68.8	992	20	W96265 Murine axin. Mus
5	61	22.1	601	21	Y90851 Castor bean casden
6	56.5	20.5	1018	21	B01769 Simian immunodef
7	55.5	20.1	301	21	G13112 Arabidopsis thalia
8	55.5	20.1	391	21	G13111 Arabidopsis thalia
9	55.5	20.1	394	21	G13110 Arabidopsis thalia
10	55.5	20.1	975	21	G45799 Arabidopsis thalia
11	54.5	19.7	566	17	W04271 B.L. neutral prote

12	54.5	19.7	594	21	G43722 Arabidopsis thalia
13	54.5	19.7	615	21	G43721 Arabidopsis thalia
14	54.5	19.7	699	21	G43720 Arabidopsis thalia
15	54	19.6	1036	13	R20599 HIV-2 polymera
16	54	19.6	1055	18	W13055 Sequence encoded b
17	53.5	19.4	314	10	P93143 Arabidopsis thalia
18	53.5	19.4	594	21	G47035 Arabidopsis thalia
19	53.5	19.4	594	21	G47041 Arabidopsis thalia
20	53.5	19.4	615	21	G47034 Arabidopsis thalia
21	53.5	19.4	615	21	G47040 Arabidopsis thalia
22	53.5	19.4	699	21	G47033 Arabidopsis thalia
23	53.5	19.4	699	21	G47039 Arabidopsis thalia
24	53	19.2	309	16	R70909 Human melanoma ant
25	53	19.2	309	20	W81548 Tumour rejection a
26	53	19.2	445	20	Y06592 CLTFA-MAGE-1-HIS f
27	53	19.2	446	20	Y06590 Lipoprotein D-MAGE
28	53	19.2	1332	20	Y01084 Human IKAP protein
29	52.5	19.0	158	21	B01778 Simian immunodef
30	52.5	19.0	329	18	W11328 Bacillus subtilis
31	52.5	19.0	616	21	G39767 Arabidopsis thalia
32	52.5	19.0	700	21	G39766 Arabidopsis thalia
33	52.5	19.0	704	21	Y77930 A. thaliana enviro
34	52.5	19.0	705	21	G39765 Arabidopsis thalia
35	52	18.8	995	20	Y04658 L.lactis HsdR subu
36	52	18.8	1337	16	R85203 huDpP-1. Homo sep
37	52	18.8	3080	10	P93285 Sequence of clone
38	52	18.8	3210	9	P81771 Deduced sequence e
39	51.5	18.7	151	19	W70219 Leishmania antigen
40	51.5	18.7	501	12	R14372 Tomato endo-1,4-B-
41	51.5	18.7	501	17	R89278 CM-cellulase. Lyc
42	51.5	18.7	620	14	R32548 Tomato hsp80. Lyc
43	51.5	18.7	659	14	R32549 Pol gene of simian
44	51.5	18.7	1061	11	R04192 Pinosylvine syntha
45	51	18.5	190	14	R33698

ALIGNMENTS

RESULT 1	
ID W93570	standard; Protein; 840 AA.
XX W93570;	
XX	
AC	
XX	
DT	17-JUN-1999 (first entry)
XX	
DE	Human conductin protein.
XX	
KW	Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour;
KW	therapy; cytoplasmic degradation; blockade; Wnt signalling pathway;
KW	Wingless signalling pathway; Adenomatous Polyposis Coll.; APC;
KW	tumour suppressor.
XX	
OS	Homo sapiens.
XX	
PN	W09911780-A2.
XX	
PD	11-MAR-1999.
XX	
PF	01-SEP-1998; 98WO-DE02621.
XX	
PR	02-SEP-1997; 97DE-1038205.
XX	
PA	(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX	
PI	Behrens J, Birchmeier W;
XX	
DR	WPI; 1999-214706/18.
XX	
PT	N-PSDB; X23370.
XX	
PT	Tumor-suppressing protein conductin - used for treatment and
XX	diagnosis of tumors

CC negative regulation of the Wnt pathway in the Nieuwkoop Center
XX
SQ Sequence 900 AA;

QY 1 LTLGHRKEQLSKKGNRYFFKKASDEFACGAVFEEIWDDEIVLPMYEGRIL 51
: ||| ||| : ||| ||| ||| ||| : ||| ||| : |||
Db 935 vtlgqfkealltkksyryyfkksvdefcgvfveevredapvlpvfeeki 985

Query Match	69.2%	Score	191;	DB	20;	Length	900;
Best Local Similarity	66.7%	Pred. No.	1.3e-17;				
Matches	34;	Conservative	9;	Mismatches	8;	Indels	0;
						Gaps	0;

Dy 1 LULGHFEQOLSKKGNRYFFKKASDEFACGAVFEEIWDDEYVLPMEYGRIL 51
::|||:::||:|||||::|||::|||::|||:
Db 843 vLlqgfkelIttkgsyryfkkvsdfdcgvvfcevredeavlpvfeekll 893

AC	Y90851;
XX	
DT	25-AUG-2000 (first entry)
...	

RESULT	4
W96265	
ID	W96265 standard; protein; 992 AA.

XX Synthase; protein co-ordinate data
KW terpenoid; 3-dimensional coordinate
KW terpenoid; 3-dimensional coordinate

AC	W96265;
XX	
DT	14-JUN-1999 (first entry)
xx	

KM pheromone; defensive agent; pigment; antitumor; steroid hormone;
KM signal transduction pathway; bile acid; affinity purification;
KM photoreceptor; enzymatic synthesis; nutrient supplement;
KM immunological research

KM axin: cancer; breast cancer; colorectal cancer;
KM gastrointestinal cancer; esophageal cancer; carcinoma; melanoma;
KM diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;
KM beta-catenin.

XX WO200017327-A2.
PN
XX
PD 30-MAR-2000.
XX

OS Mus musculus.

PF 17-SEP-1999; 99WO-US21419-

PN WO9902179-A1

PR 18-SEP-1998; 98US-0100993

PD 21-JAN-1999.

PR 23-AUG-1999;

PF 09-JUL-1998; 98WO-US14414

PA (KENT) UNIV KENTUCKY RES DI

PR 10-JUL-1997; 97US-0890865

XX

UNIV COLUMBIA NEW YORK.
(UYCO)

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PI Constant Inl F. Zend I:

DR MF1, 2000-232033/22.
DR N-PSDB: A38930.

XX	WPI; 1999-120510/10.
DR	N-PCPB; X09012
DP	

Novel terpene synthase enzymes, useful for producing terpene hydrocarbons and fragrances or antitumor agents, are derived from

PT Newly isolated nucleic acid encoding "axis inhibition" protein
PT (Axin) - useful for detecting, diagnosing and treating cancer

XX
PS Claim 106; Page 406-407; 450pp; English.

PS Claim 8; Figure 8; 95pp; English.

CC Nucleic acids encoding mutant and wild type Axin and
CC oligonucleotides derived from them are useful for detecting
CC mutations in the Axin gene and for determining whether a subject is
CC likely to develop cancer (including breast, colorectal,
CC gastrointestinal, esophagel, carcinomas or melanomas). The wild
CC type Axin and homologs of Axin are useful for treating subjects
CC who are likely to develop cancer (thyroid carcinomas). The nucleic
CC acids are also useful for diagnosing cancer and for detecting
CC mutations in cancerous cells. Wild type Axin, its antisense
CC molecule and identified compounds form pharmaceutical compositions
CC in the treatment of cancer. The compositions are also useful for
CC treating cancer by inhibiting tumorigenesis (by inducing degradation
CC of beta-catenin). The nucleic acid encoding Axin acts through
CC negative regulation of the Wnt pathway in the Nieuwkoop Center.

Sequence 992 AA:

CC nucleic acids for monitoring expression of terpene synthase

Query Match	68.8%	Score 190;	DB 20;	Length 992;
Best Local Similarly	66.7%	Pred. No. 2e-17;		
Matches 34; Conservative	9;	Mismatches 8;	Indels 0;	Gaps 0

SQ Sequence 601 AA;

Query Match 22.1%; Score 61; DB 21; Length 601;
Best Local Similarity 29.2%; Pred. No. 5.4;
Matches 14; Conservative 12; Mismatches 20; Indels 2; Gaps 2;

OY 2 TLGHRKQLSKKG-NYRY-YFKRASDEPACGAFEEIMDETVLPMYE 47
DB 399 ttfetektlaegksysvkgreatfgelrvyyleavvrdegkipsfd 446

RESULT 6
B01769
ID B01769 standard; Protein; 1018 AA.
XX
AC B01769;
DT 03-JAN-2001 (first entry)
XX
DE Simian immunodeficiency virus SIVrcm Pol protein #1.
XX
KW Red capped monkey; simian immunodeficiency virus; SIV; SIVrcm;
KM vaccination; Pol protein.
XX
OS Simian immunodeficiency virus.
XX
FH Key Location/Qualifiers
FT Misc-difference 569 /note="encoded by GACTMA"
FT
XX WO200034529-A1.
XX 15-JUN-2000.
XX 03-DEC-1999; 99WO-US28638.
XX 07-DEC-1998; 98US-0206551.
XX (UABR-) UAB RES FOUND.
XX PA
PI Hahn BH, Shaw GM, Gao F, Marx PA, Smith SM, Georges-Courbot MC;
FI Lu CY;
XX WPI: 2000-423454/36.
XX DR N-PSDB; A51008.
XX DR B01775, B01776.
XX
XX New polypeptide, useful for producing antibodies and for diagnosis of
XX simian viral infection in humans comprises complete genome of new
XX simian immunodeficiency virus isolate -
XX
XX Disclosure: Page 152-156; 173pp; English.
XX
XX The present sequence is the Pol protein from the simian immunodeficiency
XX virus found in the red capped mangabey and designated SIVrcm. This virus
XX is related to the HIV viruses that cause AIDS in humans. Knowing the
XX sequence of the Pol protein and its gene is useful as it enables
XX screening of the Pol protein and its gene in humans and animals (there is a
XX possibility that this virus undergoes cross-species transmission), allows
XX vaccines to be produced and aids research into the origin of these
XX viruses. This latter is important if an AIDS vaccine is to be found.
XX
XX Sequence 1018 AA;

Query Match 20.5%; Score 56.5; DB 21; Length 1018;
Best Local Similarity 24.2%; Pred. No. 43;
Matches 15; Conservative 12; Mismatches 24; Indels 11; Gaps 1;

OY 1 LTGHRKQLSKKG-NYRY-YFKRASDEPACGAFEEIMDETVLPMYEGR 49
DB 936 latnklqgisklqifrvyregtdlvrtpakliwkgegavvigeetgdlkvvprkxak 995

OY 50 IL 51
DB 996 IL 997

RESULT 7
G13112
ID G13112 standard; Protein; 301 AA.
XX
XX G13112;
XX
AC
XX
XX 17-OCT-2000 (first entry)
DT
XX
DE Arabidopsis thaliana protein fragment SpQ ID NO: 12483.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
XX Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX 06-SEP-2000.
PD
XX
XX 25-FEB-2000; 2000EP-0301439.
PF
XX
XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
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XX 23-MAR-1999; 99US-0125788.
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XX 06-APR-1999; 99US-0128234.
XX 08-APR-1999; 99US-0128714.
XX 16-APR-1999; 99US-0129845.
XX 19-APR-1999; 99US-0130077.
XX 21-APR-1999; 99US-0130449.
XX 23-APR-1999; 99US-0130510.
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XX 05-MAY-1999; 99US-0132485.
XX 06-MAY-1999; 99US-0132486.
XX 07-MAY-1999; 99US-0132487.
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XX 08-JUN-1999; 99US-0138094.
XX 10-JUN-1999; 99US-0138540.
XX 10-JUN-1999; 99US-0138847.
XX 14-JUN-1999; 99US-0139119.
XX 16-JUN-1999; 99US-0139452.
XX 16-JUN-1999; 99US-0139453.
XX 17-JUN-1999; 99US-0139492.

ID G3111 standard; Protein; 391 AA.
XX G3111;
AC
XX 17-OCT-2000 (first entry)
DT
XX Arabidopsis thaliana protein fragment SEQ ID NO: 12482.
DE
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX Arabidopsis thaliana.
OS
XX EP1033405-A2.
PN
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126286.
PR 29-MAR-1999; 99US-0126785.
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PR 23-AUG-1999; 99US-0149902.

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PR 31-AUG-1999; 99US-0151438.
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Query Match 19.7%; Score 54.5; DB 21; Length 594;
Best Local Similarity 34.8%; Pred. No. 42;
Matches 16; Conservative 5; Mismatches 14; Indels 11; Gaps 1;

Oy 6 FKEQLSKKGNRYYPFKASDEFCAGVFEELWDETVLPMTEGRIL 51
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RESULT 13
G43721
ID G43721 standard; Protein; 615 AA.

AC G43721;

XX 18-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 54681.

XX Protein identification: signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.

OS Arabidopsis thaliana.

XX EPI033405-A2.

PN 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

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PR 01-APR-1999; 99US-0126785.

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PR 29-OCT-1999; 99US-0162142.

Query Match 19.7%; Score 54.5; DB 21; Length 615;
Best Local Similarity 34.8%; Pred. No. 44;
Matches 16; Conservative 5; Mismatches 14; Indels 11; Gaps 1;

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Db 394 fiekllkkkyevilymwdaldelaylqllke-----fegkkl 428

RESULT 14
G43720 ID G43720 standard; Protein; 699 AA.
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AC G43720;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 54680.
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KW Protein identification: signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
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Query Match 19.7%; Score 54.5; DB 21; Length 699;
 Best Local Similarity 34.8%; Pred. No. 51;
 Matches 16; Conservative 5; Mismatches 14; Indels 11; Gaps 1;

Oy 6 FKEQLSKKGNRYFFKKASDEFACGAVFEIWDDETVLPMYEGRTL 51
 Db 478 fleklkkkyevlymwdaldehyaigqlke-----fegkkl 512

RESULT 15

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 ID R20599 standard; Protein; 1036 AA.

XX R20599;

DT 19-MAY-1992 (first entry)

DE ROD HIV-2 polymerase.

XX Human Immunodeficiency virus; AIDS.

OS Human Immunodeficiency virus-2 ROD isolate.

XX US5079342-A.

XX 07-JAN-1992.

XX 11-FEB-1987; 87US-0013477.

XX 11-FEB-1987; 87US-0013477.

XX (INSP) INST PASTEUR.

XX Allison M, Montaglier L, Gautard D, Clavel F, Sonigo P, Guyader M;

XX WPI: 1992-041067/05.

XX N-PSDB: Q20616.

XX Peptide(s) corresp. to HIV-2 amino acid sequences - used in
 PT diagnosis in vaccines and in prodn. of antibodies for diagnosis

XX Disclosure: Page 13; 30pp; English.

XX The amino acid sequence is that of a polymerase from the ROD HIV-2
 CC isolate, it is encoded by nucleotides 1829-4936. See also R20596-
 CC R20596-R20608 and R22745-R22749.

XX Sequence 1036 AA;

Query Match 19.6%; Score 54; DB 13; Length 1036;
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Search completed: June 7, 2001, 02:01:19
 Job time: 5661 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 7, 2001, 02:02:11 ; Search time 40.76 Seconds
(without alignments)
24.037 Million cell updates/sec

Title: US-09-587-574-5

Perfect score: 276

Sequence: 1 LTLGHEKLEQSLKGNRYRF.....VFEEIMDEIVLPYEGRL 51

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 1921087 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	53	19.2	309	1	US-08-465-167A-24
6	53	19.2	309	2	US-08-993-118-10
7	53	19.2	309	3	US-08-845-528C-10
8	53	19.2	1332	2	US-08-971-244-2
9	53	19.2	1332	4	US-09-286-891-2
10	52.5	19.0	477	2	US-08-432-016-3
11	52.5	19.0	477	2	US-08-684-594-3
12	52	18.8	1337	4	US-08-854-585-2
13	52	18.8	1337	5	PCR-US95-05512-2
14	52	18.8	3080	6	5233423-4
15	51.5	18.7	501	1	US-07-687-466B-2
16	51.5	18.7	501	1	US-08-434-702-2
17	51.5	18.7	501	1	US-08-271-883-2
18	51.5	18.7	501	6	5168064-4
19	50.5	18.3	328	1	US-08-826-611-6
20	50	18.1	326	1	US-08-307-499-28
21	50	18.1	314	2	US-08-928-615-2
22	49.5	17.9	3174	2	US-08-477-451-3
23	48.5	17.6	166	3	US-08-765-381-4
24	48.5	17.6	1069	1	US-07-777-715-9
25	48.5	17.6	1069	1	US-08-170-126-4
26	48.5	17.6	1069	3	US-08-954-418-4
27	48	17.4	250	1	US-08-144-121-7

28	48	17.4	250	2	US-08-460-309-7	Sequence 7, Appl1
29	48	17.4	250	2	US-08-125-077-7	Sequence 7, Appl1
30	48	17.4	250	2	US-08-735-893-7	Sequence 19, Appl1
31	47.5	17.2	187	1	US-08-644-664B-19	Sequence 19, Appl1
32	47.5	17.2	187	2	US-08-761-277A-19	Sequence 3, Appl1
33	47.5	17.2	187	5	PCR-US94-00658-3	Sequence 2, Appl1
34	47.5	17.2	193	1	US-08-192-479-2	Sequence 2, Appl1
35	47.5	17.2	193	1	US-08-637-508-2	Sequence 2, Appl1
36	47.5	17.2	193	1	US-08-417-791-2	Sequence 2, Appl1
37	47.5	17.2	193	5	PCR-US96-04546-2	Sequence 2, Appl1
38	47.5	17.2	368	4	US-09-433-428D-58	Sequence 58, Appl1
39	47.5	17.2	439	4	US-09-433-428D-57	Sequence 57, Appl1
40	47.5	17.2	471	1	US-08-257-341-9	Sequence 9, Appl1
41	47.5	17.2	524	4	US-08-557-210A-3	Sequence 3, Appl1
42	47.5	17.2	539	4	US-08-557-210A-4	Sequence 4, Appl1
43	47.5	17.2	539	4	US-08-557-210A-5	Sequence 5, Appl1
44	47	17.0	518	4	US-09-113-309-19	Sequence 19, Appl1
45	47	17.0	914	1	US-08-484-105-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1

US-08-659-251-5

Sequence 5, Application US/08659251

Patent No. 5883081

GENERAL INFORMATION:

APPLICANT: Kraus, Guenter

APPLICANT: Wong-Staal, Flossie

APPLICANT: Talbot, Randy

APPLICANT: Poeschla, Eric

TITLE OF INVENTION: Isolation of No. 5883081el HIV-2 Proviruses

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESSES:

ADDRESS: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/659,251

FILING DATE: No. 5883081 yet assigned

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/001,441

FILING DATE: 26-JUL-1995

ATTORNEY/AGENT INFORMATION:

NAME: Garrett-Wackowski, Eugenia

REGISTRATION NUMBER: 57,330

REFERENCE/DOCKET NUMBER: 02307E-0564100S

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1055 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: Protein

LOCATION: 1..1055

OTHER INFORMATION: /note="pol protein encoded by HIV-2KR"

US-08-659-251-5

TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-086-662-4

Query Match 19.7%; Score 54.5; DB 2; Length 566;
Best Local Similarity 38.5%; Pred. No. 11;
Matches 15; Conservative 5; Mismatches 16; Indels 3; Gaps 1;

OY 13 KGNRYRKRKASDEFAGAVEEIMDETLPVPM---YEG 48
DB 72 KGDYKLGKSAQDSFKVKQKADVTSTVYVMQGVYEG 110

RESULT 5
US-08-465-167A-24

Sequence 24, Application US/08465167A
Patent No. 5750395

GENERAL INFORMATION:

APPLICANT: Fikes, John D.

APPLICANT: Livingston, Brian D.

APPLICANT: Sette, Alessandro D.

APPLICANT: Sidney, John C.

TITLE OF INVENTION: DNA ENCODING MAGE-1 C-TERMINAL

TITLE OF INVENTION: IMMUNOGENIC PEPTIDES (as amended)

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESS: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th floor

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/465,167A

FILING DATE: 05-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/103,623

FILING DATE: 06-AUG-1993

ATTORNEY/AGENT INFORMATION:

NAME: Parmelee, Steven W.

REGISTRATION NUMBER: 31,990

REFERENCE/DOCKET NUMBER: 14137-60-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-467-9600

TELEFAX: 415-576-0300

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 309 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-465-167A-24

Query Match 19.2%; Score 53; DB 1; Length 309;
Best Local Similarity 50.0%; Pred. No. 8.9;
Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 34 EEIMDETLPVMEGR 49
DB 212 EEIMELSVMEYDGR 227

RESULT 6
US-08-993-118-10

Sequence 10, Application US/08993118
Patent No. 5997872

GENERAL INFORMATION:

APPLICANT: LUCAS, Sophie;

APPLICANT: DE SMET, Charles;

APPLICANT: BOON-FALLEUR, Thierry

TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING FOR TUMOR

TITLE OF INVENTION: REJECTION ANTIGEN PRECURSOR MAGE-C1 AND USES

TITLE OF INVENTION: THEREOF

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felfe & Lynch

STREET: 805 Third Avenue

CITY: New York City

STATE: New York

COUNTRY: USA

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/993,118

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/845,528

FILING DATE: April 25, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mary Anne Schofield

REGISTRATION NUMBER: 36,669

REFERENCE/DOCKET NUMBER: LUD 5455

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 309

TYPE: amino acids

STRANDEDNESS: single stranded

TOPOLOGY: linear

US-08-993-118-10

Query Match 19.2%; Score 53; DB 2; Length 309;
Best Local Similarity 50.0%; Pred. No. 8.9;
Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 34 EEIMDETLPVMEGR 49
DB 212 EEIMELSVMEYDGR 227

RESULT 7
US-08-845-528C-10
Sequence 10, Application US/08845528C
Patent No. 6027924

GENERAL INFORMATION:

APPLICANT: LUCAS, Sophie;

APPLICANT: DE SMET, Charles;

APPLICANT: BOON-FALLEUR, Thierry

TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING FOR TUMOR

TITLE OF INVENTION: REJECTION ANTIGEN PRECURSOR MAGE-C1 AND USES

TITLE OF INVENTION: THEREOF

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felfe & Lynch

STREET: 805 Third Avenue

CITY: New York City

STATE: New York

COUNTRY: USA

ZIP: 10022

TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1337 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-854-585-2

Query Match 18.8%; Score 52; DB 4; Length 1337;
Best Local Similarity 36.4%; Pred. No. 74;
Matches 12; Conservative 6; Mismatches 13; Indels 2; Gaps 1;

OY 7 KEOLSKKGNRYRYFFKKASDFACGAVFEIIMDD 39
DB 1017 KSKLRVNEFAVFFKKQADSNCG--FAFEYED 1047

RESULT 13

PCT-US95-05512-2
; Sequence 2, Application PC/TUS9505512

; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas K. and Stman, Arne
; TITLE OF INVENTION: Density Enhanced Protein Tyrosine
; TITLE OF INVENTION: Phosphatase
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESS: Borun
; STREET: 233 South Wacker Drive, Suite 6300
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05512
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27866/31954
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1337 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-05512-2

Query Match 18.8%; Score 52; DB 5; Length 1337;
Best Local Similarity 36.4%; Pred. No. 74;
Matches 12; Conservative 6; Mismatches 13; Indels 2; Gaps 1;

OY 7 KEOLSKKGNRYRYFFKKASDFACGAVFEIIMDD 39
DB 1017 KSKLRVNEFAVFFKKQADSNCG--FAFEYED 1047

RESULT 14

5223423-4
; Patent No. 5223423
; APPLICANT: FRANCHINT, GENOVEFRA, WONG-STAL, FLOSSIE;
; GALLO, ROBERT

TITLE OF INVENTION: CHARACTERIZATION OF REPLICATION COMPETENT
; HUMAN IMMUNODEFICIENCY TYPE 2 PROVIRAL CLONE HIV-2 SBL/ISY
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/331,212
; FILING DATE: 03-31-1989
; SEQ ID NO:4
; LENGTH: 3080
; 5223423-4

Query Match 18.8%; Score 52; DB 6; Length 3080;
Best Local Similarity 25.5%; Pred. No. 2e+02;
Matches 13; Conservative 11; Mismatches 17; Indels 10; Gaps 1;

OY 11 SKKGNRYRYFFKKASDEF-----ACGAVFEIIMDETVLPYEGRI 51
DB 1543 SKLKNRYFFREGNQLMNGPGLMKDGAIVYVGDIVIPRKAKTI 1593

RESULT 15

US-07-687-466B-2
; Sequence 2, Application US/07687466B

; GENERAL INFORMATION:
; APPLICANT: Bennett, Alan B.
; APPLICANT: Fischer, Robert L.
; TITLE OF INVENTION: Endo-1,4-Beta-Glucanase Genes and
; TITLE OF INVENTION: Their Use in Plants
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin L. Bastian
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/687,466B
; FILING DATE: 19910418
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 2307-304-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 501 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-687-466B-2

Query Match 18.7%; Score 51.5; DB 1; Length 501;
Best Local Similarity 46.4%; Pred. No. 26;
Matches 13; Conservative 3; Mismatches 11; Indels 1; Gaps 1;

OY 7 KEOLSKKGNRYRYFFKKASDFACGAVFE 34
DB 282 KEYLNGKSNLE-KFKKADSFICGLMPE 308

Search completed: June 7, 2001, 02:02:13
Job time: 5406 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 7, 2001, 02:03:24 ; Search time 56.43 seconds
(without alignments)
62.110 Million cell updates/sec

Title: US-09-587-574-5

Perfect score: 276
Sequence: 1 LTLGHFKKQSKKGNRYRFF.....VFEEIMDETVLPMTYEGRTL 51

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.67.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	276	100.0	838	2 T08423	Axin homolog Ax1
2	190	68.8	832	2 T08422	negative regulator
3	109.5	39.7	623	2 A49840	segment polarity p
4	95.5	34.6	716	2 JCS763	dishevelled protei
5	78.5	28.4	736	2 I51691	dishevelled homolo
6	65.5	23.7	186	1 RDBOD	dihydrofolate redu
7	65	22.6	863	2 S74447	ferrichrome-iron r
8	61.5	22.3	336	2 T19802	hypothetical prote
9	58	21.0	1616	2 T16600	vitellogenin vit-1
10	57.5	20.8	666	2 T43171	cytoplasmic signal
11	57.5	20.8	672	2 T24507	hypothetical prote
12	57	20.7	357	2 E64233	membrane transport
13	57	20.7	1238	2 S68700	Hppp beta-like tyr
14	56.5	20.5	430	1 KGR7T1	T-kininogen I prec
15	56	20.3	1034	1 GNLJCA	pol polyprotein -
16	55.5	20.1	433	2 A28055	K-kininogen, LMW I
17	55.5	20.1	499	2 S18865	heat shock protein
18	55.5	20.1	639	2 A25486	kininogen, HMW I p
19	55.5	20.1	895	2 T2191	hypothetical prote
20	55	19.9	186	2 S17984	dihydrofolate redu
21	55	19.9	273	2 T48175	transcription regu
22	55	19.9	682	2 T48175	receptor like prot
23	55	19.9	1055	1 GNLJST	pol polyprotein -
24	55	19.9	1055	2 S53092	DNA-directed RNA p
25	55	19.9	1174	2 S28976	hypothetical prote
26	55	19.9	1265	2 T21782	hypothetical prote
27	55	19.9	1465	2 T23056	vitellogenin vit-2
28	55	19.9	1613	2 A43081	calcium channel al
29	55	19.9	1851	2 T13980	

30	54.5	19.7	186	1 RDHY75	dihydrofolate redu
31	54.5	19.7	566	1 HYBSU	bacillolysin (EC 3
32	54.5	19.7	699	2 S25541	heat shock protein
33	54	19.6	509	2 S77348	glucose-6-phosphat
34	54	19.6	680	2 T42923	infected cell prot
35	53.5	19.4	303	1 OQVZF1	F1 protein - vacci
36	53.5	19.4	314	2 BVS390	replication protei
37	53.5	19.4	340	1 OQVZP1	F1 protein - vacci
38	53.5	19.4	340	2 F72159	I10R protein - var
39	53.5	19.4	340	2 S33086	G9R protein - vari
40	53.5	19.4	340	2 T28510	hypothetical prote
41	53.5	19.4	447	2 T37355	37K myristylprotei
42	53.5	19.4	447	2 B75212	amidophosphoribosy
43	53.5	19.4	650	2 D71021	hypothetical prote
44	53.5	19.4	888	2 T51593	GTP-binding regula
45	53.5	19.4	901	2 T01135	hypothetical prote

ALIGNMENTS

RESULT 1
T08423
Axin homolog Ax1 - rat
N:Alternate names: Ax1
C:Species: Rattus norvegicus (Norway rat)
C>Date: 05-Nov-1999 #sequence,revision 05-Nov-1999 #text_change 21-Jul-2000
C:Accession: T08423
R:Yamamoto, H.; Kishida, S.; Uochi, T.; Ikeda, S.; Koyama, S.; Asashima, M.; Kikuchi, M.; Cell. Biol. 18, 2867-2875, 1998
A>Title: Ax1, a member of the axin family, interacts with both glycogen synthase kin
A:Reference number: Z16414; MUID:98226558
A:Accession: T08423
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-838 <YAM>
A:Cross-references: EMBL:AF017757; NID:g3080758; PIDN:AAC40089.1; PID:g3080759
A>Note: Interacts with GSK-3beta and beta-catenin
C:Keywords: phosphoprotein; signal transduction

Query Match 100.0%; Score 276; DB 2; Length 838;
Best Local Similarity 100.0%; Pred. No. 1.9e+26;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LTLGHFKKQSKKGNRYRFFKKASDEFACGAVEEIMDETVLPMTYEGRTL 51
Db 781 LTLGHFKKQSKKGNRYRFFKKASDEFACGAVEEIMDETVLPMTYEGRTL 831

RESULT 2
T08422
negative regulator axin [imported] - rat
N:Alternate names: Axin
C:Species: Rattus norvegicus (Norway rat)
C>Date: 05-Nov-1999 #sequence,revision 05-Nov-1999 #text_change 21-Jul-2000
C:Accession: T08422
R:Ikeda, S.; Yamamoto, H.; Murai, H.; Kishida, S.; Kikuchi, A.
EMBO J. 17, 1371-1384, 1998
A>Title: Axin, a negative regulator of the Wnt signaling pathway, forms a complex wit
A:Reference number: Z16413; MUID:9815161
A:Accession: T08422
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-832 <IKE>
A:Cross-references: EMBL:AF017756; NID:g2982197; PIDN:AAC40066.1; PID:g2982198
A>Note: GSK-3beta interacting protein
C:Keywords: phosphoprotein; signal transduction

Query Match 68.8%; Score 190; DB 2; Length 832;
Best Local Similarity 64.7%; Pred. No. 1e+15;
Matches 33; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Query 1 LTGHFKRQSKKGNRYRFFKASDEFACGAVFEIWDDELVLPMEGRIL 51
DB 775 VTLGQFKELLTKGSRYYRFFKVSDEFDCGAVFEVEDEAILPFEEKIL 825

RESULT 3
A:Segment polarity protein dishevelled - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-Sep-1998
C:Accession: A49840
R:Klingensmith, J.; Nusse, R.; Perrimon, N.
Genes Dev. 8, 118-130, 1994
A:Title: The Drosophila segment polarity gene dishevelled encodes a novel protein requir
A:Reference number: A49840; MUID:94116855
A:Accession: A49840
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-623 <KLID>
A:Cross-references: GB:L26974; NID:9435043; PID:9458868
C:Genetics:
A:Gene: dsh
A:Cross-references: Flybase:FBgn0000499
C:Superfamily: GLGF domain homology
F:258-333/Domain: GLGF domain homology <GLG2>

Query Match 39.7%; Score 109.5; DB 2; Length 623;
Best Local Similarity 46.2%; Pred. No. 8.1e-06;
Matches 24; Conservative 10; Mismatches 15; Indels 3; Gaps 2;

Query 1 LTGHFKRQSKKGNRYRFFKASDEFACGAVFEIWDDELVLPMEGRIL 51
DB 35 VTLRDFKLVLRKNNKRYFFKSMADP--GVVKEEIVADSTILPCFNGRVV 84

RESULT 4
JC5763
dishevelled protein 3 - human
C:Species: Homo sapiens (man)
C:Date: 24-Jan-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000
C:Accession: JC5763
R:Bull, T.D.; Beier, D.R.; Jonsson, M.; Smith, K.; Dorrington, S.M.; Kaklamatis, L.; Keat
Biochem. Biophys. Res. Commun. 239, 510-516, 1997
A:Title: cDNA cloning of a human dishevelled DVL-3 gene, mapping to 3q27, and expression
A:Reference number: JC5763; MUID:98008870
A:Accession: JC5763
A:Molecule type: mRNA
A:Residues: 1-716 <BUU>
A:Cross-references: GB:U75651; NID:91558528; PID:AA84228.1; PID:92612833
A:Note: the authors translated the codon GTG for residue 75 as Glu and GAG for residue 2
C:Comment: This protein plays a role in the early development patterning processes, and
C:Genetics:
A:Gene: DVC-3
A:Map position: 3q27
C:Superfamily: GLGF domain homology
F:253-331/Domain: GLGF domain homology <GLG4>

Query Match 34.6%; Score 95.5; DB 2; Length 716;
Best Local Similarity 41.2%; Pred. No. 0.00052;
Matches 21; Conservative 11; Mismatches 16; Indels 3; Gaps 2;

Query 1 LTGHFKRQSKKGNRYRFFKASDEFACGAVFEIWDDELVLPMEGRIL 51
DB 28 VTLRDFKVL--GRPSYKFFKSMDDP--GVVKEEISDNNALPCFNGRVV 75

RESULT 5
151691
dishevelled homolog - African clawed frog
C:Species: Xenopus laevis (African clawed frog)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: I51691
R:Sokol, S.Y.; Klingensmith, J.; Perrimon, N.; Itch, K.
Development 121, 1637-1647, 1995
A:Title: Dorsalizing and neutralizing properties of Xdsh, a maternally expressed Xenop
A:Reference number: I51691; MUID:95324391
A:Accession: I51691
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-736 <SOK>
A:Cross-references: EMBL:U31552; NID:9445109; PID:AA800688.1; PID:9445110
C:Genetics:
A:Gene: Xdsh
C:Superfamily: GLGF domain homology
F:260-336/Domain: GLGF domain homology <GLG4>

Query Match 28.4%; Score 78.5; DB 2; Length 736;
Best Local Similarity 37.3%; Pred. No. 0.071;
Matches 19; Conservative 9; Mismatches 20; Indels 3; Gaps 2;

Query 1 LTGHFKRQSKKGNRYRFFKASDEFACGAVFEIWDDELVLPMEGRIL 51
DB 28 IRLRDFKALG-RGHAKYFRKADQDF--GVVKEEISDNNALPCFNDRVV 75

RESULT 6
RDBOD
dihydrofolate reductase (EC 1.5.1.3) - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 15-Oct-1982 #sequence_revision 15-Oct-1982 #text_change 11-Nov-1996
C:Accession: A00388
R:Leal, P.H.; Pan, Y.C.E.; Gleisner, J.M.; Peterson, D.L.; Williams, K.R.; Blakley, R.
Biochemistry 21, 3284-3294, 1982
A:Title: Structure of dihydrofolate reductase: primary sequence of the bovine liver e
A:Reference number: A00388; MUID:83000246
A:Accession: A00388
A:Molecule type: protein
A:Residues: 1-186 <LAIV>
A:Experimental source: liver
C:Superfamily: type I dihydrofolate reductase; type I dihydrofolate reductase homolog
C:Keywords: NADP; oxidoreductase
F:3-125/Domain: type I dihydrofolate reductase homolog <DFR>
F:30.34.64.70/Binding site: substrate (Glu, Phe, Asn, Arg) #status predicted

Query Match 23.7%; Score 65.5; DB 1; Length 186;
Best Local Similarity 34.1%; Pred. No. 0.68;
Matches 15; Conservative 9; Mismatches 19; Indels 1; Gaps 1;

Query 6 FKEOLSKKGNRYRFFKASDEFACGAVFEIWDDELVLPMEGRIL 48
DB 121 YKEAMNKGHVRLFTYRIMQEFESDAFPPEIDFEXYKILPEYPG 164

RESULT 7
S74447
ferriochrome-iron receptor 1 - Synechocystis sp. (strain PCC 6803)
N:Alternate names: protein sll1409
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C:Accession: S74447
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,
O.K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
S.
A:Reference number: S74322; MUID:97061201
A:Accession: S74447
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-863 <KAN>

A:Cross-references: EMBL:D90899; GB:AB001339; NID:g1651650; PIDN:BA16599.1; PID:g165167
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Genetics:
A:Gene: fruA_1
A:Start codon: GTG
A:Superfamily: ferrichrome-iron receptor 1; tonB-dependent receptor amino-terminal homol
C:Keywords: iron transport
F:240-375/Domain: tonB-dependent receptor amino-terminal homology <TNN>
F:581-863/Domain: tonB-dependent receptor carboxyl-terminal homology <TNC>

Query Match 23.6%; Score 65; DB 2; Length 863;
Best Local Similarity 28.0%; Pred. No. 4.1;
Matches 14; Conservative 14; Mismatches 14; Indels 8; Gaps 2;

OY 6 FKEQLSKGNRYRYFKKASDEFACGAFEEI-----WDETVLPMEYEG 48
Db 495 FADQDCQGSYSFY-TNAVGFSTGSVKHELLAGIDYNMSEISILTFGC 543

RESULT 8
T19802
hypothetical protein C37A5.9 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C:Accession: T19802
R:White, S.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z19180
A:Accession: T19802
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-336 <MIL>
A:Cross-references: EMBL:Z92828; PIDN:CAB07332.1; GSPDB:GN00019; CESP:C37A5.9
A:Experimental source: clone C37A5
C:Genetics:
A:Gene: CESP:C37A5.9

A:Map position: 1
A:Introns: 33/3; 124/1; 265/1; 298/2; 328/3
C:Superfamily: Caenorhabditis elegans hypothetical protein C37A5.9

Query Match 22.3%; Score 61.5; DB 2; Length 336;
Best Local Similarity 29.4%; Pred. No. 4.1;
Matches 15; Conservative 12; Mismatches 23; Indels 1; Gaps 1;

OY 1 LTGFHKEQLS-KKGNRYRYFKKASDEFACGAFEEIWDDETVLPMEYEGRI 50
Db 281 MTLAEKRRHRLPNGAHQLFKTECEDGSAFPQLLIKDHHLIPVEGRH 331

RESULT 9
T16600
vitellogenin vit-1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
C:Accession: T16600
R:Bentley, D.
submitted to the EMBL Data Library, September 1995
A:Description: The sequence of C. elegans cosmid K09F5.
A:Reference number: Z18544
A:Accession: T16600
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1616 <BEN>
A:Cross-references: EMBL:U37430; NID:g1019963; PID:g1945496; PIDN:AAB52675.1; GSPDB:GN00
A:Experimental source: strain Bristol N2; clone K09F5
C:Genetics:
A:Gene: CESP:vit-1
A:Map position: X
A:Introns: 291/3; 386/3; 1448/3; 1531/1
C:Superfamily: vitellogenin

Query Match 21.0%; Score 58; DB 2; Length 1616;
Best Local Similarity 44.4%; Pred. No. 60;
Matches 16; Conservative 7; Mismatches 7; Indels 6; Gaps 2;

OY 7 KEQLSKGNRYRY--FKKASDEFACGAFEEIWDDE 40
Db 1482 EERLSEKKNRKRYDERKYESEYS----FEETDYDE 1513

RESULT 10
T43171
cytoplasmic signaling transducer - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
C:Accession: T43171
R:Guo, C.
submitted to the EMBL Data Library, May 1998
A:Description: Mig-5, a gene that controls cell fate determination and cell migration
A:Reference number: Z22326
A:Accession: T43171
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-666 <GUO>
A:Cross-references: EMBL:AF063244; PIDN:AAC16434.1
C:Genetics:
A:Gene: mig-5

Query Match 20.8%; Score 57.5; DB 2; Length 666;
Best Local Similarity 52.4%; Pred. No. 27;
Matches 11; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

OY 2 TLGFHKEQLSKGNRYRYFKK 22
Db 37 TLGNFKNSFTKRG-YKYYAKE 56

RESULT 11
T24507
hypothetical protein T05C12.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T24507
R:Burton, J.
submitted to the EMBL Data Library, October 1995
A:Reference number: Z19901
A:Accession: T24507
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-672 <MIL>
A:Cross-references: EMBL:Z66500; PIDN:CAA91307.1; GSPDB:GN00020; CESP:T05C12.6
A:Experimental source: clone T05C12
C:Genetics:
A:Gene: CESP:T05C12.6
A:Map position: 2
A:Introns: 13/3; 63/2; 114/3; 140/1; 299/2; 340/2; 449/1; 624/1

Query Match 20.8%; Score 57.5; DB 2; Length 672;
Best Local Similarity 52.4%; Pred. No. 27;
Matches 11; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

OY 2 TLGFHKEQLSKGNRYRYFKK 22
Db 37 TLGNFKNSFTKRG-YKYYAKE 56

RESULT 12
E64233
membrane transport protein (glnQ) homolog MG303 - Mycoplasma genitalium
C:Species: Mycoplasma genitalium
C:Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 07-Dec-1999

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R:Accession: E64233
R:Frazer, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.: Fuhmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
C.A.; Venter, J.C.
Science 270, 397-403, 1995
A>Title: The minimal gene complement of Mycoplasma genitalium.
A:Reference number: A64200; MUID:96026346
A:Accession: E64233
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Residues: 1-357 <TIGR>
A:Molecule type: DNA
A:Cross-references: GB:U39711; GB:L43967; NID:g1045997; PID:g1046002; TIGR:MG303
A:Experimental source: strain G-37
C:Genetics:
A:Genetic code: GCC3
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
C:Keywords: ATP; P-loop
F:90-288/Domain: ATP-binding cassette homology <ABC>
F:107-114/Region: nucleotide-binding motif A (P-loop)

Query Match          20.7%; Score 57; DB 2; Length 357;
Best Local Similarity 30.3%; Pred. No. 16;
Matches   10; Conservative 11; Mismatches    10; Indels    2; Gaps    1;

Oy      6 FKQOLSK--KGNRYFFKKASDFACGAVFEETI 36
Db      143 YQOKITKNFKOKIGYIIQKAEDPFCDILEEV 175
        :::::| | | | | : | | | | : | | : | | :
        .....

RESULT 13
S68700
HPRP beta-like tyrosine phosphatase precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C:Accession: S68700
R:Kuramochi, S.; Matsuda, S.; Matsuda, Y.; Saitoh, T.; Ohnagi, M.; Yamamoto, T.
FEBS Lett. 378, 7-14, 1996
A>Title: Molecular cloning and characterization of Byp, a murine receptor-type tyrosine
A:Reference number: S68700; MUID:96140699
A:Accession: S68700
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1238 <KUR>
A:Cross-references: GB:D45212; NID:g1208432; PIDN:BA08146.1; PID:g1208433
C:Genetics:
A:Map position: 2E1-2
C:Superfamily: protein-tyrosine-phosphatase, receptor type J; fibronectin type III repee
C:Keywords: phosphoprotein
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-1238/Product: HPRP beta-like tyrosine phosphatase #status predicted <MAT>
F:267-347/Domain: fibronectin type III repeat homology <3FR>
F:966-1188/Domain: protein-tyrosine-phosphatase homology <PTP>
F:1140/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1146/Binding site: substrate phosphate (Arg) #status predicted

Query Match          20.7%; Score 57; DB 2; Length 1238;
Best Local Similarity 33.3%; Pred. No. 60;
Matches   16; Conservative 7; Mismatches    19; Indels    6; Gaps    2;

Oy      7 KEQLSKGNRYFFKKASDFACGAVFEETIMDETV---LPMYGRI 50
Db      918 KSLIRVENFEAYFRKOADSNG--FAEEYEDLKLGISLPKYAEI 963
        I : I : I : I : I : I : I : I : I : I : I :
        ..:::..:::..:::..:::..:::..:::..:::..

RESULT 14
KGRTTI
T-kininogen I precursor - rat
N:Alternate names: 73K protein; LMW kininogen T-I
N:Contains: bradykinin; T-kinin
C:Species: Rattus norvegicus (Norway rat)
C:Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 22-Jun-1999

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C:Accession: A01286; D25486; A28526; P10193; J00027; B25488; A28525; S68036
J:Funuro-Kato, S.; Matsumoto, A.; Kitamura, N.; Nakanishi, S.
J. Biol. Chem. 260, 12054-12059, 1985
A:Title: Primary structures of the mRNAs encoding the rat precursors for bradykinin a
inhibitor.
A:Reference number: A92496; MUID:86008264
A:Accession: A01286
A:Molecule type: mRNA
A:Residues: 1-430 <EUR>
A:Cross-references: GB:M11883; NID:g205084; PIDN:AAA449.1; PID:g205085
J:Kitagawa, H.; Kitamura, N.; Hayashida, H.; Miyata, T.; Nakanishi, S.
J. Biol. Chem. 262, 2190-2198, 1987
A:Title: Differing expression patterns and evolution of the rat kininogen gene family
A:Reference number: A92625; MUID:87137443
A:Accession: D25486
A:Molecule type: DNA
A:Residues: 375-430 <KIT>
R:Enyoji, K.; Kato, H.; Hayashi, I.; Oh-Ishi, S.; Iwanaga, S.
J. Biol. Chem. 263, 973-979, 1988
A:Title: Purification and characterization of rat T-kininogens isolated from plasma o
A:Reference number: A92729; MUID:88087226
A:Accession: A28526
A:Molecule type: protein
A:Residues: 1-70-48;376-430 <ENJ>
R:Kanda, S.; Sugiyama, K.; Takahashi, M.; Shumiyu, S.; Tomino, S.; Nagase, S.
Jpn. J. Cancer Res. 81, 63-68, 1990
A:Title: Identification of a protein increasing in serum of Nagase analbuminemic rats
A:Reference number: P10193; MUID:90216390
A:Accession: P10193
A:Molecule type: mRNA
A:Residues: 330-420; 'R', 422-429, 'P' <KAN>
R:Anderson, K.P.; Croyle, M.L.; Lingrel, J.B.
Gene 81, 119-128, 1989
A:Title: Primary structure of a gene encoding rat T-kininogen.
A:Reference number: J00027; MUID:90034172
A:Accession: J00027
A:Molecule type: DNA
A:Residues: 1-60, 'E', 62-113, 'R', 115-165, 'F', 167-178, 'TKI', 182-211, 'F', 213-256, 'S', 258
A:Experimental source: strain Sprague-Dawley
R:Kageyama, R.; Kitamura, N.; Ohkubo, H.; Nakanishi, S.
J. Biol. Chem. 262, 2345-2351, 1987
A:Title: Differing utilization of homologous transcription initiation sites of rat K
A:Reference number: A25488; MUID:87137465
A:Accession: B25488
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-48 <KAS>
A:Cross-references: GB:M14356; NID:g205090; PIDN:AAA4492.1; PID:g205091
R:Enyoji, K.; Kato, H.; Hayashi, I.; Oh-Ishi, S.; Iwanaga, S.
J. Biol. Chem. 263, 965-972, 1988
A:Title: Purification and characterization of two kinds of low molecular weight kinin
A:Reference number: A28525; MUID:88087225
A:Accession: A28525
A:Molecule type: protein
A:Residues: 376-430 <EN2>
R:Stieria, F.; Walter, R.; Vautravers, P.; Guigoz, Y.
Arch. Biochem. Biophys. 322, 333-338, 1995
A:Title: Identification of several isoforms of T-kininogen expressed in the liver of
A:Reference number: S68034; MUID:96032652
A:Accession: S68036
A:Molecule type: mRNA
A:Residues: 340-430 <SID>
A:Experimental source: clone pSG17
C:Comment: At least three types of LMW kininogen precursors are present in rat plasma
ceding bradykinin.
C:Comment: T-kininogens contain T-kinin (I-S-bradykinin), a novel kinin isolated afte
d of an Arg or Lys, it is probably not released from its precursor by either tissue o
C:Comment: The T-kininogens are produced in response to an inflammatory stimulant.
C:Genetics:
A:Introns: 65/3; 102/3; 130/1; 187/3; 223/2; 252/1; 309/3; 345/3; 374/3; 398/3
C:Superfamily: kininogen; cystatin homology
C:Keywords: acute phase; bradykinin; cysteine proteinase inhibitor; duplication; glycy
F:1-18/Domains: signal sequence #status predicted <IG>

F:19-430/Product: T-kininogen I #status experimental <MAT>
 F:19-130/Domain: cystatin homology <CY1>
 F:141-252/Domain: cystatin homology <CY2>
 F:263-374/Domain: cystatin homology <CY3>
 F:378-386/Product: bradykinin #status predicted <BDY>
 F:19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimenter
 F:82,126,168,204,326/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:83-94,107-125,141-144,205-217,228-247,263-266,327-339,350-369/Disulfide bonds: #status

Query Match 20.5%; Score 56.5; DB 1; Length 430;
 Best Local Similarity 33.3%; Pred. No. 22;
 Matches 12; Conservative 8; Mismatches 11; Indels 5; Gaps 1;

QY 3 LGHFKQLSKGNRYF-----KASDEFACGAVF 33
 DB 281 LGHSIAQLNAQHNIFFKIDTVKATSQVAGVIV 316

RESULT 15

GNLJCA
 pol polyprotein - human immunodeficiency virus type 2 (isolate CAM2/Guinea-Bissau)
 N:Contains: endonuclease (EC 3.1.-.-); retropepsin (EC 3.4.23.16); RNA-directed DNA poly
 C:Species: human immunodeficiency virus type 2, HIV-2
 A:Note: host Homo sapiens (man)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 31-Jan-1997
 C:Accession: B38475; J00974
 R:Ristlem, M.; Hill, F.; Karpas, A.
 J. Gen. Virol. 72, 721-724, 1991
 A:Title: Nucleotide sequence of a Guinea-Bissau-derived human immunodeficiency virus ty
 A:Reference number: A38475; MUID:91170959
 A:Accession: B38475
 A:Molecule type: DNA
 A:Residues: 1-1034 <TRI>
 A:Note: readthrough of the terminator TGA may occur between codons ATT for 564-Ile and G
 C:Comment: The cleavage sites of this polyprotein have not been determined.
 C:Genetics:
 A:Gene: pol
 C:Superfamily: pol polyprotein
 C:Keywords: AIDS; aspartic protease; endonuclease; hydrolase; immunodeficiency; nucleoc
 F:85-183/Product: retropepsin #status predicted <RTP>
 F:109/Active site: Asp (shared with dimeric partner) #status predicted

Query Match 20.3%; Score 56; DB 1; Length 1034;
 Best Local Similarity 25.5%; Pred. No. 66;
 Matches 13; Conservative 11; Mismatches 17; Indels 10; Gaps 1;

QY 11 SKKGNRYFVKASDEF-----ACGAVEEIMDETIVLPMYEGRTL 51
 DB 959 SKLKNRYFREGRODLMKPGELMKGDGAVIVKGTIDIKIIPRRKAKIT 1009

Search completed: June 7, 2001, 02:03:25
 Job time: 5038 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 7, 2001, 02:10:32 ; Search time 39.03 seconds
(without alignments)
44.761 Million cell updates/sec

Title: US-09-587-574-5

Sequence: 1 LTCHKEQLSKKGNRYTF.....VFEEIMDEVLPVMEGRIL 51

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 3425486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	276	100.0	838	1	AXN2_RAT
2	276	100.0	840	1	AXN2_MOUSE
3	272	98.6	843	1	AXN2_HUMAN
4	246	89.1	812	1	AXN2_BRARE
5	197	71.4	841	1	AXN_CHICK
6	195	70.7	842	1	AXN_XENLA
7	191	69.2	900	1	AXN1_HUMAN
8	190	68.8	893	1	AXN1_RAT
9	190	68.8	992	1	AXN1_MOUSE
10	175	63.4	835	1	AXN1_BRARE
11	109.5	33.7	623	1	DSH_PROME
12	102	37.0	736	1	DVL2_HUMAN
13	102	37.0	736	1	DVL2_MOUSE
14	95.5	34.6	716	1	DVL3_HUMAN
15	95.5	34.6	716	1	DVL3_MOUSE
16	95	34.4	670	1	DVL1_HUMAN
17	95	34.4	670	1	DVL1_MOUSE
18	95	34.4	695	1	DVL1_MOUSE
19	95	34.4	695	1	DVL1_MOUSE
20	85	30.8	745	1	AXN1_MOUSE
21	78.5	28.4	736	1	DVL2_XENLA
22	65.5	23.7	186	1	DYR_BOVIN
23	62.5	22.6	417	1	MTE8_ECOLI
24	58	21.0	1616	1	VIRL1_CAEL
25	57	20.7	357	1	P303_MYCGE
26	57	20.5	1238	1	PRPJ_MOUSE
27	56.5	20.5	430	1	KNL1_RAT
28	56	20.3	146	1	TDM_BP186
29	56	20.3	1034	1	POL_HVZCA
30	55.5	20.1	499	1	HS82_TOBAC
31	55.5	20.1	639	1	KNG_RAT
32	55	19.9	186	1	DYR_AEDAL
33	55	19.9	273	1	BLTR_BACSU

34	55	19.9	1035	1	POL_HVZKR	074120 human immun
35	55	19.9	1055	1	POL_HVZST	P20876 human immun
36	55	19.9	1174	1	RPB2_HUMAN	P30876 human sapien
37	55	19.9	1613	1	VIR2_CAEL	P05690 caenorhabd1
38	55	19.9	1851	1	CCAA_DROME	P91645 drosophilla
39	54.5	19.7	186	1	DYR_MESAU	P04753 mesocricetu
40	54.5	19.7	566	1	NPRE_BACCE	P05806 bacillus ce
41	54.5	19.7	699	1	HS82_ORYSA	P33126 oryza sativ
42	54	19.6	509	1	G6PD_SYNY3	P73411 synecchocyst
43	53.5	19.4	303	1	VG09_VACCV	P07611 vaccinia vl
44	53.5	19.4	314	1	REP_LACHI	P35857 lactobacill
45	53.5	19.4	340	1	VG09_VACCC	P21030 vaccinia vl

ALIGNMENTS

RESULT 1	ID	AXN2_RAT	STANDARD:	PRT:	838 AA.
AC	070240;				
DT	01-OCT-2000 (Rel. 40, Created)				
DT	01-OCT-2000 (Rel. 40, Last sequence update)				
DT	01-OCT-2000 (Rel. 40, Last annotation update)				
DE	AXIN 2 (AXIS INHIBITION PROTEIN 2) (CONDUCTIN) (AXIN-LIKE PROTEIN) (AXIL).				
GN	AXIN2.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_Taxid-10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Brain;				
RX	MEDLINE=98226558; PubMed=9566905;				
RA	Yamamoto H., Kishida S., Uochi T., Ikeda S., Koyama S., Asashima M., Kikuchi A.				
RT	"Axil, a member of the Axin family, interacts with both glycogen synthase kinase 3beta and beta-catenin and inhibits axis formation of xenopus embryos."				
RT	Mol. Cell. Biol. 18:2867-2875(1998).				
CC	- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-CATENIN AND APC BY GSK-3B (BY SIMILARITY).				
CC	- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B) AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN.				
CC	TERMINAL COMPLEX.				
CC	- SUBCELLULAR LOCATION: CYTOPLASMIC.				
CC	- TISSUE SPECIFICITY: EXPRESSED IN LUNG AND THYMUS.				
CC	- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY PP2A.				
CC	- SIMILARITY: CONTAINS 1 RGS DOMAIN.				
CC	-----				
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CC	-----				
CC	EMBL: AF017757; AAC40089.1; -				
DR	HSSP: P49799; IAGR.				
DR	InterPro: IPR000342; -				
DR	InterPro: IPR001158; -				
DR	Pfam: PF00615; RGS; 1.				
DR	Pfam: PF00778; DIX; 1.				
DR	PROSITE: PS50132; RGS; 1.				
KW	Developmental protein; Phosphorylation.				
FT	DOMAIN 81 200 RGS.				
FT	DOMAIN 327 413 GSK-3B BINDING SITE (BY SIMILARITY).				

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FT DOMAIN 413 476 BETA-CATENIN BINDING SITE (BY
FT DOMAIN 469 474 SIMILARITY).
FT DOMAIN 756 838 DIX.
SQ SEQUENCE 838 AA: 92947 MW: 45B825C13BA07F37 CRC64:

Query Match 100.0%; Score 276; DB 1; Length 838;
Best Local Similarity 100.0%; Pred. No. 3.3e-27;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTLGHFKQLSKKGNRYRYFKKASDFACGAVFEIIMDETVLPMYEGRI 51
DB 781 LTLGHFKQLSKKGNRYRYFKKASDFACGAVFEIIMDETVLPMYEGRI 831

RESULT 2
AXN2_MOUSE STANDARD; PRT: 840 AA.
ID AXN2_MOUSE 090XJ6;
AC 088566;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN 2 (AXIS INHIBITION PROTEIN 2) (CONDUCTIN) (AXIN-LIKE PROTEIN)
DE (AXIL).
CN AXIN2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98221239; PubMed=9554852;
RA Behrens J., Jernchow B.A., Wuertele M., Grimm J., Asbrand C.,
RA Wiltz R., Kuehl M., Wedlich D., Birchmeier W.;
RA "Functional interaction of an axin homolog, conductin, with beta-
RA catenin, APC, and GSK3beta.";
RL Science 280:596-599(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G.,
RA Jenkins N.A., Warburton D., Costantini F.;
RA "Properties of mouse Axin2 and human AXIN2: chromosomal location,
RA expression pattern, interaction with Axin and effects on embryonic
RA axis formation.";
RL Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATENIN AND APC BY GSK-3B (BY SIMILARITY).
CC -1- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)
CC AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN
CC OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN.
CC TENNARY COMPLEX (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC PP2A (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: AF073788; AAC26047.1; -
CC EMBL: AF205889; AAF22800.1; -
CC MGP: MGI:1270862; Axin2.
CC HSSP: P49799; IAGR.
CC InterPro: IPR000342; -
CC InterPro: IPR001158; -

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DR Pfam; PF00615; RGS; 1.
DR Pfam; PF00778; DIX; 1.
DR PRINTS; P01301; RGSBP/PROTEIN.
DR PROSITE; PS50132; RGS; 1.
KW Anti-oncogene; Phosphorylation.
FT DOMAIN 81 200
FT DOMAIN 327 413 GSK-3B BINDING SITE (BY SIMILARITY).
FT DOMAIN 413 478 BETA-CATENIN BINDING SITE (BY
FT DOMAIN 469 476 SIMILARITY).
FT DOMAIN 758 840 POLY-HIS.
FT CONFLICT 101 101 DIX.
FT CONFLICT 474 474 R -> K (IN REF. 2).
FT CONFLICT 484 484 H -> Y (IN REF. 2).
FT CONFLICT 503 503 S -> P (IN REF. 2).
FT CONFLICT 603 603 F -> S (IN REF. 2).
FT CONFLICT 603 603 G -> A (IN REF. 2).
SQ SEQUENCE 840 AA: 92934 MW: A07D5EFB25DE7277 CRC64:

Query Match 100.0%; Score 276; DB 1; Length 840;
Best Local Similarity 100.0%; Pred. No. 3.3e-27;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTLGHFKQLSKKGNRYRYFKKASDFACGAVFEIIMDETVLPMYEGRI 51
DB 783 LTLGHFKQLSKKGNRYRYFKKASDFACGAVFEIIMDETVLPMYEGRI 833

RESULT 3
AXN2_HUMAN STANDARD; PRT: 843 AA.
ID AXN2_HUMAN 09Y2T1; Q9UH84;
AC 09Y2T1; Q9UH84;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN 2 (AXIS INHIBITION PROTEIN 2) (CONDUCTIN) (AXIN-LIKE PROTEIN)
DE (AXIL).
CN AXIN2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99168905; PubMed=10049590;
RA Mai M., Qian C., Yokomizo A., Smith D.I., Liu W.;
RA "Cloning of the human homolog of conductin (AXIN2), a gene mapping to
RA chromosome 17q23-q24.";
RL Genomics 55:341-344(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G.,
RA Jenkins N.A., Warburton D., Costantini F.;
RA "Properties of mouse Axin2 and human AXIN2: chromosomal location,
RA expression pattern, interaction with Axin and effects on embryonic
RA axis formation.";
RL Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATENIN AND APC BY GSK-3B (BY SIMILARITY).
CC -1- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)
CC AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN
CC OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN.
CC TENNARY COMPLEX (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN AND LYMPHOBLAST.
CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC PP2A (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -----
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DR EMBL: AF078165; AAD20976.1; -
DR EMBL: AF205888; AAF22799.1; -
DR MIM: 604023; -
DR InterPro: IPR000342; -
DR InterPro: IPR001158; -
DR Pfam: PF00615; RGS; 1.
DR Pfam: PF00778; DIX; 1.
DR PROSITE: PRO1301; RGS-PROTEIN.
DR PROSITE: PS50132; RGS; 1.
KW Developmental protein; Phosphorylation.
FT DOMAIN 81 200 RGS.
FT DOMAIN 327 413 GSK-3B BINDING SITE (BY SIMILARITY).
FT DOMAIN 413 476 BETA-CATENIN BINDING SITE (BY
SIMILARITY).
FT DOMAIN 469 474 DIX.
FT DOMAIN 761 843 POLY-HIS.
FT CONFLICT 37 62 OPGVKGQVTKPMSSVSNTRNEDGL -> HHGGQGPQHQT
DIX.
FT CONFLICT 346 346 Q -> R (IN REF. 2).
FT CONFLICT 572 636 MISSING (IN REF. 2).
FT CONFLICT 687 687 P -> S (IN REF. 2).
FT CONFLICT 696 696 Q -> H (IN REF. 2).
SQ SEQUENCE 843 AA; 93557 MW; F7B62BED6A84664D CRC64;

Query Match 98.6%; Score 272; DB 1; Length 843;
Best Local Similarity 98.0%; Pred. No. 1; Ie-26;
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LTLGHFEQLSKKGNRYFFKASDEFACGAVFEIIMDETVLPMYEGRL 51
Db 786 LTLGHFEQLSKKGNRYFFKASDEFACGAVFEIIMDETVLPMYEGRL 836

RESULT 4
AXN2_BRARE STANDARD; PRT; 812 AA.
AC P57095;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN 2 (AXIS INHIBITION PROTEIN 2).
GN AXIN2.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20171051; Pubmed=10704853;
RA Shimizu T., Yamanaoka Y., Ryu S.-L., Hashimoto H., Yabe T., Hirata T.,
Rae Y.-K., Hibi M., Hirano T.;
RT "Cooperative roles of Bozozok/Dharma and Nodal-related proteins in the
formation of the dorsal organizer in zebrafish.";
RL Mech. Dev. 91:293-303(2000).
CC -|- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CATENIN AND APC BY GSK-3B (BY SIMILARITY).
CC -|- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -|- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
PP2A (BY SIMILARITY).
CC -|- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -|- SIMILARITY: CONTAINS 1 DIX DOMAIN.
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DR EMBL: AB032263; BAA92440.1; -
DR HSSP: P49799; IAGR.
DR InterPro: IPR000342; -
DR InterPro: IPR001158; -
DR Pfam: PF00615; RGS; 1.
DR Pfam: PF00778; DIX; 1.
DR PROSITE: PS50132; RGS; 1.
KW Developmental protein; Phosphorylation.
FT DOMAIN 84 203 RGS.
FT DOMAIN 329 415 GSK-3B BINDING SITE (BY SIMILARITY).
FT DOMAIN 415 467 BETA-CATENIN BINDING SITE (BY
SIMILARITY).
FT DOMAIN 412 419 POLY-SER.
FT DOMAIN 730 812 DIX.
SQ SEQUENCE 812 AA; 91496 MW; 465DA6DE2240CC CRC64;

Query Match 89.1%; Score 246; DB 1; Length 812;
Best Local Similarity 86.3%; Pred. No. 2e-23;
Matches 44; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Oy 1 LTLGHFEQLSKKGNRYFFKASDEFACGAVFEIIMDETVLPMYEGRL 51
Db 755 LTLGHFEQLSKKGNRYFFKASDEFACGAVFEIIMDETVLPMYEGRL 805

RESULT 5
AXN_CHICK STANDARD; PRT; 841 AA.
ID OA2400;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN (AXIS INHIBITION PROTEIN).
GN AXIN OR AXN.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=97373830; Pubmed=9230313;
RA Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perry W.L. III,
Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F.;
RT "The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling
pathway that regulates embryonic axis formation.";
RL Cell 90:181-192(1997).
CC -|- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CATENIN AND APC BY GSK-3B (BY SIMILARITY).
CC -|- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -|- DEVELOPMENTAL STAGE: EXPRESSED AT STAGE 12 TO 15.
CC -|- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
PP2A (BY SIMILARITY).
CC -|- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -|- SIMILARITY: CONTAINS 1 DIX DOMAIN.
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CC -----
DR EMBL: AF009012: AAC60245.1;
DR HSP: P49799: IAGR.
DR InterPro: IPR000342;
DR InterPro: IPR001158;
DR Pfam: PF00615: RGS; 1.
DR Pfam: PF00778: DIX; 1.
DR PROSITE: PS50132: RGS; 1.
DR Developmental protein: Phosphorylation.
KM DOMAIN 88 211 RGS-3B BINDING SITE (BY SIMILARITY).
FT DOMAIN 348 433 BETA-CATENIN BINDING SITE (BY
FT DOMAIN 434 508 SIMILARITY).
FT DOMAIN
SQ SEQUENCE 841 AA; 94931 MW; 400D0C90E72506FE CRC64;

Query Match 71.4%; Score 197; DB 1; Length 841;
Best Local Similarity 66.7%; Pred. No. 3.2e-17;
Matches 34; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

Qy 1 LTLGHFKQLSKKGNRYRYFKKASDFACGAFVEEIMDEVLPYEGRIIL 51
Db 784 VTGGFKELLTKKGNRYRYFKKVSDFDGVFEEVREDMDILPYEKII 834

RESULT 6
AXN_XENLA STANDARD: PRT; 842 AA.
ID AXN_XENLA
AC 09GY0;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN (AXIS INHIBITION PROTEIN) (AXIN).
GN AXIN OR AXN.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99173782; PubMed=10072781;
RA Hedgepeth C.M., Deardorff M.A., Klein P.S.;
RT "Xenopus axin interacts with glycogen synthase kinase-3 beta and is
RT expressed in the anterior midbrain."
RL Mech. Dev. 80:147-151(1999).
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATEENIN AND APC BY GSK-3B (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- DEVELOPMENTAL STAGE: WEAKLY AND UBQUITOUSLY EXPRESSED THROUGHOUT
CC EARLY DEVELOPMENT, AND HIGHLY EXPRESSED IN THE ANTERIOR
CC MESENCEPHALON ADJACENT TO THE FOREBRAIN-MIDBRAIN BOUNDARY.
CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC PP2A (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
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CC or send an email to license@sib-sib.ch).
CC EMBL: AF097313: AAC71036.1;
CC HSP: P49799: IAGR.
CC InterPro: IPR000342;
CC InterPro: IPR001158;
CC Pfam: PF00615: RGS; 1.
CC Pfam: PF00778: DIX; 1.
CC PROSITE: PS50132: RGS; 1.
CC Developmental protein: Phosphorylation.
CC NON_TER 1

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DR PROSITE: PS50132: RGS; 1.
DR Developmental protein: Phosphorylation.
KM DOMAIN 88 211 RGS-3B BINDING SITE (BY SIMILARITY).
FT DOMAIN 348 433 BETA-CATENIN BINDING SITE (BY
FT DOMAIN 434 508 SIMILARITY).
FT DOMAIN
SQ SEQUENCE 842 AA; 94459 MW; BDAL52734C97191E CRC64;

Query Match 70.7%; Score 195; DB 1; Length 842;
Best Local Similarity 66.7%; Pred. No. 5.7e-17;
Matches 34; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

Qy 1 LTLGHFKQLSKKGNRYRYFKKASDFACGAFVEEIMDEVLPYEGRIIL 51
Db 785 VTGGFKELLTKKGNRYRYFKKVSDFDGVFEEVREDMDILPYEKII 835

RESULT 7
AXN1_HUMAN STANDARD: PRT; 900 AA.
ID AXN1_HUMAN
AC 015169;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN1 (AXIS INHIBITION PROTEIN 1) (AXIN1) (FRAGMENT).
GN AXIN1 OR AXIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97373830; PubMed=9230313;
RA Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perry W.L. III,
RA Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F.;
RT "The mouse fused locus encodes Axin, an inhibitor of the wnt signaling
RT pathway that regulates embryonic axis formation."
RL Cell 90:181-192(1997).
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATEENIN AND APC BY GSK-3B.
CC -1- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)
CC AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN
CC OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN.
CC TERNARY COMPLEX. MAY ALSO BINDS TO PLAKOGLOBIN (GAMA-CATENIN),
CC APC, DVL AND PP2A.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: UBQUITOUSLY EXPRESSED.
CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC PP2A.
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -----
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CC or send an email to license@sib-sib.ch).
CC EMBL: AF009674: AAC51624.1;
CC HSP: P49799: IAGR.
CC MIM: 603816;
CC InterPro: IPR000342;
CC InterPro: IPR001158;
CC Pfam: PF00615: RGS; 1.
CC Pfam: PF00778: DIX; 1.
CC PROSITE: PS50132: RGS; 1.
CC Developmental protein: Phosphorylation.
CC NON_TER 1

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FT DOMAIN 125 248 RGS.
FT DOMAIN 365 470 GSK-3B BINDING SITE (BY SIMILARITY).
FT DOMAIN 471 540 BETA-CATENIN BINDING SITE (BY
FT DOMAIN 818 900 SIMILARITY).
SQ SEQUENCE 900 AA: 99803 MW: EESF990B11FC7B3B CRC64;

Query Match 69.2%; Score 191; DB 1; Length 900;
Best Local Similarity 66.7%; Pred. No. 2e-16;
Matches 34; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

OY 1 LTGHEKQSLKGNRYFKKASDEFCAGVFEIWDDETVLPMYEGRII 51
Db 843 VTIGQFKELLTKGSTRYFKKVSDEDFCGVFEVREDAVLPVEEKII 893

RESULT 8
AXNI_RAT STANDARD; PRT; 893 AA.
AC 070239;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN 1 PROTEIN (AXIS INHIBITION PROTEIN 1) (RAXIN) (FRAGMENT).
GN AXIN1 OR AXIN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=98151361; PubMed=9482734;
RA Ikeda S., Kishida S., Yamamoto H., Murali H., Koyama S., Kikuchi A.;
RT *Axin, a negative regulator of the Wnt signaling pathway, forms a
RT complex with GSK-3beta and beta-catenin and promotes GSK-3beta-
RT dependent phosphorylation of beta-catenin.*;
RL EMO J. 1711371-1384(1998).
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
CC -1- SUBUNIT: INTERACTS WITH GSK-3B AND BETA-CATENIN. THE INTERACTION
CC BETWEEN AXIN AND BETA-CATENIN OCCURS VIA THE ARMA/ILLO REPEATS
CC CONTAINED IN BETA-CATENIN. TERNARY COMPLEX. ALSO BINDS TO
CC PLASOGLOBIN (GAMMA-CATENIN), APC, DVL AND PP2A (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS, THYMUS AND LUNG.
CC FOLLOWED BY CEREBRUM, CEREBELLUM, HEART, KIDNEY, SKELETAL MUSCLE,
CC SPLEEN AND LIVER.
CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC PP2A (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -----
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CC -----
CC EMBL: AF017756; AAC40066.1; ALT_INIT.
CC HSSP: P49799; IAGR.
CC InterPro: IPR000342; -.
CC InterPro: IPR001158; -.
CC Pfam: PF00615; RGS; 1.
CC Pfam: PF00778; DIX; 1.
CC PROSITE: PS50132; RGS; 1.
CC Developmental protein; Phosphorylation.
KW NON_TER 1 1
FT DOMAIN 154 277 RGS.

```

```

FT DOMAIN 414 498 GSK-3B BINDING SITE.
FT DOMAIN 499 567 BETA-CATENIN BINDING SITE.
FT DOMAIN 811 893 DIX.
SQ SEQUENCE 893 AA: 99188 MW: 3CCBD2242EDD384C CRC64;

Query Match 68.8%; Score 190; DB 1; Length 893;
Best Local Similarity 64.7%; Pred. No. 2.6e-16;
Matches 33; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

OY 1 LTGHEKQSLKGNRYFKKASDEFCAGVFEIWDDETVLPMYEGRII 51
Db 836 VTIGQFKELLTKGSTRYFKKVSDEDFCGVFEVREDAVLPVEEKII 886

RESULT 9
AXNI_MOUSE STANDARD; PRT; 992 AA.
AC 035625;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN 1 (AXIS INHIBITION PROTEIN 1) (FUSED PROTEIN) (FRAGMENT).
GN AXIN1 OR AXIN OR FU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=97373830; PubMed=9230313;
RA Zeng L., Fagotto F., Zhang T., Hsu W., Vasilek T.J., Perry W.L. III,
RA Lee J.J., Tligman S.M., Gumbiner B.M., Costantini F.;
RT The mouse fused locus encodes Axin, an inhibitor of the Wnt signaling
RT pathway that regulates embryonic axis formation.*;
RL Cell 90:181-192(1997).
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
CC -1- SUBUNIT: INTERACTS WITH GSK-3B AND BETA-CATENIN. THE INTERACTION
CC BETWEEN AXIN AND BETA-CATENIN OCCURS VIA THE ARMA/ILLO REPEATS
CC CONTAINED IN BETA-CATENIN. TERNARY COMPLEX. ALSO BINDS TO
CC PLASOGLOBIN (GAMMA-CATENIN), APC, DVL AND PP2A (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2: ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN EMBRYONIC STEM CELLS.
CC -1- DEVELOPMENTAL STAGE: WIDELY EXPRESSED AT E10.5 TO E16.5 DAY.
CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC PP2A.
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -----
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CC -----
CC EMBL: AF009011; AAC53285.1; -.
CC HSSP: P49799; IAGR.
CC MGD: MGI:1096327; Axin1.
CC InterPro: IPR000342; -.
CC InterPro: IPR001158; -.
CC Pfam: PF00615; RGS; 1.
CC Pfam: PF00778; DIX; 1.
CC PROSITE: PS50132; RGS; 1.
CC Developmental protein; Phosphorylation; Alternative splicing.
KW NON_TER 1 1
FT DOMAIN 217 340 POLY-ALA.

```

FT DOMAIN 477 561 GSK-3B BINDING SITE (BY SIMILARITY).
 FT DOMAIN 562 630 BETA-CATENIN BINDING SITE (BY
 FT DOMAIN 910 992 DIX.
 FT VARSLIC 860 895 MISSING (TN ISOFORM 2).
 SQ SEQUENCE 992 AA: 109917 MW: 70EBB53D387BD26F CRC64;

Query Match 68.8%; Score 190; DB 1; Length 992;
 Best Local Similarity 66.7%; Pred. No. 2,9e-16;
 Matches 34; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 LTIGHFEQSLSKNGNRYRFFKASDEPAACAVFEIIMDETFLPMYGRIL 51
 :||| ||| :|||:||||| ||| ||| ||| :|||: |||:
 Db 935 VTLGGFELLTKKSGYRFFKVSDEPDCCGVFEFEVREDEFLVFEKKII 985

RESULT 10
 AXN1_BRAE STANDARD; PRT; 835 AA.
 AC P57094;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DE AXIN 1 (AXIS INHIBITION PROTEIN 1).
 GN AXIN1.
 OS Brachydanio rerio (zebrafish) (zebra danio).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Rasbora; Danio.
 NC NCBI_TaxID=955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20171051; PubMed-10704853;
 RA Shimizu T., Yamana Y., Ryu S.-L., Hashimoto H., Yabe T., Hirata T.,
 RA Bae Y.-K., Hibi M., Hirano T.,
 RT "Cooperative roles of Bozozok/Dharma and Nodal-related proteins in the
 RT formation of the dorsal organizer in zebrafish.";
 RL Mech. Dev. 91:293-303(2000).
 CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
 CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
 CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- PPM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
 CC PP2A (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.

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 CC -----

DR EMBL; AB032262; BAA92439.1; -
 DR HSSP; P49799; IAGR.
 DR InterPro; IPR000342; -
 DR InterPro; IPR001158; -
 DR Pfam; PF00615; RGS; 1.
 DR Pfam; PF00778; DIX; 1.
 DR PROSITE; PS50132; RGS; 1.
 KW Developmental protein; Phosphorylation.
 FT DOMAIN 92 214 RGS:
 FT DOMAIN 351 436 GSK-3B BINDING SITE (BY SIMILARITY).
 FT DOMAIN 437 512 BETA-CATENIN BINDING SITE (BY
 FT DOMAIN SIMILARITY).
 FT DOMAIN 753 835 DIX.
 SQ SEQUENCE 835 AA: 94351 MW: 1C62FCF1F5937C87 CRC64;

Query Match 63.4%; Score 175; DB 1; Length 835;

Best Local Similarity 58.8%; Pred. No. 1,9e-14;
 Matches 30; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY 1 LTIGHFEQSLSKNGNRYRFFKASDEPAACAVFEIIMDETFLPMYGRIL 51
 :||| ||| :|||:||||| ||| ||| ||| :|||: |||:
 Db 778 VTLGGFELLTKKSGYRFFKVSDEPDCCGVFEFEVREDEFLVFEKKII 828

RESULT 11
 DSH_DROME STANDARD; PRT; 623 AA.
 ID DSH_DROME
 AC P51140;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE SEGMENT POLARITY PROTEIN DISHEVELLED.
 GN DSH.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NC NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-94116855; PubMed-8288125;
 RA Klingensmith J., Nusse R., Perrimon N.;
 RT "The Drosophila segment polarity gene dishevelled encodes a novel
 RT protein required for response to the wingless signal.";
 RL Genes Dev. 8:118-130(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-94200163; PubMed-8149913;
 RA Theisen H., Purcell J., Bennett M., Karsagana D., Syed A., Marsh J.L.;
 RT "Dishevelled is required during wingless signaling to establish both
 RT cell polarity and cell identity.";
 RL Development 120:347-360(1994).
 RN [3]
 RP PHOSPHORYLATION.
 RX MEDLINE-95262901; PubMed-7744250;
 RA Yanagawa S.-I., van Leeuwen F., Wodarz A., Klingensmith J., Nusse R.;
 RT "The dishevelled protein is modified by wingless signaling in
 RT Drosophila.";
 RL Genes Dev. 9:1087-1097(1995).

CC -1- FUNCTION: REQUIRED TO ESTABLISH COHERENT ARRAYS OF POLARIZED CELLS
 CC AND SEGMENTS IN EMBRYOS. PLAYS A ROLE IN WINGLESS (WG) SIGNALING,
 CC POSSIBLY THROUGH THE RECEPTION OF THE WG SIGNAL BY TARGET CELLS
 CC AND SUBSEQUENT REDISTRIBUTION OF ARM PROTEIN IN RESPONSE TO THAT
 CC SIGNAL IN EMBRYOS. THIS SIGNAL SEEMS TO BE REQUIRED TO ESTABLISH
 CC PLANAR CELL POLARITY AND IDENTITY.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC. ASSOCIATED WITH THE MEMBRANE
 CC WHEN HYPERPHOSPHORYLATED.
 CC -1- TISSUE SPECIFICITY: FOUND IN EGG CHAMBERS OF THE OVARY AND
 CC UTRICULUS THROUGHTOUT EMBRYOGENESIS AND IN DISCS. EXPRESSION IS
 CC NOT SEEN IN SALIVARY GLANDS, MUSCLES OR VENTRAL GANGLIA BUT IS
 CC OBSERVED IN BRAIN LOBES.
 CC -1- PPM: PHOSPHORYLATED. WG SIGNALING GENERATES HYPERPHOSPHORYLATED
 CC FORMS OF DSH WHICH ARE THE ACTIVE FORMS.
 CC -1- SIMILARITY: BELONGS TO THE DSH FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 DEP DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 PDZ/DIR DOMAIN.
 CC -----

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 CC -----

DR EMBL; L26974; AAA16535.1; -
 DR EMBL; U02491; AAA20216.1; -
 DR FlyBase; FBgn0000499; dsh.
 DR InterPro; IPR000591; -


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FT DOMAIN 7 12 POLY-GLY.
FT DOMAIN 112 122 POLY-PRO.
FT DOMAIN 235 240 POLY-ANG.
FT DOMAIN 267 339 PDZ.
FT DOMAIN 433 507 DEP.
FT DOMAIN 686 691 POLY-PRO.
SQ SEQUENCE 736 AA; 78802 MW; 9237C3DD3C92A60 CRC64;

Query Match 37.0%; Score 102; DB 1; Length 736;
Best Local Similarity 41.2%; Pred. No. 2.8e-05;
Matches 21; Conservative 8; Mismatches 20; Indels 2; Gaps 1;

OY 1 LTLGHFKQLSKRGYRYFFKASDFACGAFEEIMDEVLPMYEGRIIL 51
    :||| | | : :||| : | | | | | | | : ||| :
Db 38 ITLDPEKSVLQRPAGAKYFFKSMDDF--GYVKEEISDNRALPCFNGRV 86

RESULT 14
DVL3_HUMAN STANDARD; PRT; 716 AA.
ID DVL3_HUMAN Q92997; Q92607; O14642; Q13531;
AC Q92997; Q92607; O14642; Q13531;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE SEGMENT POLARITY PROTEIN DISHEVELLED HOMOLOG DVL-3 (DISHEVELLED-3)
DE (DSH HOMOLOG 3).
DE DVL3 OR KIAA0208.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain;
RA MEDLINE=98008870; PubMed=9344861;
RA Bui T.D., Belder D.R., Jonsson R., Sussman D.J., Harris A.L.,
RA Kallmanis L., Kearney L., Regan R., Sussman D.J., Harris A.L.,
RA "cDNA cloning of a human dishevelled DVL-3 gene, mapping to 3q27, and
RA expression in human breast and colon carcinomas.";
RT Blochem. Biophys. Res. Commun. 239:510-516(1997).
RL [2]
RN SEQUENCE FROM N.A.
RP MEDLINE=97336056; PubMed=9192851;
RA Semenov M.V., Snyder M.;
RA "Human dishevelled genes constitute a DHR-containing multigene
RA family.";
RL Genomics 42:302-310(1997).
RN [3]
RN SEQUENCE FROM N.A.
RP TISSUE-Brain;
RC MEDLINE=9641301; PubMed=8817329;
RA Pizanti A., Anati F., Calabrese G., Mari A., Colosimo A., Silani V.,
RA Gliziano L., Ratti A., Pensio D., Calza L., Palka G., Scariato G.,
RA Novelli G., Dallapiccola B.;
RA "cDNA characterisation and chromosomal mapping of two human homologues
RA of the Drosophila dishevelled polarity gene.";
RT Hum. Mol. Genet. 5:953-958(1996).
RL [4]
RN SEQUENCE FROM N.A.
RP TISSUE-Bone marrow;
RC MEDLINE=97191544; PubMed=9039502;
RA Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayashi Y.,
RA Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;
RA "Prediction of the coding sequences of unidentified human genes. VI.
RA The coding sequences of 80 new genes (KIA0201-KIA0280) deduced by
RA analysis of cDNA clones from cell line KG-1 and brain.";
RL DNA Res. 3:321-329(1996).
RN -1- FUNCTION: MAY PLAY A ROLE IN THE SIGNAL TRANSDUCTION PATHWAY
RN MEDIATED BY MULTIPLE WNT GENES.
RN -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
RN -1- SIMILARITY: BELONGS TO THE DSH FAMILY.
RN -1- SIMILARITY: CONTAINS 1 DEP DOMAIN.

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CC -1- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
CC -----
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CC -----
DR EMBL; U75651; AAB84228.1; -
DR EMBL; AF006013; AAB65244.1; -
DR EMBL; U49262; AAB47447.1; -
DR EMBL; D86963; BAA13199.1; -
DR HSSP; P31016; LBFE.
DR MIM; 601368; -
DR InterPro; IPR000591; -
DR InterPro; IPR001158; -
DR InterPro; IPR001478; -
DR Pfam; PF00610; DEP; 1.
DR Pfam; PF00778; DIX; 1.
DR Pfam; PF00595; PDZ; 1.
DR PROSITE; PS50186; DEP; 1.
DR PROSITE; PS50106; PDZ; 1.
KW Developmental protein.
FT DOMAIN 249 321
FT DVL3_HUMAN 422 496
FT CONFICT 2 2
FT CONFICT 76 76
FT CONFICT 102 102
FT CONFICT 151 151
FT CONFICT 182 182
FT CONFICT 218 218
FT CONFICT 222 222
FT CONFICT 230 230
FT CONFICT 233 233
FT CONFICT 236 236
FT CONFICT 239 239
FT CONFICT 242 242
FT CONFICT 303 303
FT CONFICT 431 431
FT CONFICT 450 450
FT CONFICT 465 465
FT CONFICT 472 472
FT CONFICT 543 543
FT CONFICT 553 554
FT CONFICT 629 629
FT CONFICT 633 633
FT CONFICT 682 716
SQ SEQUENCE 716 AA; 78054 MW; B1A55BF9507D06E CRC64;

Query Match 34.6%; Score 95.5; DB 1; Length 716;
Best Local Similarity 41.2%; Pred. No. 0.00018;
Matches 21; Conservative 11; Mismatches 10; Indels 3; Gaps 2;

OY 1 LTLGHFKQLSKRGYRYFFKASDFACGAFEEIMDEVLPMYEGRIIL 51
    :||| | | : :||| : | | | | | | | : ||| :
Db 28 VTLADPEKSVLQRPAGAKYFFKSMDDF--GYVKEEISDNRALPCFNGRV 75

RESULT 15
DVL3_MOUSE STANDARD; PRT; 716 AA.
ID DVL3_MOUSE Q61062;
AC Q61062;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE SEGMENT POLARITY PROTEIN DISHEVELLED HOMOLOG DVL-3 (DISHEVELLED-3)
DE (DSH HOMOLOG 3).
GN DVL3.
OS Mus musculus (Mouse).

```


OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE-Brain;
RX MEDLINE-97081279; PubMed-8922524;
RA Tsang M., Lijam N., Yang Y., Belter D.R., Wynshaw-Boris A.,
Susman D.J.;
RT Isolation and characterization of mouse dishevelled-3";
RL Dev. Dyn. 207:253-262(1996).
CC -1- FUNCTION: MAY PLAY A ROLE IN THE SIGNAL TRANSDUCTION PATHWAY
CC MEDIATED BY MULTIPLE WNT GENES.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: UBIQUITOUS.
CC -1- SIMILARITY: BELONGS TO THE DSH FAMILY.
CC -1- SIMILARITY: CONTAINS 1 DEP DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
CC -----
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CC -----
DR EMBL: U41285; AAB01761.1; -.
DR HSSP: P31016; 1BFE.
DR MGD: MGI:108100; Dv13.
DR InterPro: IPR000591; -.
DR InterPro: IPR001158; -.
DR InterPro: IPR001478; -.
DR Pfam: PF00610; DEP; 1.
DR Pfam: PF00778; DIX; 1.
DR Pfam: PF00595; PDZ; 1.
DR PROSITE: PS50186; DEP; 1.
DR PROSITE: PS50106; PDZ; 1.
KW Developmental protein.
KW DOMAIN 249 321 PDZ.
FT DOMAIN 422 496 DEP.
SQ SEQUENCE 716 AA; 78122 MW; 55412C03202301F0 CRC64;

Query Match 34.6%; Score 95.5; DB 1; Length 716;
Best Local Similarity 41.2%; Pred. No. 0.00018;
Matches 21; Conservative 11; Mismatches 16; Indels 3; Gaps 2;

OY 1 LVTGHEKELSKRGNYRYEKKASDEFACGAYFEETIMDETVLPMEGRRL 51
DB 28 VTLADKGYL-QRPSTKFFKSMDDF--GVVKEETISDNKLPFCNGRYV 75

Search completed: June 7, 2001, 02:10:34
Job time: 422 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 7, 2001, 02:09:43 ; Search time 81.06 Seconds
(without alignments)
73.743 Million cell updates/sec

Title: US-09-587-574-5
Perfect score: 276
Sequence: 1 LTGHRFKQSLSKGNRYRFF.....VFEEIMDETVLPMYEGRTL 51

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues
Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP unclassified:*
13: SP vertebrate:*
14: SP virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	276	100.0	838	11 070240	070240 ratius norv
2	276	100.0	840	11 088566	088566 mus musculu
3	276	100.0	840	11 090XJ6	090XJ6 mus musculu
4	272	98.6	777	4 090H84	090H84 homo sapien
5	272	98.6	843	4 09Y2T1	09Y2T1 homo sapien
6	197	71.4	841	13 042400	042400 gallus gall
7	195	70.7	842	13 09YGY0	09YGY0 xenopus lae
8	191	69.2	900	4 015169	015169 homo sapien
9	190	68.8	832	11 070239	070239 ratius norv
10	190	68.8	992	11 035625	035625 mus musculu
11	159	57.6	706	13 09P7P2	09P7P2 xenopus lae
12	109.5	39.7	623	5 09VY29	09VY29 drosophila
13	102.5	37.1	685	5 09NL46	09NL46 clona intes
14	95	34.4	695	11 090UG5	090UG5 ratius norv
15	85	30.8	743	5 09XVC1	09XVC1 drosophila
16	85	30.8	745	5 09V407	09V407 drosophila
17	66	23.6	561	10 081634	081634 elaeis olei
18	65	23.6	863	2 P72599	P72599 synechocyst
19	61.5	22.3	336	5 062090	062090 caenorhabd1

20	59	21.4	511	10 09MB73	09MB73 citrus unsh
21	57.5	20.8	666	5 061720	061720 caenorhabd1
22	57.5	20.8	672	5 022227	022227 caenorhabd1
23	57	20.7	361	11 061373	061373 mus musculu
24	57	20.7	1216	11 062884	062884 ratius norv
25	56.5	20.5	430	11 063581	063581 ratius norv
26	56	20.3	1035	14 073194	073194 human immun
27	55.5	20.1	205	14 073955	073955 human immun
28	55.5	20.1	895	5 045631	045631 caenorhabd1
29	55.5	20.1	930	10 09LG18	09LG18 arabidopsis
30	55.5	20.1	1702	10 09LEP3	09LEP3 arabidopsis
31	55	19.9	212	10 09LLY3	09LLY3 nicotiana t
32	55	19.9	381	6 09MZ21	09MZ21 sus scrofa
33	55	19.9	682	10 09M021	09M021 arabidopsis
34	55	19.9	827	10 09ZS85	09ZS85 arabidopsis
35	55	19.9	1019	5 09VDC9	09VDC9 drosophila
36	55	19.9	1059	14 076630	076630 human immun
37	55	19.9	1265	5 062231	062231 caenorhabd1
38	55	19.9	1347	4 015050	015050 homo sapien
39	55	19.9	1465	5 017909	017909 caenorhabd1
40	55	19.9	1848	5 09VTR8	09VTR8 drosophila
41	54.5	19.7	260	11 064742	064742 citreulius
42	54.5	19.7	316	5 018516	018516 aplysia cal
43	54.5	19.7	566	2 032309	032309 bacillus th
44	54.5	19.7	699	10 003986	003986 arabidopsis
45	54.5	19.7	700	10 09XGFI	09XGFI triticum ae

ALIGNMENTS

RESULT	ID	PRELIMINARY	PRT	838 AA.
070240	070240			
AC	070240			
DT	01-AUG-1998 (TREMblrel. 07, Created)			
DT	01-AUG-1998 (TREMblrel. 07, Last sequence update)			
DT	01-OCT-2000 (TREMblrel. 15, Last annotation update)			
DE	AXIL.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.			
OX	NCBI_TaxId=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98226558; PubMed=9566905;			
RA	Yamamoto H., Kishida S., Uochi T., Ikeda S., Koyama S., Asashima M.,			
RA	Kikuchi A.;			
RT	"Axil, a member of the Axin family, interacts with both glycogen			
RT	synthase kinase 3beta and beta-catenin and inhibits axis formation of			
RT	Xenopus embryos."			
RL	MOL. Cell. Biol. 18:2867-2875(1998).			
DR	EMBL; AF017757; AAC40089.1;			
DR	HSSP; P49799; IAGR.			
DR	INTERPRO: IPR000342; -			
DR	INTERPRO: IPR001158; -			
DR	PFAM: PF00615; KGS; 1.			
DR	PFAM: PF00778; DIX; 1.			
DR	PRODOM; PD001580; -; 1.			
DR	PRODOM; PD003639; -; 1.			
SO	SEQUENCE 838 AA; 92947 MW; 45B825C13BA07F37 CRC64;			

Query Match 100.0%; Score 276; DB 11; Length 838;
Best Local Similarity 100.0%; Pred. No. 4.7e-26;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTGHRFKQSLSKGNRYRFFPKASDEPACGVFEEIMDETVLPMYEGRTL 51
DB 781 LTGHRFKQSLSKGNRYRFFPKASDEPACGVFEEIMDETVLPMYEGRTL 831

RESULT 2

DR PFAM: PF00778; DIX: 1.
SQ SEQUENCE 843 AA; 93557 MW; F7B62BED6AB4664D CRC64;

Query Match 98.6%; Score 272; DB 4; Length 843;
Best Local Similarity 98.0%; Pred. No. 1.5e-25;
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTLGHFEQLSKGNRYFFKASDEFACGAVEEIMDETVLPMYEGRTL 51
DB 786 VTLGQFRELTLTKKGNRYFFKASDEFACGAVEEIMDETVLPMYEGRTL 836

RESULT 6
ID 042400 PRELIMINARY; PRT; 841 AA.

AC 042400;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE AXIN.
GN AXIN.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97373830; PubMed=9230313;
RA Zeng L., Fagotto F., Zhang T., Hsu W., Vasilek T.J., Perry W.L.,
RA Ili Lee J.J., Tilghman S.M., Gumbiner B.M., Constantini F.;
RT "The mouse fused locus encodes Axin, an inhibitor of the Wnt signaling
pathway that regulates embryonic axis formation.";
RL Cell 90:181-192(1997).
DR EMBL: AF009012; AAC60245.1; -.
DR HSSP: P49799; IAGR.
DR INTERPRO: IPR000342; -.
DR INTERPRO: IPR001158; -.
DR PFAM: PF00615; RGS; 1.
DR PFAM: PF00778; DIX; 1.
DR PRODOM: PD001580; -; 1.
DR PRODOM: PD003639; -; 1.
SQ SEQUENCE 841 AA; 94931 MW; 400D0C90E72506FE CRC64;

Query Match 71.4%; Score 197; DB 13; Length 841;
Best Local Similarity 66.7%; Pred. No. 3.1e-16;
Matches 34; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

OY 1 LTLGHFEQLSKGNRYFFKASDEFACGAVEEIMDETVLPMYEGRTL 51
DB 784 VTLGQFRELTLTKKGNRYFFKASDEFACGAVEEIMDETVLPMYEGRTL 834

RESULT 7
ID 09YGYO PRELIMINARY; PRT; 842 AA.

AC 09YGYO;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE AXIN.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OC NCBI_TaxID=6355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99173782; PubMed=10072781;
RA Hedepeeth C.M., Deardorff M.A., Klein P.S.;
RT "Xenopus axin interacts with glycogen synthase kinase-3 beta and is

RT expressed in the anterior midbrain.";
RL Mech. Dev. 80:147-151(1999).
DR EMBL: AF097313; AAC71036.1; -.

DR HSSP: P49799; IAGR.
DR INTERPRO: IPR000342; -.
DR INTERPRO: IPR001158; -.
DR PFAM: PF00615; RGS; 1.
DR PFAM: PF00778; DIX; 1.
DR PRODOM: PD001580; -; 1.
DR PRODOM: PD003639; -; 1.
SQ SEQUENCE 842 AA; 94459 MW; BDA152734C97191E CRC64;

Query Match 70.7%; Score 195; DB 13; Length 842;
Best Local Similarity 66.7%; Pred. No. 5.6e-16;
Matches 34; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

OY 1 LTLGHFEQLSKGNRYFFKASDEFACGAVEEIMDETVLPMYEGRTL 51
DB 785 VTLGQFRELTLTKKGNRYFFKASDEFACGAVEEIMDETVLPMYEGRTL 835

RESULT 8
ID 015169 PRELIMINARY; PRT; 900 AA.

AC 015169;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE AXIN (FRAGMENT).
GN AXIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97373830; PubMed=9230313;
RA Zeng L., Fagotto F., Zhang T., Hsu W., Vasilek T.J., Perry W.L.,
RA Ili Lee J.J., Tilghman S.M., Gumbiner B.M., Constantini F.;
RT "The mouse fused locus encodes Axin, an inhibitor of the Wnt signaling
pathway that regulates embryonic axis formation.";
RL Cell 90:181-192(1997).
DR EMBL: AF009674; AAC51624.1; -.
DR HSSP: P49799; IAGR.
DR INTERPRO: IPR000342; -.
DR INTERPRO: IPR001158; -.
DR PFAM: PF00615; RGS; 1.
DR PFAM: PF00778; DIX; 1.
DR PRINTS: PR01301; RGSPPROTEIN.
DR NON_TER
SQ SEQUENCE 900 AA; 99803 MW; EE5F90B11FC7B3B CRC64;

Query Match 69.2%; Score 191; DB 4; Length 900;
Best Local Similarity 66.7%; Pred. No. 1.9e-15;
Matches 34; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

OY 1 LTLGHFEQLSKGNRYFFKASDEFACGAVEEIMDETVLPMYEGRTL 51
DB 843 VTLGQFRELTLTKKGNRYFFKASDEFACGAVEEIMDETVLPMYEGRTL 893

RESULT 9
ID 070239 PRELIMINARY; PRT; 832 AA.

AC 070239;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE AXIN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98151361; PubMed=9482734;
RA Ikeda S., Yamamoto H., Murai H., Kishida S., Kikuchi A.;
RT Axin, a negative regulator of the Wnt signaling pathway, forms a
RT complex with GSK-3beta and beta-catenin and promotes GSK-3beta-
RT dependent phosphorylation of beta-catenin."
RL EMBL J. 17:1371-1384(1998).
DR EMBL; AF017756; AAC40066.1; -.
DR HSP; P49799; IAGR.
DR INTERPRO: IPR000342; -.
DR INTERPRO: IPR001158; -.
DR PFAM: PF00615; RGS; 1.
DR PFAM: PF00778; DIX; 1.
DR PRODOM: PD001580; -; 1.
DR PRODOM: PD003639; -; 1.
SQ SEQUENCE 832 AA; 92856 MW; B489504C7E594347 CRC64;

Query Match 68.8%; Score 190; DB 11; Length 832;
Best Local Similarity 64.7%; Pred. No. 2.3e-15;
Matches 33; Conservative 10; Mismatches 8; Indels 0; Gaps 0;
OY 1 LTLGFKKQSLKSKGNRYFFKASDEFACGAVFEETIMDETVLPMEGRIL 51
Db 775 VTLGQFKELTKKSGYRYFFKASDEFACGAVFEETIMDETVLPMEGRIL 825

RESULT 10
035625 PRELIMINARY; PRT; 992 AA.
AC 035625;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE AXIN (FRAGMENT).
GN AXIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97373830; PubMed=9230313;
RA Zeng L., Fagotto F., Zhang T., Hsu W., Vasilek T.J., Perry W.L.,
RA Ili Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F.;
RT "The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling
RT pathway that regulates embryonic axis formation."
RL Cell 90:181-192(1997).
DR EMBL; AF009011; AAC53285.1; -.
DR HSP; P49799; IAGR.
DR MGD; MGI:1096327; Axin.
DR INTERPRO: IPR000342; -.
DR INTERPRO: IPR001158; -.
DR PFAM: PF00615; RGS; 1.
DR PFAM: PF00778; DIX; 1.
DR PRINTS: PR01301; RGSPTROTEIN.
FT NON_TER 1
SQ SEQUENCE 992 AA; 109917 MW; 70EEB53D387BD26F CRC64;

Query Match 68.8%; Score 190; DB 11; Length 992;
Best Local Similarity 66.7%; Pred. No. 2.8e-15;
Matches 34; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

OY 1 LTLGFKKQSLKSKGNRYFFKASDEFACGAVFEETIMDETVLPMEGRIL 51
Db 935 VTLGQFKELTKKSGYRYFFKASDEFACGAVFEETIMDETVLPMEGRIL 985

RESULT 11

Q9PFP2
ID Q9PFP2 PRELIMINARY; PRT; 706 AA.
AC Q9PFP2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE AXIN-RELATED PROTEIN.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=83355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-OVARY;
RA Itoh K., Antipova A., Ratcliffe M., Sokol S.;
RT "Dishevelled transduces a signal by displacing GSK3 from axin-GSK3
RT complex."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF140243; AAF22574.1; -.
DR INTERPRO: IPR000342; -.
DR INTERPRO: IPR001158; -.
DR PFAM: PF00778; DIX; 1.
DR PRINTS: PR01301; RGSPTROTEIN.
SQ SEQUENCE 706 AA; 79196 MW; C3D0AF0D9540F162 CRC64;

Query Match 57.6%; Score 159; DB 13; Length 706;
Best Local Similarity 56.9%; Pred. No. 1.4e-11;
Matches 29; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

OY 1 LTLGFKKQSLKSKGNRYFFKASDEFACGAVFEETIMDETVLPMEGRIL 51
Db 649 LTLGFKKQSLKSKGNRYFFKASDEFACGAVFEETIMDETVLPMEGRIL 699

RESULT 12
09VYZ9 PRELIMINARY; PRT; 623 AA.
ID 09VYZ9
AC 09VYZ9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE DSH PROTEIN.
GN DSH.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Arroll J.F., Agdayani A., An H.-J., Andrews-Plankoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borikova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fostler C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostlin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,

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OM nucleic - nucleic search, using sw model

Run on: June 6, 2001, 18:46:26 ; Search time 4956.99 Seconds
(without alignments)
8404.839 Million cell updates/sec

Title: US-09-587-574-6

Perfect score: 2825
Sequence: 1 cagccgtcgcgatgatatt.....accctgtctcagcctaagc 2825

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1283235 segs, 7373929652 residues

Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba1: *
2: gb_ba3: *
3: gb_ba3: *
4: gb_in1: *
5: gb_in2: *
6: gb_in3: *
7: gb_om: *
8: gb_ov: *
9: gb_pat1: *
10: gb_pat2: *
11: gb_ph: *
12: gb_pi1: *
13: gb_pi2: *
14: gb_pi3: *
15: gb_pi4: *
16: em_ba1: *
17: em_ba2: *
18: em_fun: *
19: em_htgo_hum: *
20: em_htgo_inv: *
21: em_htgo_rnd: *
22: em_htg_hum1: *
23: em_htg_hum2: *
24: em_htg_hum3: *
25: em_htg_hum4: *
26: em_htg_hum5: *
27: em_htg_hum6: *
28: em_htg_hum7: *
29: em_htg_hum8: *
30: em_htg_inv1: *
31: em_htg_inv2: *
32: em_htg_other: *
33: em_htg_rnd: *
34: em_hum1: *
35: em_hum2: *
36: em_hum3: *
37: em_hum4: *
38: em_hum5: *
39: em_hum6: *
40: em_hum7: *
41: em_in: *
42: em_om: *
43: em_or: *

44: em_ov: *
45: em_pat: *
46: em_pi: *
47: em_pi1: *
48: em_ro: *
49: em_sts: *
50: em_sy: *
51: em_un: *
52: em_v1: *
53: gb_sts1: *
54: gb_sts2: *
55: gb_sts3: *
56: gb_sy: *
57: gb_un: *
58: gb_v11: *
59: gb_v12: *
60: gb_htg1: *
61: gb_htg2: *
62: gb_htg3: *
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64: gb_htg5: *
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68: gb_htg9: *
69: gb_htg10: *
70: gb_htg11: *
71: gb_htg12: *
72: gb_htg13: *
73: gb_htg14: *
74: gb_htg15: *
75: gb_htg16: *
76: gb_htg17: *
77: gb_htg18: *
78: gb_htg19: *
79: gb_htg20: *
80: gb_htg21: *
81: gb_htg22: *
82: gb_htg23: *
83: gb_htg24: *
84: gb_htg25: *
85: gb_pi1: *
86: gb_pi2: *
87: gb_pi3: *
88: gb_pi4: *
89: gb_pi5: *
90: gb_pi6: *
91: gb_pi7: *
92: gb_pi8: *
93: gb_pi9: *
94: gb_pi10: *
95: gb_pi11: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2825	100.0	2825	9 A98521	A98521 Sequence 6
2	2825	100.0	2825	9 AF073788	AF073788 Mus muscu
3	2645.2	93.6	3016	94 AF205889	AF205889 Mus muscu
4	2389.2	84.6	3216	94 AF017757	AF017757 Rattus no
5	1944.4	68.8	3072	88 AF078165	AF078165 Homo sapi
6	1571.2	55.6	2538	88 AF205888	AF205888 Homo sapi
7	1359.2	48.1	2104	89 AK025718	AK025718 Homo sapi
8	955	33.8	191041	69 AC024114	AC024114 Mus muscu
9	850.2	30.1	3485	8 AB032263	AB032263 Danio rer
10	698.2	24.7	184263	85 AC004805	AC004805 Homo sapi
11	490.6	17.4	191041	69 AC024114	AC024114 Mus muscu

12	401.8	14.2	3411	88	AF009674	Homo sapi
13	378.6	13.4	1863	88	AB052751	Homo sapi
14	369	13.1	369	9	A98522	Sequence 7
15	337.6	12.0	3761	94	AF009011	Mus muscu
16	316	11.2	3156	8	AF009012	Gallus ga
17	312.2	11.1	3460	94	AF017756	Rattus no
18	265	9.4	2529	8	AF097313	Xenopus l
19	256.6	9.1	3066	8	AB033262	Danio rer
20	209.4	7.4	23786	91	HS415C1	
21	209.4	7.4	35054	91	HS335B10	
22	209.4	7.4	39170	85	AC005202	Homo sapi
23	209.4	7.4	133069	70	AC026836	Homo sapi
24	209.4	7.4	187272	74	AC069076	Homo sapi
25	207	7.3	207	9	A98524	Sequence 9
26	165.8	5.9	2121	8	AF140243	Xenopus 1
27	162	5.7	162	9	A98523	Sequence 8
28	153	5.4	153	9	A98525	Sequence 10
29	79.2	2.8	31557	91	HS13434	
30	79.2	2.8	133069	70	AC026836	Homo sapi
31	79.2	2.8	187272	74	AC069076	Homo sapi
32	65.2	2.2	910	7	AF011361	Bos tauru
33	63.2	2.2	22029	91	HS419C1	
34	63.2	2.2	36418	85	AC004652	Homo sapi
35	63.2	2.2	278229	76	AC074332	Homo sapi
36	59.4	2.1	278229	76	AC074332	Homo sapi
37	59.2	2.1	2638	93	HS077655	
38	58.8	2.1	2132	93	HS094829	
39	58.8	2.1	2383	10	165400	
40	58.8	2.1	2383	93	HS070426	
41	58.8	2.1	2406	9	AR035805	Sequence
42	58.8	2.1	2406	9	AR035832	Sequence
43	57.2	2.0	606	9	AR035823	Sequence
44	57.2	2.0	606	9	AR035850	Sequence
45	56.4	2.0	1505	94	AF215669	Mus muscu

ALIGNMENTS

Dp	61	AGCGTTTGCTGTAAAAAGAGGAGGCTCACATCAGGCCCTCGTGAATTAAAGAGACCA	120
Oy	121	agccgatgtcgtgagaggaacttgaagaagaaagagagagagagaaagacaaac	180
Dp	121	AGCCGATTGCTGAGAGGCAACTGGAAGAAAGAAAAAGGAGGAGGCAAAAAAGCAAAAC	180
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 REFERENCE 1 (bases 1 to 2825)
 AUTHORS Behrens,J., Jerchow,B.-A., Wurtzle,M., Grimm,J., Asbrand,C.,
 Wirtz,R., Kuhl,M., Wedlich,D. and Birchmeier,W.
 TITLE Functional interaction of an axin homolog, conductin, with
 beta-catenin, APC, and GSK3beta
 JOURNAL Science 280 (5363), 596-599 (1998)
 MEDLINE 98221239
 REFERENCE 2 (bases 1 to 2825)
 AUTHORS Behrens,J., Jerchow,B.-A. and Birchmeier,W.
 TITLE Direct Submission
 JOURNAL Submitted (22-JUN-1998) Cellular Biology, Max Delbrueck Center for
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AUTHORS	Zhang, T., Fagotto, F., Hsu, W., Zeng, L., Gilbert, D., Copeland, N.G., Jenkins, N.A., Warburton, D. and Costantini, F.				
TITLE	Properties of mouse Axin2 and human AXIN2: chromosomal location, expression pattern, interaction with Axin and effects on embryonic axis formation				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 3016)				
AUTHORS	Zhang, T. and Costantini, F.				
TITLE	Direct Submision				
JOURNAL	Submitted (16-NOV-1999) Genetics & Development, Columbia University, 701 M168th St. HHSC 1416, New York, NY 10032, USA				
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BASE COUNT	766 a 858 c 837 g 555 t				
ORIGIN					
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Qy	288	cggttccgggaagaagaggagagccacacggtgtcagcctagtggtggcaaggtccagt	347		
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Qy	348	ccacacacatagcccggttcccttaatgtcagcgggaatgaagaatgcagctggggagc	407		
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Db	1328	ttccTACCTCCGGAGGATGATGAAGAGGACCCAAACCAATTGTGGACGACCACTTCGA	1387
QY	1548	gggttcctaagaaccccgcgctgtcaatcccttggttggtgtcgtacagcccaagctcc	1607
Db	1388	gggttcTCAAAACCCCGGCGCTGTCAATCCCTGTGTGGGTGCTTACACCCCAAGGTCC	1447
QY	1608	gtcccccagaccacacacacacagcaccaccacacatagcagtgctacacctcttcga	1667
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Oy	2668	tcccatctgacgaagcagagatcctctgagcaaaagtgcagagatcgcactgaagccttgcct	2747	
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LOCUS	AF017757	3216 bp	mRNA	ROD
DEFINITION	Rattus norvegicus GSK-3beta interacting protein, Ax11 mRNA, complete cds.			24-Apr-1998
ACCESSION	AF017757			
VERSION	AF017757.1	GI:3080758		
KEYWORDS				
SOURCE	Norway rat.			
ORGANISM	Rattus norvegicus			
REFERENCE	1 (bases 1 to 3216)			
AUTHORS	Yamamoto, H., Kishida, S., Uochi, T., Ikeda, S., Koyama, S., Asashima, M.			
TITLE	Ax11, a member of the Axin family, interacts with both glycogen synthase kinase 3beta and beta-catenin and inhibits axis formation of Xenopus embryos			
JOURNAL	Mol. Cell. Biol. 18 (5), 2867-2875 (1998)			
MEDLINE	98226558			
REFERENCE	2 (bases 1 to 3216)			
AUTHORS	Yamamoto, H., Ikeda, S., Murai, H., Kishida, S. and Kikuchi, A.			
TITLE	Direct Submission			
JOURNAL	Submitted (08-AUG-1997) Biochemistry, Hiroshima University, School of Medicine, 1-2-3 Kasumi, Minami-Ku, Hiroshima, Hiroshima 734, Japan			
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	ORIGIN
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Best Local Similarity	93.7%; Pred. No. 0;
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OY	251 ccacagcagaagattccggagagatgcctccggccccggcttccggagaaagaaaggagag 310
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OY	311 acccccacgcgtgcaagcctaigtgtgggcaaagttccagttccacaacaaactaagccgtttcc 370
DB	181 ACCCCACCGCTGTCAAGCTTAGCGTGCGGCAAGTGCAGTCCACCAAACCTATGCGCTGTCC 240
OY	371 tctaatgtatagacggaatgaagaatggacttgggggagcccgagggcgccctcccccgat 430
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VERSION AF078165.1 GI:4454790
KEYWORDS
SOURCE
ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 3072)
Majumder, M., Qian, C., Yokomizo, A., Smith, D.I. and Liu, W.
Cloning of the human homolog of conductin (Axin2), a gene mapping
to chromosome 17q23-q24
JOURNAL Genomics 55 (3), 341-344 (1999)
MEDLINE 99168905
REFERENCE 2 (bases 1 to 3072)
AUTHORS Majumder, M., Qian, C., Smith, D.I. and Liu, W.
TITLE Direct Submission
JOURNAL Submitted (15-JUL-1998) Lab Medicine and Pathology, Mayo Clinic,
200 First Street SW, Rochester, MN 55905, USA
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DB 277 GGGAGCCGGAAGGGGCGGATCTCCGGATTCCTCTGACCCGGTGACCAACTCTTAC 336
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 2538)
 Zhan, T., Fagotto, F., Hsu, W., Zeng, L., Gilbert, D., Copeland, N.G.,
 Jenkins, N.A., Warburton, D. and Costantini, F.,
 TITLE Properties of mouse Axin2 and human AXIN2: chromosomal location,
 expression pattern, interaction with Axin and effects on embryonic

axis formation
 Unpublished
 2 (bases 1 to 2538)
 Zhan, T. and Costantini, F.
 Direct Submission
 Submitted (16-NOV-1999) Genetics & Development, Columbia
 University, 701 W168th St. HHSC 1416, New York, NY 10032, USA
 Location/Qualifiers
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AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
	1 (sites)		
TITLE	Kawabata,A., Hikiji,T., Kobtake,N., Inagaki,H., Ikema,Y.,		
JOURNAL	Okamoto,S., Oktani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,		
REFERENCE	Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.		
AUTHORS	Unpublished (2000)		
	2 (bases 1 to 2104)		
TITLE	Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,		
JOURNAL	Shibahara,T., Tanaka,T. and Nakamura,Y.		
	Direct Submission		
	Submitted (29-AUG-2000) to the DDBJ/EMBL/GenBank databases. Sumio		
	Sugano, Institute of Medical Science, University of Tokyo,		
	Laboratory of Genome Structure Analysis, Human Genome Center;		
	Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan		
	(E-mail:cdna@ems.u-tokyo.ac.jp, Tel:81-3-5449-5286,		
	Fax:81-3-5449-5416)		
COMMENT	NEDO human cDNA sequencing project supported by Ministry of		
	International Trade and Industry of Japan; cDNA full insert		
	sequencing: Research Association for Biotechnology; cDNA library		
	construction, 5'-6' and one pass sequencing; Depart of		
	Virology and Human Genome Center, Institute of Medical Science,		
	University of Tokyo (partly supported by Science and Technology		
	Agency).		
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0y	964	gtccagcaaaactcttggggccaacgcgagtgtagatccacggaaacagctggaacag	1023
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0y	1024	attcaagtccttaagagaagcgaccacagtcacatcctatacagctaggtccgactatg	1083

D	b	121	ATACAGGCTCTTAAGAGGAGGAGCAGCATCTCTTATCTCTTATACATAGTTCTGGCTATGT	180
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O	y	1144	ttccatctccatctgcagcaagtagcgtagatctgaagtcctctcttaaccgatctggagataa	1203
D	b	241	TTCCATGTGCTATGACGGACAGCAGTGTAGATGGAATTCCTCTTATCTGTGTGGGACGTA	300
O	y	1204	gaaaacgctccagagagagatgcatcgcaagtgtgaagcccaatgyccaagtgctctctac	1263
D	b	301	GAACACAGCTCCAGAGAGAAATATGCATGTGCATGTGAAGGGCAATGGCCAAAGTCTCTAC	360
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D	b	361	TCATTTTCCCGAAGAACCCACGCCCTGTGCCCAAGAGATATGCCCCGTGTGAACCCGCCACTT	420
O	y	1324	cgcgcgcgagctcatctctccagcgtctggagaaactgaaactgtgagcttggaaagccgcatag	1383
D	b	421	TGCAGCTGAGCTGTATCTCGAGGCTGGAAAAAGCTGGAAGCTGTGAGTTGGAAGCCGCCACAG	480
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O	y	1792	ggagagagatcggagcgagaaagccacacagagagtgccgtctcttctctgggggaaacga	1851
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O	y	1852	ttattattgtacttccaaatgycaaaaagccacccgaaggtctcagagccctctcgtggga	1911
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AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 191041)		
	Metzker, M.L., Lewis, L.R.,		
	Deederich, D., Thomas, S., Okunou, G., Carlack, C., Garner, T.,		
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	Bunyah, C., Bunac, C., Burkett, C., Chacko, J., Chen, G., Chen, Z.,		
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	Fernandez, C., Ferraguto, D., Forcum-Tansey, J., Gill, R.,		
	Gorell, J.T.H., Gunaratne, P., Haller, G., Hernandez, J., Hogue, M.,		
	Hosak, H., Hou, X., Huber, J., Jackson, L., Jia, Y., Kelly, J., Kelly, S.,		
	Kovari, C., Liu, J., Liu, W., Louisied, H., Lozano, R.J., Martin, R.,		
	Massey, E., McLeod, M.P., Mel, G., Moore, S., Morgan, M., Morris, S.,		
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	Perez, L., Reller, D., Say, J., Shen, H., Vasquez, J., Watlington, S.,		
	Williams, A., Wrenford, G., Zhou, X., Bouck, J., Hodgson, A.,		
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	Worley, K. and Gibbs, R.		
TITLE	Direct Submission		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 191041)		

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ACCESSION AF009011
VERSION AF009011.1 GI:2252815
KEYWORDS
SOURCE house mouse.
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Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS 1 (bases 1 to 3761)
Zeng, L., Fagotto, F., Zhang, T., Han, W., Vasicek, T.J., Perry, W.L.
3rd, Lee, J.J., Tilghman, S.M., Gumbiner, B.M. and Costantini, F.
The mouse fused locus encodes Axin, an inhibitor of the Wnt
signaling pathway that regulates embryonic axis formation
Cell 90 (1), 181-192 (1997)
JOURNAL 2 (bases 1 to 3761)
MEDLINE 97373830
TITLE Zeng, L., Zhang, T., Perry, W.L. III, Lee, J.J. and Costantini, F.
AUTHORS Direct Submission
TITLE Submitted (13-JUN-1997) Genetics and Development, Columbia
JOURNAL University, 701 W. 168th Street, New York, NY 10032, USA
location/Qualifiers
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BASE COUNT 890 a 1012 c 1088 g 771 t
ORIGIN

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Qy 2730	tcgaatgagcttgctctctc	2751
Db 2974	TGGACTGAGCACTGGGCACAC	2995

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 6, 2001, 22:08:02 ; Search time 276.75 Seconds
(without alignments)
5959.105 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 678276 seqs, 291890651 residues
Total number of hits satisfying chosen parameters: 1356552

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2825	100.0	2825	20	X23369 Human conductin DN
2	2523	89.3	2523	20	X23370 Human conductin CD
3	401.8	14.2	3411	20	X09012 Human axin gene.
4	337.6	12.0	3761	20	X09013 Murine axin gene.
5	322.2	11.4	1205	21	A77843 cDNA encoding huma
6	317.8	11.2	401	21	A77754 cDNA encoding huma
7	58.8	2.1	2383	17	T11418 p53 response prote
8	58.8	2.1	2406	18	T43376 Human cytokine res
9	58.8	2.0	606	21	A39650 Human CRI cDNA. H
10	57.2	2.0	606	21	A39678 Cytokine response
11	57.2	2.0	746	19	V34780 Human RATH.1 DNA.

12	50.8	1.8	2272	19	V34779 Mouse RATH.1 DNA.
13	49.2	1.7	7720	21	A53800 Genomic DNA encodi
14	48.2	1.7	1505	15	O55750 Genomic clone G11F
15	42.6	1.5	2006	22	A89195 Wheat phytochelati
16	42.2	1.5	10732	21	A10594 Gene encoding a su
17	40.6	1.4	18660	21	A58472 Nucleotide sequenc
18	40.6	1.4	2172	19	V02996 Mammalian Ena (Men
19	39.8	1.4	1848	18	T97129 Human netrin-1 cDN
20	39.6	1.4	2356	21	A87736 Human secreted pro
21	39.4	1.4	1000	21	A02484 Human colon cancer
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23	39	1.4	1691	21	Z36910 cDNA encoding a re
24	39	1.4	1721	17	T39752 Macaque mucosal ad
25	39	1.4	1923	20	X51745 DNA encoding a hum
26	38.6	1.4	1337	20	Z1263 Human gene expres
27	38.4	1.4	4839	18	T85642 Ras-binding protei
28	38.2	1.4	5059	20	X84332 Stealth virus nucl
29	38	1.3	756	12	O15508 Modified Flt-3-specif
30	38	1.3	1164	21	A52090 Murine RGS protein
31	37.8	1.3	379	21	A31144 Plant microsatellit
32	37.4	1.3	1933	21	F14882 Trichoderma reesei
33	37.4	1.3	2898	19	V02998 Mouse neural Wena+
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44	36.6	1.3	5452	20	X90923 Anti-sense strand
45	36.6	1.3	8705	20	Z23778 Vector pShuttle DN

ALIGNMENTS

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AC X23369;	
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KW Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour;	
KW therapy; cytoplasmic degradation; blockade; Wnt signalling pathway;	
KW Wntless signalling pathway; Adenomatous Polyposis Coll; APC;	
KW tumour suppressor; ss.	
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OS Homo sapiens.	
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FT	/tag- b
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XX MO9911760-A2.
XX 11-MAR-1999.
XX 01-SEP-1998; 98MO-DE02621.
XX 02-SEP-1997; 97DE-1038205.
XX (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX Behrens J, Birchmeier W;
XX WPI; 1999-214706/18.
XX P-PSDB; W93569.
XX Tumor-suppressing protein conductin - used for treatment and
XX diagnosis of tumors
XX
XX Claim 18; Fig 2; 22pp; German.
XX
XX This invention describes a novel human conductin protein which has
XX anti-tumour activity. Detecting the presence or amount of conductin,
XX at protein or nucleic acid levels, is used to diagnose tumours, while
XX agents that (re)activate conductin are used for tumour therapy.
XX Conductin binds to beta-catenin and induces its cytoplasmic degradation,
XX resulting in blockade of the Wnt/Wingless signalling pathway in
XX vertebrates. Conductin also binds to Adenomatous Polyposis Coll (APC)
XX fragments and, in conjunction with APC, acts as a tumour suppressor.
XX
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QY 455 tcttaacactctctgttggtgtagacagatagtgtacatcccttcggaaacttccttgag 514
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QY 515 agggagaatgtgtgtagacagctggaacttcggttctgttgaatgggttcagcagatg 574
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Oy	2555	caaaagcttgacctcgggccactccaagggagcagctcagcaaaaaggaaattacagtat	2614*
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Oy	2615	tatttcagaagaagcgagtgacgaattgcctgcggagcacagtttttgagagagatctgggac	2674*
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Oy	2675	gacgagacgaatgtctcccacgatcgaagacagagatcctctggcacaagtctgagagagtcac	2733*
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Oy	2735	tga 2737	
Db	2521	tga 2523	
 RESULT 3 XO9012 ID XO9012 standard; DNA; 3411 BP.			
XX	AC	XO9012;	
XX	DT	14-JUN-1999 (first entry)	
XX	DE	Human axin gene.	
KW	Axin; cancer; breast cancer; colorectal cancer;		
KM	gastrointestinal cancer; esophageal cancer; carcinoma; melanoma;		
KX	diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;		
XX	beta-catenin; ss.		
OS	Homo sapiens.		
XX	Key	Location/Qualifiers	
FH	CDS	2..2704	
FT		/*tag= a	
FT		/product= Axin	
XX	M09902179-A1.		
PN	21-JAN-1999.		
PD			
XX	09-JUL-1998; 98MO-US14414.		
PP			
XX	10-JUL-1997; 97US-0890865.		
PR			
XX	(UYCO) UNIV COLUMBIA NEW YORK.		
PA			
XX	Constantini F, Zeng L;		
P1			
XX	WPI: 1999-120510/10.		
DR	P-PSDB: W96264.		
DR			
XX			
XX			
PT	Newly isolated nucleic acid encoding "axis inhibition" protein		
PT	(Axin) - useful for detecting, diagnosing and treating cancer		
XX			
XX			
XX	Disclosure; Figure 10A-10B; 95pp; English.		
CC	Nucleic acids encoding mutant and wild type Axin and		
CC	oligonucleotides derived from them are useful for detecting		
CC	mutations in the Axin gene and for determining whether a subject is		
CC	likely to develop cancer (including breast, colorectal,		
CC	gastrointestinal, esophageal, carcinomas or melanomas). The wild		
CC	type Axin and homologues of Axin are useful for treating subjects		
CC	who are likely to develop cancer (thyroid carcinomas). The nucleic		
CC	acids are also useful for diagnosing cancer and for detecting		
CC	mutations in cancerous cells. Wild type Axin, its antisense		
CC	molecule and identified compounds form pharmaceutical compositions		
CC			

CC In the treatment of cancer. The compositions are also useful for
CC treating cancer by inhibiting tumorigenesis (by inducing degradation
CC of beta-catenin). The nucleic acid encoding Axin acts through
CC negative regulation of the Wnt pathway in the Nieuwkoop Center.
XX
SQ Sequence 3411 BP, 752 A, 1010 C, 1066 G, 582 T, 1 other;

Query Match	14.2%	Score 401.8;	DB 20;	Length 3411;
Best Local Similarity	52.7%;	Pred. No. 1.6e-97;		
Matches 1297;	Conservative	0;	Mismatches 1052;	Indels 114;
				Gaps 15;

QY	404	gagccgagggcgcgagcgtcccccgcgattccctcttgacccaaggttgagccaagctttaaac	463
Db	323	gagccttgaggcagctgctcccccacccccaactctgaagggcgctgagctacatcgcat	382
QY	464	tcctctgttgggttgacccaagatctgtgtacatacctctcccggaacttcccttgagagagagaa	523
Db	383	tcctctgcttgatgacccaagatggataagcgtcttcaaggaacttccctgaagagagagggc	442
QY	524	tgtgtgtgatacgcgtgacctctgctgttgccttgtaatggatctcaagcagatg-----	574
Db	443	tgtgcgcgactgtgcgaactctctgtgttgcctctgcgaactgccttcagagagctgagaccgtc	502
QY	575	aacctgaaaggtatccaaaactcttgccgagctggtccaaagcatctataagggtaac---tt	631
Db	503	gactctgaaacgagagaaagagctgaagactctggcgagagatcataccgaaagatatactctc	562
QY	632	gagaaacaacagcgtctgtctccaaagcagctgaagcccgcccaagacataataagat	691
Db	563	gataacaaatgcatcgtgtctcccggaagccaagcccgcccaagagctctcataaaggcc	622
QY	692	ggacataaagaaagcaacagatctgcgtctgatactgtgacaaagtcacagacgagataacag	751
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QY	812	gtgagagagctgggggggaaacaacagctctatactgaagtaacggg-----ggaactgggagac	865
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QY	866	ctaaaggtcttaattctgtgactactcccccacactctgaatgaagaaagaggtgagacgtgtgc	925
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QY	926	gaacctcaagctgcaaaactctcaacccaacccgctgtgtgtgctgtgtccagcaaaactctcgg--	982
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QY	983	-----ggccacgcgaggtgtgagatacca-----cgaaacaagctgaaaac	1022
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Qy 1910 gagcagcttctgtagaagctgtagaagctgtagaagctgtagaagctgtagaagctgtagaagctgtagaagctgtagaagctgtagaag 1969
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Db 1857 gcttgcgcgcgcctgtagaagctgtagaagctgtagaagctgtagaagctgtagaagctgtagaagctgtagaagctgtagaag 1915
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```

Db 2270 aagagagagagctgtagaagctgtagaagctgtagaagctgtagaagctgtagaagctgtagaagctgtagaagctgtagaag 2329
Qy 2372 -----gacagagagagagctgtagaagctgtagaagctgtagaagctgtagaagctgtagaagctgtagaagctgtagaag 2422
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2330 ccgcgcgcgcctgtagaagctgtagaagctgtagaagctgtagaagctgtagaagctgtagaagctgtagaagctgtagaag 2389
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2423 ccaagagagagagctgtagaagctgtagaagctgtagaagctgtagaagctgtagaagctgtagaagctgtagaagctgtagaag 2482
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2390 atgagagctcctccgagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagag 2449
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2483 ccgcgcgcgcctgtagaagctgtagaagctgtagaagctgtagaagctgtagaagctgtagaagctgtagaagctgtagaagctgtagaag 2542
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2450 ccgcgcgcgcctgtagaagctgtagaagctgtagaagctgtagaagctgtagaagctgtagaagctgtagaagctgtagaagctgtagaag 2509
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2543 atgctgagagagctcctccgagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagag 2602
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2510 ctggttgagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagag 2569
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2603 aattacagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagag 2662
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2570 agctacagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagag 2629
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2663 gaggtctgtagaagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagag 2722
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2630 gaggtctgtagaagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagag 2689
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2723 gagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagag 2782
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2690 gagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagagag 2749
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2783 cac 2785
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2750 cac 2752
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 4
X09013 standard; DNA: 3761 BP.
ID X09013
XX
AC X09013;
XX
DT 14-JUN-1999 (first entry)
XX
DE Murine axin gene.
XX
KW Axin; cancer; breast cancer; colorectal cancer;
KW gastrointestinal cancer; esophageal cancer; carcinoma; melanoma;
KW diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;
KW beta-catenin; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 1..2981
FT /tag= a
FT /product= Axin
XX
PN W09902179-A1.
XX
PD 21-JAN-1999.
XX
PE 09-JUL-1998; 98MO-US14414.
XX
PR 10-JUL-1997; 97US-0890865.
XX
PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX
PI Constantini F, Zeng L;
XX
XX WPI; 1999-120510/10.
XX
DR P-PSDB; W96265.
XX
PT Newly isolated nucleic acid encoding "axin inhibition" protein

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PT (Axlin) - useful for detecting, diagnosing and treating cancer
XX
PS Claim 7: Figure 9A-9B: 95bp; English.
XX
CC Nucleic acids encoding mutant and wild type Axlin and
CC oligonucleotides derived from them are useful for detecting
CC mutations in the Axlin gene and for determining whether a subject is
CC likely to develop cancer (including breast, colorectal,
CC gastrointestinal, esophageal, carcinomas or melanomas). The wild
CC type Axlin and homologues of Axlin are useful for treating subjects
CC who are likely to develop cancer (thyroid carcinomas). The nucleic
CC acids are also useful for diagnosing cancer and for detecting
CC mutations in cancerous cells. Wild type Axlin, its antisense
CC molecule and identified compounds form pharmaceutical compositions
CC in the treatment of cancer. The compositions are also useful for
CC treating cancer by inhibiting tumorigenesis (by inducing degradation
CC of beta-catenin). The nucleic acid encoding Axlin acts through
CC negative regulation of the Wnt pathway in the Nieuwkoop Center.
XX
SQ Sequence 3761 BP; 890 A; 1012 C; 1088 G; 771 T; 0 other:

Query Match 12.0%; Score 337.6; DB 20; Length 3761;
Best Local Similarity 51.1%; Pred. No. 2,7e-80;
Matches 1238; Conservative 0; Mismatches 1084; Indels 100; Gaps 15;

QY 404 gggccgagggggggggcctcccccggatcccttggaccgagtgagaccagtttccac 463
DB 600 gggccgagggggggggcctcccccggatcccttggaccgagtgagaccagtttccac 659
QY 464 tcccttggtagaccgagtagtgatcatccttcggagagctccctggagggagaa 523
DB 660 tcccttggtagaccgagtagtgatcatccttcggagagctccctggagggagaa 719
QY 524 tggtagtagaccgagtagtgatcatccttcggagagctccctggagggagaa 574
DB 720 tggtagtagaccgagtagtgatcatccttcggagagctccctggagggagaa 779
QY 575 aacctgtagaccgagtagtgatcatccttcggagagctccctggagggagaa 631
DB 780 aacctgtagaccgagtagtgatcatccttcggagagctccctggagggagaa 839
QY 632 gggag 691
DB 840 gggag 899
QY 692 gggag 751
DB 900 gggag 959
QY 752 gggag 811
DB 960 gggag 1019
QY 812 gggag 865
DB 1020 gggag 1079
QY 866 gggag 925
DB 1080 gggag 1139
QY 926 gggag 971
DB 1140 gggag 1199
QY 972 gggag 1021
DB 1200 gggag 1259
QY 1022 gggag 1081
DB 1260 gggag 1319

QY 1082 gggag 1141
DB 1320 gggag 1379
QY 1142 gggag 1201
DB 1380 gggag 1436
QY 1202 gggag 1261
DB 1437 gggag 1493
QY 1262 gggag 1321
DB 1494 gggag 1550
QY 1322 gggag 1381
DB 1551 gggag 1610
QY 1382 gggag 1441
DB 1611 gggag 1670
QY 1442 gggag 1496
DB 1671 gggag 1730
QY 1497 gggag 1556
DB 1731 gggag 1790
QY 1557 gggag 1616
DB 1791 gggag 1848
QY 1617 gggag 1676
DB 1849 gggag 1908
QY 1677 gggag 1736
DB 1909 gggag 1968
QY 1737 gggag 1796
DB 1969 gggag 2028
QY 1797 gggag 1856
DB 2029 gggag 2088
QY 1857 gggag 1916
DB 2089 gggag 2148
QY 1917 gggag 1976
DB 2149 gggag 2208
QY 1977 gggag 2036
DB 2209 gggag 2259
QY 2037 gggag 2096
DB 2260 gggag 2316
QY 2097 gggag 2156
DB 2317 gggag 2373

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QY 2157 gtgcggcccaaggaagatcagccgacacatctgttgaggcgagacatccc 2216
DB 2374 ggccttctgcatcagcgtctcgtggcgctgcaccccttggtcagcgtcgttggga 2433
QY 2217 gctcagtgccggcgctaccacattacccagagccctgcacatgctcccttaccac 2276
DB 2434 attctgcccagcctctctatcttctatccaaagatccacacatgccacacacagcc 2493
QY 2277 ccaacacttggcagcagtagaagaagccttcgcagagctgcagaggtgttcga----- 2331
DB 2494 ctatccctctaccacagctggaagagcccgacgctgttgaaagaagaagaagagag 2553
QY 2332 -----gcccagagcagcgctgcgtgcgtgcagtcagcagaggg----- 2371
DB 2554 caaacaactcctcccaagcagagaggtatgtgcagagcagtcagcagcgaggagcact 2613
QY 2372 --gacaggaacacactcgtcgtcgttcagcagcagcctcacccttcgcaacccagcc 2429
DB 2614 gtgtcagcagcagctgtgtcaccggtgctgagtggtgtacacagcgtgtcagacttggaac 2673
QY 2430 tgcgtccagagatcaacaagaagcacaagaactgcagagtgctcagcgtccagagcca 2489
DB 2674 tctccgagacagagacaacaatcacaaagaagcaggtgcggtgagtgacacacatgtg 2733
QY 2490 gtgagctggtgtcactcactcttctgtgagaagaattccatcacaggaagatgtga 2549
DB 2734 acagcatgtgtgtggtgctacatctctgtggtggaacccatccctcaccgagacccgtgga 2793
QY 2550 aggtcacaagcttgaccccttgagccactcaagagcagctcagcaaaaagaaattaca 2609
DB 2794 gggcgctgctgtcacccttgagccagctcaagagcgtgtcaacaaagagggagactaca 2853
QY 2610 ggtatatttcaagaagcagatgtacgaattgtcctgcgagcagcttcttgagagatc 2669
DB 2854 gatactacttcaagaagtgatgtgattgtgactgtgtgtgtgatttgaggaagtcac 2913
QY 2670 gggagcagcagcagctgcccacatgtacgaagcagagatccttggtggaagagga 2729
DB 2914 gggagagatgagagccgtctgtcctgtcttgaaagaagaagatcatcgcaagtgagaaag 2973
QY 2730 tgcagtagccttggtcctcctc 2751
DB 2974 tggactgagcactgggagcagcac 2995

```

RESULT 5

A77843 standard; CDNA: 1205 BP.

AC A77843:

14-NOV-2000 (first entry)

CDNA encoding human colon tumour polypeptide. SEQ ID NO:123.

Human colon tumour polypeptide; tumour antigen; cancer; vaccine;

immunotherapy; diagnosis; progression; ss.

Homo sapiens.

WO200037643-A2.

29-JUN-2000.

23-DEC-1999; 99MO-US30909.

23-DEC-1998; 98US-0221298.

22-SEP-1999; 99US-0347496.

19-NOV-1999; 99US-0444242.

02-DEC-1999; 99US-0454150.

(CORI-) CORIXA CORP.

```

XX Xu J, Lodes MJ, Secrist H, Benson DR, Meagher MJ, Stolk J;
PI Wang T, Yugu J;
XX WPI: 2000-442671/38.
DR New colon tumor polypeptides used to inhibit the development of cancer,
XX especially colon cancer, and for diagnosing and monitoring the
PT progression of the cancer -
PS Claim 1; Page 125-126; 229pp; English.
XX
CC Sequences A77722-A78199 represent 478 cDNAs encoding proteins or
CC portions of proteins which are associated with human colon tumors.
CC The invention also specifically discloses 8 human colon tumour proteins
CC (B11897-B11904). The nucleic acids, the polypeptides they encode, and
CC antigen presenting cells (APCs, preferably dendritic cells) expressing
CC such polypeptides may be used in vaccines that target tumour cells,
CC especially colon tumour cells, thereby inhibiting the development of
CC cancer. T-cells specific for the polypeptide expressed by the APC are
CC used to remove tumour cells from biological samples, especially blood or
CC fractions thereof. The sample or the isolated T-cells specific for the
CC polypeptide can then be used to inhibit cancer development. CD4+ and/or
CC CD8+ T-cells from a patient may be incubated with a polypeptide or
CC nucleic acid of the invention, or an APC expressing such a polypeptide,
CC to cause the proliferation of specific T-cells. The T-cells can be
CC cloned and then administered back to the patient to inhibit cancer
CC development. Nucleic acids encoding the polypeptides and antibodies
CC against the polypeptides may be used to determine the expression level
CC of a tumour protein of the invention, and therefore to determine whether
CC cancer cells are present. Such diagnostic methods may also be used to
CC monitor the progression of a cancer by repeating the processes at time
CC intervals, and comparing the current result to previous results. The
CC present sequence represents a cDNA encoding a human colon tumour
XX polypeptide.
SQ Sequence 1205 BP; 316 A; 248 C; 324 G; 317 T; 0 other:

```

Query Match 11.4%; Score 322.2; DB 21; Length 1205;
Best Local Similarity 89.0%; Pred. No. 2,1e-76;
Matches 348; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

```

QY 2358 ccagtcagcagagggagcaggaacacactgctgctgtgtagcagagcctacccctcg 2417
DB 1 ccagtcagcagagggagcaggaacacactgctgctgtgtagcagagcctacccctct 60
QY 2418 ccaaccagcctgctcagcagagatcacacaagaagcacaagaactggaagtgccacg 2477
DB 61 ccaaccagcctgctcagcagagatcacacaagaagcacaagaactggaagtgccacg 120
QY 2478 cgtccagagcagtgagctggtgtgtacactcttctgtggaagaagaattccataca 2537
DB 121 cgtccagagcagtgagctggtgtgtacactcttctgtggaagaagaattccataca 180
QY 2538 ggaagatgctgaagctcaagcttgacccttgagccacttcaaggagagcagcagcaaaa 2597
DB 181 ggaagatgctgaagctcaagcttgacccttgagccacttcaaggagcagcagcaaaa 240
QY 2598 aggaattacagatatttcaagaagcgagtgacgaatttgcttcgagagcagttt 2657
DB 241 aggaattacagatatttcaagaagcgagtgacgaatttgcttcgagagcagttt 300
QY 2658 ttgagagatcttggaagcagagagcagtgctcccatgtacgaagcagagatcttgga 2717
DB 301 ttgagagatcttggaagcagagagcagtgctcccatgtacgaagcagagatcttgga 360
QY 2718 aagtgagagagatcagatgagccttgccctc 2748
DB 361 aagtgagagagatcagatgagccttgccctc 391

```

RESULT 6

A77754
 A77754 standard; cDNA; 401 BP.
 A77754;
 14-NOV-2000 (first entry)
 cDNA encoding human colon tumour polypeptide, SEQ ID NO:33.
 Human colon tumour polypeptide; tumour antigen; cancer; vaccine;
 immunotherapy; diagnosis; progression; ss.
 Homo sapiens.
 M0200037643-A2.
 29-JUN-2000.
 23-DEC-1999; 99MO-US30909.
 23-DEC-1999; 98US-0221298.
 02-JUL-1999; 99US-0347496.
 22-SEP-1999; 99US-0401064.
 19-NOV-1999; 99US-0444242.
 02-DEC-1999; 99US-0454150.
 (CORI-) CORIXA CORP.
 Xu J, Lodes MJ, Secrist H, Benson DR, Meagher MJ, Stolk J;
 Wang T, Yuqiu J;
 WPI: 2000-442671/38.
 New colon tumor polypeptides used to inhibit the development of cancer,
 especially colon cancer, and for diagnosing and monitoring the
 progression of the cancer -
 Claim 1; Page 96-97; 229pp; English.
 Sequences A77722-A78199 represent 478 cDNAs encoding proteins or
 portions of proteins which are associated with human colon tumours.
 The invention also specifically discloses 8 human colon tumour proteins
 (B11897-B11904). The nucleic acids, the polypeptides they encode, and
 antigen presenting cells (APCs, preferably dendritic cells) expressing
 such polypeptides may be used in vaccines that target tumour cells,
 especially colon tumour cells, thereby inhibiting the development of
 cancer. T-cells specific for the polypeptide expressed by the APC are
 used to remove tumour cells from biological samples, especially blood or
 fractions thereof. The sample or the isolated T-cells specific for the
 polypeptide can then be used to inhibit cancer development. CD4+ and/or
 CD8+ T-cells from a patient may be incubated with a polypeptide or
 nucleic acid of the invention, or an APC expressing such a polypeptide,
 to cause the proliferation of specific T-cells. The T-cells can be
 cloned and then administered back to the patient to inhibit cancer
 development. Nucleic acids encoding the polypeptides and antibodies
 against the polypeptides may be used to determine the expression level
 of a tumour protein of the invention, and therefore to determine whether
 cancer cells are present. Such diagnostic methods may also be used to
 monitor the progression of a cancer by repeating the processes at time
 intervals, and comparing the current result to previous results. The
 present sequence represents a cDNA encoding a human colon tumour
 polypeptide.
 Sequence 401 BP; 105 A; 88 C; 123 G; 85 T; 0 other;

	Query Match	Similarity	Best Local	Score	DB	Length
Matches	343	Conservative	0	Mismatches	42	Indels
						Gaps
QY	2364	agcagaagagacaggaaccacatcgtcgtcgtcgtgtaacgagagacaccccttcgcgaacc	2423			
Db	1	agcagaagagacaggaaccacatcgtcgtcgtcgtgtaacgagagacaccccttcgcgaacc	60			

QY	2424	caagccggtctcagaagatcacaaaagacgcaaaagaacttgcgaattgtccacggtcc	2483
	1111111111		
Db	61	caagcccggtccccaagaagacacaaaagacgaagaaacttgcgaagtgtccacggtcc	120
QY	2484	agcgcaatcgagctgtgttcacctaactttctctgtgtgaagaagaattcatatcagaagaa	2543
	1111111111		
Db	121	agcgcaatcgaggtgtgtgttcacttaactttttctctgtgtgaagaagaattcatatcagaa	180
QY	2544	tgtctgaagctcacaagctctgacctctggtccactctcaagagcagctcagcaaaaaggaa	2603
	1111111111		
Db	181	tgtctgaagctcagaagctctgacctctggtccactcttaagagcagctcagcaaaaaggaa	240
QY	2604	attcacagatattatttcaagaagaagcgatgtgaagaaatttcctctggtgagcagtttttgag	2663
	1111111111		
Db	241	attcacagatattacttcaaaaagaacgagatgagttttcctctgtgtgaagcgtgtgtttgag	300
QY	2664	agatcttggaacgagagacaagtctccccccttgcagcaagaagcaggtctcctgtgcacaagtg	2723
	1111111111		
Db	301	agatcttggaagagagacaagtgctccccccttgcagatcagaaagccgagatctcgtgcacaagtg	360
QY	2724	agaagatcgaactagccttgcctc	2748
	1111111111		
Db	361	agcgatcgaattgagccctgtggtc	385

RESULT	7
ID	T11418
AC	T11418 standard; cDNA; 2383 BP.
CC	T11418;
CC	15-APR-1996 (first entry)
CC	p53 response protein PIGI-1 coding sequence.
CC	Response protein; PIGI-1; oncogenesis; cancer; tumour; p53; ss.
CC	Homo sapiens.
CC	Key
CC	Location/Qualifiers
CC	93..701
CC	/*Lag- a
CC	/product= p53 response protein PIGI-1.
CC	W09601907-A1.
CC	25-JAN-1996.
CC	10-JUL-1995; 95MO-US08597.
CC	12-JUL-1994; 94US-0274118.
CC	(BRIM) BRISTOL-MYERS SQUIBB CO.
CC	Buckbinder L, Kley N, Seizinger BR, Talbott R;
CC	WPI: 1996-097636/10.
CC	P-PSDB; R89895.
CC	New isolated nucleic acid encoding p53 response protein PIGI-1
CC	used to develop prods. for the study, diagnosis and treatment of
CC	tumours and cancer
CC	Claim 3; Figure 6; 58pp; English.
CC	Recombinant production of PIGI-1 allows the study of the structure,
CC	function and role in oncogenesis of the protein. PIGI-1 and
CC	nucleic acid encoding it can also be used to develop products for
CC	use in treating tumours and cancer and in the diagnosis of cancer.
CC	Sequence 2383 BP; 561 A; 603 C; 657 G; 562 T; 0 other;

XX	18-SEP-2000	(first entry)
DT		
XX		
DE		
XX	Human CRI CDNA.	
XX		
KW	CR2: human; antibody; cytokine response gene; cytostatic; anti-allergic;	
KW	immunosuppressive; antimicrobial; therapy; cell proliferation; treatment;	
KW	cell differentiation; cancer; immune disease; rheumatologic disease;	
KW	transplant rejection; anti-infective; CRI; ss.	
XX		
OS	Homo sapiens.	
XX		
EH	Key	Location/Qualifiers
FT	CDS	116..724
FT		/*tag= a
XX		/product= "CRI"
PN	US6057427-A.	
PD	02-MAY-2000.	
XX		
PE	05-JUN-1996;	96US-0652446.
XX		
PR	20-NOV-1991;	91US-0796066.
PR	10-AUG-1993;	93US-0104736.
PR	27-OCT-1994;	94US-0330108.
PR	05-JUN-1996;	96WO-US08992.
XX		
PA	(DART-) DARTMOUTH COLLEGE.	
XX		
PI	Beadling C, Smith KA;	
XX		
DR	WPI: 2000-338623/29.	
XX		
XX	P-PSDB: Y87952.	
PT		
PT	Novel antibody or antibody fragment which selectively binds to a	
XX	polypeptide encoded by cytokine response gene 2	
XX		
PS	Example IV; Column 75-78; 66pp; English.	
XX		
CC	This invention describes a novel isolated antibody or antibody fragment	
CC	(I) which selectively binds to a polypeptide encoded by cytokine response	
CC	gene 2 (cr2) and modulates cr2 activity. The products of the invention	
CC	have cytostatic, anti-allergic, immunosuppressive and antimicrobial	
CC	activity. The antibodies are useful as therapeutic agents for regulating	
CC	cellular proliferation and differentiation and for treating all kinds of	
CC	cancers, immune diseases such as allergic, autoimmune, and rheumatologic	
CC	diseases, transplant rejection, and as anti-infectives for fighting	
CC	viral, bacterial, parasitic and fungal infections. This sequence encodes	
CC	the human CRI protein described in the invention.	
XX		
XX	Sequence 2406 BP; 565 A; 621 C; 656 G; 564 T; 0 other;	

	Query Match	Similarity	2.13:	Score 58.8:	DB 21:	Length 2406:
	Best Local	Similarity	47.28:	Pred. No.1.le-05:		
	Matches	251:	Conservative	0:	Matches 272:	Indels 9, Gaps 2:
Qy	444	ggtggacccaagtccttaacatcctctgttctgggtgagccagaatggtcatatcctcttcgga	503			
Db	297	ggtggagagagctgtctgcagccctgcctgcagcagcaaaaatgtagtgcctgccttcacg	356			
Qy	504	ctctctctggagaaaggagaaatgctgtgatacgcctgcagctctctgttctcttaatgggt	563			
Db	357	ctctctctgaagacaagatgctcagctggaggaaccttggaaatcttcggcttcgccttctggagagt	416			
Qy	564	tcaggcagatggaacccctggaaaggataccaaaactcttcgagctggcgcacaaagacataaag	623			
Db	417	tca---agaagatccgcagctacagctaccaagctgcgcctcagggcacacaacagatccttggg	473			
Qy	624	ggtacatctggaaacaacacgcgtctgtctccaagcagcctgaagcccgccacaaagacctaca	683			
Db	474	agttcaattcgg-----cagctgagggcccttaagaaggtacaactttacatgagaccgcg	527			

QY	684	tacgaagtcgtcatcaagaagaacacagatcggtcgggtcaatgttttacccaaggaacacgcg	743
Db	528	agctgcacgaggaatgaacctgcagactgtccacacagacacatgtctttatgtcgtgcctcaggga	587
QY	744	agatccacgagagtgatctgagaagaataatgctaccacaggtgtctcttgactctgaacattacc	803
Db	588	agacacgttacccctgatctgagaagaagactcctctaccacagctcctctgaagtcgcctgttacc	647
QY	804	tggaaatctgtgaggaagtgtggggggaataacacagcttacaatgaatgaacggtggactggga	863
Db	648	gggagctgtgctgcaccaagcctcagccgctctctgcacactgtctccacgctgcagctgcagcc	707
QY	864	gcctaaagctcttatctgtgtgtctaccctccacacttgatgaagaagagatgagactgtg	923
Db	708	agccctacacacactgctcgtctccacagcgagctgagaagaacgacgagcggaagaagagttgag	767
QY	924	ccgacctcacaatgtaaacactctcacccacgcgtgtgtgctgtctgcacgaacaaac	975
Db	768	tcaccatcccccagagtggtgctgcctctgtgtggaggaagagcttcgcgaagc	819
RESULT	10		
ID	A39678	A39678 standard; cDNA; 606 BP.	
XX	AC	A39678;	
XX	DT	18-SEP-2000 (first entry)	
XX	DE	Cytokine response gene-related cDNA sequence (seq ID 27).	
KW	CR2; human; antibody; cytokine response gene; cytostatic; anti-allergic;		
KW	immunosuppressive; antimicrobial; therapy; cell proliferation; treatment;		
KW	cell differentiation; cancer; immune disease; rheumatologic disease;		
KW	transplant rejection; anti-infective; ss.		
XX	OS	Unidentified.	
PN	US6057427-A.		
PD	02-MAY-2000.		
XX	05-JUN-1996;	96US-0652446.	
XX	20-NOV-1991;	91US-0796066.	
PR	10-AUG-1993;	93US-0104736.	
PR	27-OCT-1994;	94US-0330108.	
PR	05-JUN-1996;	96WO-US08992.	
XX	(DART-) DARTMOUTH COLLEGE.		
XX	Beadling C, Smith KA;		
XX	WPI: 2000-338623/29.		
PT	Novel antibody or antibody fragment which selectively binds to a		
PT	polypeptide encoded by cytokine response gene 2		
XX	Disclosure; Column 113-116; 66pp; English.		
XX	This invention describes a novel isolated antibody or antibody fragment		
CC	(1) which selectively binds to a polypeptide encoded by cytokine response		
CC	gene 2 (CR2) and modulates CR2 activity. The products of the invention		
CC	have cytostatic, anti-allergic, immunosuppressive and antimicrobial		
CC	activity. The antibodies are useful as therapeutic agents for regulating		
CC	cellular proliferation and differentiation and for treating all kinds of		
CC	cancers, immune diseases such as allergic, autoimmune, and rheumatologic		
CC	diseases, transplant rejection, and as anti-infectives for fighting		
CC	viral, bacterial, parasitic and fungal infections. This sequence is		
CC	presented in the Seq ID list but is not described in the specification.		
QY	Sequence 606 BP; 147 A; 172 C; 170 G; 117 T; 0 other;		

	RESULT	10
ID A39678	A39678 standard; cDNA; 606 BP.	
XX AC		
XX AC	A39678;	
DT DT	18-SEP-2000 (first entry)	
XX DE	Cytokine response gene-related cDNA sequence (Seq ID 27).	
XX KR	CR2; human; antibody; cytokine response gene; cytosolic; anti-a-	
KW KW	mmunosuppressive; antimicrobial; therapy; cell proliferation; t	
KM KM	cell differentiation; cancer; immune disease; rheumatologic dise	
KM KM	transplant rejection; anti-infective; ss.	
XX OS	Unidentified.	
PN PN	US6057427-A.	
PD PD	02-MAY-2000.	
PF PF	05-JUN-1996; 96DS-0652446.	
PR PR	20-NOV-1991; 91US-0796066.	
PR PR	10-AUG-1993; 93US-0104736.	
PR PR	27-OCT-1994; 94US-0330108.	
PR PR	05-JUN-1996; 96WO-US08992.	
PA PA	(DART-) DARTMOUTH COLLEGE.	
PI PI	Beadling C, Smith KA.	
DR DR	WPL; 2000-338623/29.	
PT PT	Novel antibody or antibody fragment which selectively binds to a	
PS PS	polypeptide encoded by cytokine response gene 2 -	
XX XX	Disclosure; Column IJ3-I16; 66pp; English.	
CC CC	This invention describes a novel isolated antibody or antibody f	
CC CC	(I) which selectively binds to a polypeptide encoded by cytokinele	
CC CC	gene 2 (CR2) and modulates CR2 activity. The products of the inv	
CC CC	have cytostatic, anti-allergic, immunosuppressive and antmicrob	
CC CC	activity. The antibodies are useful as therapeutic agents for re	
CC CC	cellular proliferation and differentiation and for treating all i	
CC CC	cancers, immune diseases such as allergic, autoimmune, and rhum	
CC CC	diseases, transplant rejection, and as anti-infectives for fight	
CC CC	viral, bacterial, parasitic and fungal infections. This sequenc	
CC CC	presented in the Seq ID list but is not described in the specifi	
XQ XQ	Sequence 606 BP; 147 A; 172 C; 170 G; 117 T; 0 other:	

XX 09-APR-1998.
 PD 06-OCT-1997; 97WO-US18259.
 XX 06-JUN-1997; 97US-0870815.
 XX PR 04-OCT-1996; 96US-0726228.
 XX (MILL-) MILLENNIUM PHARM INC.
 PA Glimeno CJ, Levinson DA;
 XX MPI: 1998-240085/21.
 XX P-PSDB: M59293.
 DR
 XX
 XX New activated T helper cell specific gene, RATH - used for
 PT developing products for treating e.g. autoimmune disorders,
 PT arthritis, graft rejection, asthma, allergy, infections or neoplasms
 XX
 PS Claim 1: Fig 1A-C: 127pp: English.
 XX
 CC This sequence encodes a novel member of the mouse regulator of G-protein
 CC signalling (RGS) gene family, RATH1.1. The encoded protein participates
 CC in the regulation, control and/or modulation of G-protein mediated
 CC signal transduction, involved in T cell activation, including T-helper
 CC (TH) cell and TH cell subpopulation activation. The protein can be
 CC used to develop products for treating autoimmune disorders, arthritis,
 CC graft rejection, asthma, allergy, infections or neoplasms.
 XX
 SQ Sequence 2272 BP; 548 A; 584 C; 625 G; 515 T; 0 other;

Query Match 1.8%; Score 50.8; DB 19; Length 2272;
 Best Local Similarity 50.3%; Pred. No. 0.0015;

Matches 183; Conservative 0; Mismatches 172; Indels 9; Gaps 2;

OY 444 gctgagaccagcttaccctctctctgttgggtgagaccagatgtgtcatcctcttcgga 503
 DB 219 gactgagagagatcttgcgtctgctgaacagtaaaatgggggtcgtccttcacatg 278
 OY 504 ctctccctgagagggagaaatgtgtgtaacgctgagcttctggttctgttaatgggt 563
 DB 279 cctctctaaagcgaatcatcgtgaggaagaacctgagcttctggttctggtcgaagagt 338
 OY 564 tcaaggcagatgaacctgaaagataccaaaaccttgcgagltggccaaagaatctataaga 623
 DB 339 tca---agaagatcgcgtacgaccacaacctggtccaggggtccacacatctttgacg 395
 OY 624 ggtacatctgagaacaacagcgttcttccaagcagctgaaagcccgccacaaagacttaca 683
 DB 396 agtacct-----ccgcagcgaagccctaaagaggttgacataagatcagagaccgag 449
 OY 684 tagcagatgcatcacaagaacagacagctgcgtcgtgtcatgtttgaccagcagacgg 743
 DB 450 aactgacccaagaacaaacccaacagctgcacactacacagtgcttgatgtggtcagaaggga 509
 OY 744 agatccagcagtgatgaggaagaatgctaccacaggltgttctgtacatctgtacattacc 803
 DB 510 agaccgcacatgtatgtggaagagactctatccgcgtctcctcacaagtaccagcttacc 569
 OY 804 tggga 807
 DB 570 gcga 573

RESULT 13

AS3800 ID AS3800 standard; DNA: 7720 BP.

AC AS3800;

XX 19-DEC-2000 (first entry)

DE Genomic DNA encoding M68 TNF receptor related protein.
 XX
 XX M68: tumour necrosis factor; TNF; programmed cell death; apoptosis;
 KW receptor; immune response; cell differentiation; ligand; cancer;
 KW bone disease; systemic lupus erythematosus; Hashimoto's thyroiditis;
 KW Grave's disease; idiopathic myxedema; autoimmune diabetes;
 KW thrombotic thrombocytopenic purpura; multiple sclerosis;
 KW liver diseases; autoimmune gastritis; ulcerative colitis;
 KW glomerulonephritis; pulmonary fibrosis; heart failure;
 KW atherosclerosis; aplastic anaemia; myelodysplastic syndromes;
 KW osteoporosis; Alzheimer's disease; Parkinson's disease; stroke;
 KW myocardial infarction; human; ds.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH exon 5580..6003
 FT /*tag= a
 FT /*label= Exon 1
 FT intron 6004..6139
 FT /*tag= b
 FT /*label= Intron 1
 FT exon 6140..6334
 FT /*tag= c
 FT /*label= Exon 2
 FT intron 6335..7091
 FT /*tag= d
 FT /*label= Intron 2
 FT exon 7092..7375
 FT /*tag= e
 FT /*label= Exon 3
 XX
 PN WO200046247-A1.
 XX
 PD 10-AUG-2000.
 XX
 XX 04-FEB-2000; 2000MO-US03037.
 XX
 XX 05-FEB-1999; 99US-0118902.
 PR 20-DEC-1999; 99US-0172754.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Bai C;
 XX
 XX MPI: 2000-506066/45.
 DR P-PSDB: Y97246.
 XX
 PT Isolated human M68 nucleic acids and proteins which are part of the
 PT tumor necrosis factor receptor (TNFR) family, useful for identifying
 PT modulators that may be used to treat various diseases e.g. cancer,
 PT osteoporosis, Alzheimer's disease
 XX
 PS Claim 19; Page 76-78; 80pp: English.
 XX
 XX The M68 protein is a member of a family of proteins which have
 CC roles in immune responses, cell death, cell proliferation and
 CC stimulation of cell differentiation. M68 lacks a transmembrane domain
 CC and is a secreted factor suggesting that it functions as a natural
 CC inhibitor for its ligand. The altered expression pattern of M68 in a
 CC multitude of tissues suggests that M68 may play a role in cancer by
 CC binding to its ligand and blocking apoptotic cell death induced by
 CC such a ligand. This anti-apoptotic role of M68 suggests that
 CC modulators of M68 will be useful in treatment of apoptosis-related
 CC diseases such as various forms of cancer and various bone disorders.
 CC M68 nucleic acids and proteins are therefore useful for treating
 CC conditions involving atypical apoptosis and for identifying
 CC modulators of M68. Modulators of M68 are useful for treatment of
 CC cancer and other diseases associated with abnormal levels of
 CC apoptosis including systemic lupus erythematosus, Hashimoto's
 CC thyroiditis, Grave's disease, idiopathic myxedema, autoimmune
 CC diabetes, thrombotic thrombocytopenic purpura, multiple sclerosis,
 CC liver diseases, autoimmune gastritis, ulcerative colitis,


```

Db 274 GGTGAGAGAGAGTCTGTCAGCTGCTGCTGAGCAGTAAATAATGAGTGGCTTCACAG 333
QY 504 cttcccgagagagagagaaatgltgtaagctgagcttctgttctgttaatggt 563
Db 334 CTTTCTGAGACAGAGAGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 393
QY 564 tcaggcagatgaactgaagagataccaaacttgcagagtgagcgaagaaactataaga 623
Db 394 TCA---AGAGATCCGATCAGCTACAGCTGAGCTCCAGGACACACAGATCTTTGAGG 450
QY 624 ggtcattgtaaaacaacagcgttcttccaaagcgtgaagcccgcccaagcactaca 683
Db 451 AGTTCATTG---CAGTAGAGGCCCTTAAAGAGGTCACATTGACATGACATGACCGCG 504
QY 684 tagcagatgagatcaagaagacacagatcggtcgtcatgtttgacagagcagagcgg 743
Db 505 AGCTGACAGAGATGAGCTGACAGACTGCCACAGCCACATGCTTTGATTCGGCTCAGGGGA 564
QY 744 agatccagcagatgagagagaaatgctaccagagtgcttgcatacttgcatactaac 803
Db 565 AGACACGTAACCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 624
QY 804 tggaaatgtaagagagtgaggagaaacacagcttaacatgaagagagagagagag 863
Db 625 GGGACCTGCTGCCCAAGCTCAGCGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 684
QY 864 gcttaagagcttattgtgtctaccctccacacttgatgaagaagagagagagagag 923
Db 685 AGCCTTCACACACCTGATGATCTCCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGT 744
QY 924 cgaagcctaagtgcaactctcaccacagtggtgtgtgtgtgtgtgtgtgtgtgtgt 975
Db 745 TCACCATCCCGAGAGTGCTGCCCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 796

RESULT 2
; Sequence 1, Application US/08754108
; Patent No. 5886149
; GENERAL INFORMATION:
; APPLICANT: Buckbinder, Leonard
; APPLICANT: Talbott, Randy
; APPLICANT: Seizinger, Bernd R.
; APPLICANT: Kley, Nikolai
; TITLE OF INVENTION: No. 5886149el p53 Response Genes
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/754,108
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/274,318
; FILING DATE: 11-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bogden, James M.
; REGISTRATION NUMBER: 32,962
; REFERENCE/DOCKET NUMBER: ONO127-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-727-3688
; TELEFAX: 206-727-3601
; INFORMATION FOR SEQ ID NO: 1:

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```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 2383 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-754-108-1

Query Match
Best Local Similarity 47.2%; Pred. No. 2.5e-06;
Matches 251; Conservative 0; Mismatches 272; Indels 9; Gaps 2;

QY 444 ggtgaccagatcttaccctctgttgggtgagcagagatgagatgagatgagatgag 503
Db 274 GGTGAGAGAGAGTCTGTCAGCTGCTGCTGAGCAGTAAATAATGAGTGGCTTCACAG 333
QY 504 cttcccgagagagagagaaatgltgtaagctgagcttctgttctgttaatggt 563
Db 334 CTTTCTGAGACAGAGAGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 393
QY 564 tcaggcagatgaactgaagagataccaaacttgcagagtgagcgaagaaactataaga 623
Db 394 TCA---AGAGATCCGATCAGCTACAGCTGAGCTCCAGGACACACAGATCTTTGAGG 450
QY 624 ggtcattgtaaaacaacagcgttcttccaaagcgtgaagcccgcccaagcactaca 683
Db 451 AGTTCATTG---CAGTAGAGGCCCTTAAAGAGGTCACATTGACATGACATGACCGCG 504
QY 684 tagcagatgagatcaagaagacacagatcggtcgtcatgtttgacagagcagagcgg 743
Db 685 AGCCTTCACACACCTGATGATCTCCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGT 744
QY 744 agatccagcagatgagagagaaatgctaccagagtgcttgcatacttgcatactaac 803
Db 505 AGCTGACAGAGATGAGCTGACAGACTGCCACAGCCACATGCTTTGATTCGGCTCAGGGGA 564
QY 804 tggaaatgtaagagagtgaggagaaacacagcttaacatgaagagagagagagag 863
Db 625 GGGACCTGCTGCCCAAGCTCAGCGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 684
QY 864 gcttaagagcttattgtgtctaccctccacacttgatgaagaagagagagagagag 923
Db 685 AGCCTTCACACACCTGATGATCTCCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGT 744
QY 924 cgaagcctaagtgcaactctcaccacagtggtgtgtgtgtgtgtgtgtgtgtgtgt 975
Db 745 TCACCATCCCGAGAGTGCTGCCCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 796

RESULT 3
; Sequence 1, Application US/08463081B
; Patent No. 5871960
; Patent No. 5871960 5837487
; GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A. & Beadling, Carol
; TITLE OF INVENTION: Nucleic Acids Encoding CRP Polypeptide,
; Expression Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER & POPILMSKI
; STREET: 444 South Flower St. - Suite 1900
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0,
; Version #1.25

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463.081B
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/104,736
FILING DATE: 10-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38150 (DART-060)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2406 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 116..722
US-08-463-081B-1

Query Match 2.1%; Score 58.8; DB 2; Length 2406;
Best Local Similarity 47.2%; Pred. No. 2.5e-06;
Matches 251; Conservative 0; Mismatches 272; Indels 9; Gaps 2;

OY 444 ggtggaacagctcttaccctctgtgtggtgagcaagatggtacatcctctccgga 503
DB 297 GGTGAGAGAGTCGTTGACGCTGCTGAGCAGTAAATGAGTGGCTGCTTCACG 356
OY 504 cttctcgtgagagggagaaatggtgtgatacgtgactctggtctgtctgtaaggt 563
DB 357 CTTTCTTGAAAGACAGATTGACGTGAGGAGAACCTGAGTGGCTGCTGTGAGGAGT 416
OY 564 tcagggcagatgagcctgaagagatgacaaactctgcagtggtgccaagaatctataaga 623
DB 417 TCA---AGAGATCCGATACGATACCAAGCTGCTCCAGGGCAGACAGATCTTGAGG 473
OY 624 gttacattgagaacacagcgtgtgtctccaagcagctgaagccgcacaaagactaca 683
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DB 538 AGCTGACGAGGTGAACCTGACACTGCGACAGCCACATGCTTGTGCGCTGACAGGGA 587
OY 744 agatccagagcaatgtagaggaataatgctaccaggtgtcttgaactctgacattacc 803
DB 588 ACACACGATACCTGATGAGAGAGACTCTACCAACGCTTCTGTAAGTGGCTGCTTACC 647
OY 804 tggaaatagtgaagagtggtggggggaacacacagctacatagtgaacggggagtgga 863
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OY 864 gcttaaaaggtcttaagtgtctacatcccaacttgaaataaagaaggggtgtgaagtg 923
DB 708 AGCCTTCACACACCTGAGTCTCCACGCGAGTGAAGAGCCACCGGGAAGAGGTTGAG 767
OY 924 ccgacctcaagtgcaaaactcaccacacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 975
DB 768 TCACCATCCCGAGGTGGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 819

RESULT 4
US-08-461-379A-1
; Sequence 1, Application us/08461379A

Patent No. 5871961
GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
TITLE OF INVENTION: Vector and Transformed Cell Thereof, and
TITLE OF INVENTION: Expression thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESS: Ratner & Prestia
ADDRESS: (B) STREET: One Westlakes-Berwyn
CITY: Valley Forge
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,379A
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/330,108; 08/104,736
APPLICATION NUMBER: 6 07/796,066
FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: DART-070
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)470-0700
TELEFAX: (610)470-0701
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2406 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 116..722
US-08-461-379A-1

Query Match 2.1%; Score 58.8; DB 2; Length 2406;
Best Local Similarity 47.2%; Pred. No. 2.5e-06;
Matches 251; Conservative 0; Mismatches 272; Indels 9; Gaps 2;

OY 444 ggtggaacagctcttaccctctgtgtggtgagcaagatggtacatcctctccgga 503
DB 297 GGTGAGAGAGTCGTTGACGCTGCTGAGCAGTAAATGAGTGGCTGCTTCACG 356
OY 504 cttctcgtgagagggagaaatggtgtgatacgtgactctggtctgtctgtaaggt 563
DB 357 CTTTCTTGAAAGACAGATTGACGTGAGGAGAACCTGAGTGGCTGCTGTGAGGAGT 416
OY 564 tcagggcagatgagcctgaagagatgacaaactctgcagtggtgccaagaatctataaga 623
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DB 528 AGCTGACGAGGTGAACCTGACACTGCGACAGCCACATGCTTGTGAGCGCTGACGGGA 587
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Db      648 GGGAGCTGGCGGCCCAAGCCNCACCGCGCTCTTGCCACTCTGTCCAGCTGCAGCCTTGACC 707
QY      864 gccataagttcatgtgtgtacctccacccttgaatgaaagaagaggtagcgttg    923
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Db      708 AGCCCTCACACACTGTGACTCTCCACGGCAGTAGAGAGAAACCGCGGAAGAGAGGTTAG 767
QY      924 ccagactcaagtgcaaacctcacaccacgcgtgtgtgtgtlccagcaaac    975
        |||
Db      768 TCACCACCTCCCCGAGGTGGCTGCCCTGTGTGGGAGCGCAGGTTCTGCAAAGC 819

RESULT          5
US-08-462-390B-1
; Sequence 1, Application US/08462390B
; Patent No. 5882894
GENERAL INFORMATION:
APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and
NUMBER OF INVENTIONS: Transformed Cell Thereof, and Expression Thereof
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestlia
                (B) STREET:One Westlakes-Berwyn
City: Valley Forge
State: Pennsylvania
Country: USA
Zip: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,390B
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/330,108
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: DART-040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)407-0700
TELEFAX: (610)407-0701
INFORMATION FOR SEQ ID NO.: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2406 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 116..722
US-08-462-390B-1

Query Match          2.1%; Score 58.8; DB 2; Length 2406;
Best Local Similarity 47.2%; Pred. No. 2.5e-06;
Matches 251; Conservative 0; Mismatches 272; Indels 9; Gaps 2

OY      444 ggtgaccaagctcttaacctctctgttgtgtggcgacagagatggtgatatacctcttcgga 503
        |||
Db      297 GTGTGAGAGAGGCTGTCGCGCTGCTGCTGAGCAGTAAATGAGATGGCTGCTTCCACG 356
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OY	504	cttccctcggagaggaagaataatgtytgatatacgttcgtaattccttggttgccttgtaagcgggt	563
Db	357	cttttcttgcgaacacgaagtctcagtaggagaaacctggcgggttcttgcttgcttgacagact	416
OY	564	tcagacagatlaaaccttgaaagatatccaaaacttgcagtytgcccaagcaatcatalaaga	623
Db	417	TCA---AGAAATCTCGAATCAAGCTTCAAGCTGGCCCTTCAGGACACACAGATCTTTGAGG	473
OY	624	ggtcattctgagaacaacacagcgtgtgtctccaagcagctcgaagcccgccacaagaactaca	683
Db	474	AGTTTCATTGG-----CAGTGAGGCCCTTAAAGAGGTCAACATTGACCATGAAACCCGCG	527
OY	684	tacgagatgcatcaagaagaacaagatacgtcgtcgtcatcgttcttgacaagacagacgcg	743
Db	528	AGCTGACGACGATGATACCTGCACTGCAGACTGCCACAGCCACATGCTTTGANGCGGCTCAGGGGA	587
OY	744	agatccagcagctgatacggagagaaatgctaccacagctgtcttccttgactcttcgacattacc	803
Db	588	AGACACGTCATCCCTGATGAGAGAGACTCTTACCCACGCTTCTGTAACTCCCTCGCTTACC	647
OY	804	tggaaatgtgtagagatgtygggggagaaacacagcttaccatgagttaaaggggagactgggga	863
Db	648	GGGACCTTGCTGCCCAAGCCTCACCAGCCGCTTGCCCACTGTGTCCAGTGTGCAGGCTGGACC	707
OY	864	gcttaagaagcttctatgtgtgctactctcccccacttgaatgaagaagagagtgtaactgtg	923
Db	708	AGCCCTTCACACACCTGAGTCTCCACGGCAGTGAAGAAAGCCAGCCGGGAAAGAGAGGTTGAG	767
OY	924	cggactctaagtgaanaactcaccacacacggtyggttgctgtgtccaggaanaac	975
Db	768	TCACCATTCGCCAGGTGGCTGCCCTCTGTGTGGAGAGCAGGTTCTGCAAAAGC	819

RESULT 6
 US-08-463-074B-1
 : Sequence 1, Application US/08463074B
 : Patent No. 6020155
 : GENERAL INFORMATION:
 : APPLICANT: Smith, Kendall A. & Beadling, Carol
 : TITLE OF INVENTION: Nucleic Acids Encoding CRI Fusion Protein, Vector an
 : NUMBER OF SEQUENCES: 35
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: PRETTY, SCHROEDER & POPLAMSKI
 : ADDRESSSEE: (B) STREET:
 : CITY: Los Angeles
 : STATE: California
 : COUNTRY: USA
 : ZIP: 90071
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentin Release #1.0,
 : SOFTWARE: Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/463,074B
 : FILING DATE: 5-JUN-1995
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 08/104,736
 : FILING DATE: 10-AUG-1993
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 07/796,066
 : FILING DATE: 20-NOV-91
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Viviana Amzel, Ph. D.
 : REGISTRATION NUMBER: 30,930
 : REFERENCE/DOCKET NUMBER: P66 38143 (PART-020)
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (213) 622-7700
 : TELEFAX: (213) 489-4210
 : INFORMATION FOR SEQ ID NO: 1:
 : SEQUENCE CHARACTERISTICS:
 :

LENGTH: 2406 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 116..722
US-08-463-074B-1

Query Match 2.1%; Score 58.8; DB 3; Length 2406;
Best Local Similarity 47.2%; Pred. No. 2.5e-06;
Matches 251; Conservative 0; Mismatches 272; Indels 9; Gaps 2;

QY 444 ggtgagcaagctcttaccctccttggtggtgagcagatggtacatcttcgga 503
DB 297 ggtgagagagctggttcgactgctgagcagatggtgagtggtgcttcacg 356
QY 504 cttctcgtgaggggagaaatggtggtatagctggtggttctgttgaatggt 563
DB 357 cttctcgtgagggagaaatggtggtatagctggtggttctgttgaatggt 563
QY 564 tcagagcagatgagctgaaagatggtacaaacttgctgagtggtgagcagatcaga 623
DB 417 tca---agaaatccgagatgagctgagcagctgagcagcagcagcagcagcagc 473
QY 624 ggtgagcagatgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 683
DB 474 agttcatttg-----cagtgagggccctaaagagctcaaatgagcagcagcagcagc 527
QY 684 taccgagatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 743
DB 528 agctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 587
QY 744 agatccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 803
DB 588 agacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 647
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QY 924 ccgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 975
DB 768 tcacccatcccgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 819

RESULT 7
US-08-465-585C-1
Sequence 1, Application US/08465585C
Patent No. 6027914
GENERAL INFORMATION:
APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR6 Polypeptide, Vector
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHRÖDER & POPLAWSKI
ADDRESS: (B) STREET: 444South Flower St. - Suite 190
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 900071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,585C
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/330,108
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 20-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38149 (DART-050)
TELEPHONE: (213) 622-7700
TELEFAX: (213) 4894210
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2406 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 116..722
US-08-465-585C-1

Query Match 2.1%; Score 58.8; DB 3; Length 2406;
Best Local Similarity 47.2%; Pred. No. 2.5e-06;
Matches 251; Conservative 0; Mismatches 272; Indels 9; Gaps 2;

QY 444 ggtgagcaagctcttaccctccttggtggtgagcagatggtacatcttcgga 503
DB 297 ggtgagagagctggttcgactgctgagcagatggtgagtggtgcttcacg 356
QY 504 cttctcgtgagggagaaatggtggtatagctggtggttctgttgaatggt 563
DB 357 cttctcgtgagggagaaatggtggtatagctggtggttctgttgaatggt 563
QY 564 tcagagcagatgagctgaaagatggtacaaacttgctgagtggtgagcagatcaga 623
DB 417 tca---agaaatccgagatgagctgagcagcagcagcagcagcagcagcagcagc 473
QY 624 ggtcagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 743
DB 474 agttcatttg-----cagtgagggccctaaagagctcaaatgagcagcagcagcagc 527
QY 684 taccgagatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 743
DB 528 agctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 587
QY 744 agatccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 803
DB 588 agacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 647
QY 804 tggaaatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 863
DB 648 gggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 707
QY 864 ggtcagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 923
DB 708 accctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 767
QY 924 ccgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 975
DB 768 tcacccatcccgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 819

RESULT 8
US-08-652-446-1

Sequence 1, Application US/08652446
Patent No. 6057427

GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Reading, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CRS
TITLE OF INVENTION: Polypeptide, Vector and Transformed Cell Thereof, and
TITLE OF INVENTION: Expression Thereof
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
ADDRESSER: (B) STREET:
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,446
FILING DATE:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP App. # 96921319.8
FILING DATE: 5-JAN-1998
APPLICATION NUMBER: PCT/US/96/09194
FILING DATE: 5-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,108
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/463,074
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,337
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,390
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,585
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/463,081
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/461,379
FILING DATE: 5-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/739,523
FILING DATE: 29-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: FP66 40035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
INFORMATION FOR SRD ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2406 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:

NAME/KEY: CDS
LOCATION: 116..722
US-08-652-446-1

444 South Flower St. - Suite 1900

```
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38150 (DART-060)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 606 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-463-081B-27

Query Match          2.0%; Score 57.2; DB 2; Length 606;
Best Local Similarity 51.4%; Pred. No. 3.4e-06;
Matches 187; Conservative 0; Mismatches 168; Indels 9; Gaps 2;

OY 444 ggtagcaagtccttaccctccttggtggtgacagatggtgcatcctcttcgga 503
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 182 ggtgagagagtcgttcgacgtgctgacagatgagaaatgagtgcttcacag 241

OY 504 ctttcctgagagaggaagaaatgltggtgatacgtctgactcttggtcttgaatggt 563
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DB 242 ctttcttgaaagacagatgctgagtgagAACCTGGAGTTCTGGCTGGAGAGT 301

OY 564 tcaggcagatgacctgaaagatgatacaaaacttgagtgagtgccaaagaatctataaga 623
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DB 302 tca---AGAGATCCGATACGATACCAAGCTGCTCCAGGGCACCAGATCTTTGAGG 358

OY 624 ggtacatgagaacaacagcgtgtgtctccaagcagctgaaagccgacaaagactaca 683
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 359 ACTTCATTG-----CACTGAGGCCCTAAAGAGTCAACATTTGACATGAGACCCGGG 412

OY 684 ttcgagatgcatcagaagaacagatcgctcggtcgtgcatglttgaccagagcaagcgg 743
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 413 AGCTGACGAGATGAACCTGACAGACTGCCACAGCCCATGCTTTGATGCGCTCAGGGGA 472

OY 744 agatccagcagtgatgaggaagaatgctaccaggtgttcttgacttgacattacc 803
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 473 AGACACGATACCTGATGGAAGAGACTCTTACCACAGCTTCTGGAAGTCCCTGCTTACC 532

OY 804 tggg 807
    |||
DB 533 GGGA 536

RESULT 10
US-08-461-379A-27
; Sequence 27, Application US/08461379A
; Patent No. 5871961
; GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A. & Beadling, Carol
; TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
; TITLE OF INVENTION: Vector and Transformed Cell Thereof, and
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; CITY: Valley Forge
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0,
; SOFTWARE: Version #1.25
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,379A
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/330,108; 08/104,736
APPLICATION NUMBER: 6 07/796,066
FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: DART-070
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)470-0700
TELEFAX: (610)470-0701
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 606 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-461-379A-27

Query Match          2.0%; Score 57.2; DB 2; Length 606;
Best Local Similarity 51.4%; Pred. No. 3.4e-06;
Matches 187; Conservative 0; Mismatches 168; Indels 9; Gaps 2;

OY 444 ggtagcaagtccttaccctccttggtggtgacagatggtgcatcctcttcgga 503
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 182 ggtgagagagtcgttcgacgtgctgacagatgagaaatgagtgcttcacag 241

OY 504 ctttcctgagagaggaagaaatgltggtgatacgtctgactcttggtcttgaatggt 563
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 242 ctttcttgaaagacagatgctgagtgagAACCTGGAGTTCTGGCTGGAGAGT 301

OY 564 tcaggcagatgacctgaaagatgatacaaaacttgagtgagtgccaaagaatctataaga 623
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 302 tca---AGAGATCCGATACGATACCAAGCTGCTCCAGGGCACCAGATCTTTGAGG 358

OY 624 ggtacatgagaacaacagcgtgtgtctccaagcagctgaaagccgacaaagactaca 683
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 359 ACTTCATTG-----CACTGAGGCCCTAAAGAGTCAACATTTGACATGAGACCCGGG 412

OY 684 ttcgagatgcatcagaagaacagatcgctcggtcgtgcatglttgaccagagcaagcgg 743
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 413 AGCTGACGAGATGAACCTGACAGACTGCCACAGCCCATGCTTTGATGCGCTCAGGGGA 472

OY 744 agatccagcagtgatgaggaagaatgctaccaggtgttcttgacttgacattacc 803
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 473 AGACACGATACCTGATGGAAGAGACTCTTACCACAGCTTCTGGAAGTCCCTGCTTACC 532

OY 804 tggg 807
    |||
DB 533 GGGA 536

RESULT 11
US-08-462-390B-27
; Sequence 27, Application US/08462390B
; Patent No. 5882894
; GENERAL INFORMATION:
; APPLICANT: Smith, K. A., & Beadling, C.
; TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and
; TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; CITY: Valley Forge
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19482
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 6, 2001, 18:41:56 ; Search time 3054.04 Seconds
(without alignments)
8080.928 Million cell updates/sec

Title: US-09-587-574-6

Perfect score: 2825
Sequence: 1 cagccgtcgcgatgatc.....accctgtctcagcctacgc 2825

Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 4368049070 residues

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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190: em_gss_pin1:*	17.0	798	140	BE872155	BE872155 601446262	
191: em_gss_pin2:*	15.5	591	102	A1818109	A1818109 WK27C05.x	
192: em_gss_pro:*	15.2	732	140	BE882875	BE882875 601509279	
193: em_gss_rod1:*	14.9	621	122	AW962356	AW962356 EST374429	
194: em_gss_rod2:*	13.9	543	177	A1220032	A1220032 9978B02.x	
195: em_gss_rod3:*	13.3	548	7	AA463378	AA463378 z558B07.f	
196: em_gss_rod4:*	13.1	427	149	BF521997	BF521997 UT-R-Y0-R	
197: em_gss_rod5:*	13.0	471	169	BF812711	BF812711 RC3-C1019	
198: em_gss_vrt1:*	12.8	521	168	BF757617	BF757617 MR2-CT059	
199: em_gss_vrt2:*	12.1	463	103	A1912345	A1912345 tz24C04.x	
200: em_gss_vrt3:*	11.9	1068	231	CNS03YD0	AL266841 Tetradon	
201: gb_gss1:*	11.7	830	230	CNS03YD0	AL172875 Tetradon	
202: gb_gss2:*	11.6	399	8	AA489748	AA489748 aa43B02.f	
203: gb_gss3:*	11.5	487	18	A1307112	A1307112 q189F01.x	
204: gb_gss4:*	11.4	460	20	A1419942	A1419942 tg40D11.x	
205: gb_gss5:*	11.1	459	18	A1722864	A1722864 q143B03.x	
206: gb_gss6:*	10.7	308	142	BF021386	BF021386 ux56a02.x	
207: gb_gss7:*	10.4	444	13	AA937585	AA937585 of71h02.s	
208: gb_gss8:*						
209: gb_gss9:*						
210: gb_gss10:*						
211: gb_gss11:*						
212: gb_gss12:*						
213: gb_gss13:*						
214: gb_gss14:*						
215: gb_gss15:*						
216: gb_gss16:*						
217: gb_gss17:*						
218: gb_gss18:*						
219: gb_gss19:*						
220: gb_gss20:*						
221: gb_gss21:*						
222: gb_gss22:*						
223: gb_gss23:*						
224: gb_gss24:*						
225: gb_gss25:*						
226: gb_gss26:*						
227: gb_gss27:*						
228: gb_gss28:*						
229: gb_gss29:*						
230: gb_gss30:*						
231: gb_gss31:*						
232: gb_gss32:*						
233: gb_gss33:*						
234: gb_gss34:*						

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

C	19	290.6	10.3	546	13	AA915999	AA915999 oh86g11.s
	20	285	10.1	495	139	BE755017	BE755017 208720 MA
	21	276.8	9.8	447	13	AA903395	AA903395 ok62b09.s
	22	271.8	9.6	418	103	AI858567	AI858567 w164d08.x
	23	266.8	9.4	902	231	CNS03G20	AI243621 Tetracodon
	24	261.4	9.3	409	8	AA489644	AA489644 aa43d02.s
	25	257	9.1	375	5	AA305361	AA305361 EST176379
	26	256.4	9.1	413	19	AI336613	AI336613 q062c07.x
	27	247	8.7	363	18	AI262837	AI262837 qk3b08.x
	28	240	8.5	408	23	AI660139	AI660139 we61a09.x
	29	236.2	8.4	257	135	BB523213	BB523213 BB523213
	30	219.6	7.8	345	24	AI742962	AI742962 wq76d09.x
	31	214.6	7.6	383	112	AM207598	AM207598 UT-H-B11-
	32	208	7.4	651	141	BE894571	BE894571 601433182
	33	207.8	7.4	391	13	AA884421	AA884421 am16d12.s
	34	206.6	7.3	282	134	BB481314	BB481314 BB481314
	35	201.6	7.1	975	230	CNS03J74	AI226201 Tetracodon
	36	179.4	6.4	299	19	AI363868	AI363868 qy60a10.x
	37	175.4	6.2	956	150	BF582324	BF582324 602101153
	38	174.4	6.2	217	150	BF559312	BF559312 UT-R-E1-f
	39	170.2	6.0	585	140	BE854108	BE854108 ux27g03.y
	40	170	6.0	654	219	AZ315171	AZ315171 1M0032016
	41	168.6	6.0	269	161	BB597228	BB597228 BB597228
	42	168.2	6.0	546	138	BE668565	BE668565 158407 MA
	43	166	5.9	539	3	AA198606	AA198606 mu15d04.r
	44	162.2	5.7	285	117	AA56657	AA56657 fk03a11.y
	45	154	5.5	428	8	AA502360	AA502360 me26c11.s

ALIGNMENTS

RESULT 1
LOCUS BE872155 798 bp mRNA
DEFINITION 60146262F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850502 5',
mRNA sequence.
ACCESSION BE872155
VERSION BE872155.1 GI:10320931
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 798)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LHAM9569 row: k column: 15
High quality sequence stop: 544.
Location/Qualifiers
1. 798
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3850502"
/clone_lib="NIH_MGC_65"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: colon; Vector: pCMV-Sport6; Site:1: NotI;
Site:2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.8 kb. Library constructed by Life
Technologies."

FEATURES

source
BASE COUNT 218 a 229 c 207 g 144 t

ORIGIN
Query Match 17.0%; Score 480; DB 140; Length 798;
Best Local Similarity 81.7%; Pred. No. 1,5e-112;
Matches 629; Conservative 0; Mismatches 130; Indels 11; Gaps 6;

571 ggtgaacctgaagatcaccaaaacttgctgagtgagccaaagcaatcctataaggtacat 630
1 GATGAACCTGAAGATACCAAACTTACAGATACCAAAAGCATCTCAAAAGGTACAT 60
631 tggacaacaacagctgtgtctccaagcagcctgaagcccgccacaagaactatacag 690
61 TGAGAACAAAGCAGCTGTCTCCAAAGCAGCTGAAGCCCTCCCAAGACCTTAAGAGA 120
691 tggcatcaagaacaacagatcgctcgatcagtttgaccagagcagacagatca 750
121 TGCCATCAACAAAGCAGCTGTATTCATCATCATGTTGACAGCGCAGACAGATCCA 180
751 ggcagtgatgaggaatcctaccagcgtgtcttcttcttcttcttcttcttcttctg 810
181 GTGGGTATGAGAGAAATGCTTACAGATGTTTGTACTTGTGATTAATACCTGATA 240
811 tgtgagagtgaggggggaagaacaacagcttaccatgagtaacggggagcctaa 870
241 TGTGAGAGAGTGGGGGAGAAACACAGCTTACATGATTAATGGGGAGCTCGGAGCTAAA 300
871 gttctatgtgtgtacctcccaaccttgaaatgaagaagagtgagtggtgcagact 930
301 GT 360
931 caagtgaacacttccaccacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 990
361 CAAGTGAACCTTTCGCAACCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
991 ggtgtgagatccacggaacacagctgaagaacgagat-tcaggtctctca--gagaagcga 1047
421 GAGGTGAGGTCCACGGAACCTGTTGACAGTGGATCAAGGTCTTCAAGCAGAGACGA 480
1048 cccagtaactcctatcaagtaagttccggtatg-tctttgacacagcagcagcgca 1106
481 TCCTGTCAATCTTATACATAGATCTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGT 540
1107 acgacagcaggtc--atccagcagcagcagcagcagcagcagcagcagcagcagcag 1164
541 ACAGCATGATGATCATCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
1165 tagcgtatgagatccctctcctt--accgcatggggagtaagaacag---ctccagaga 1219
601 CCGGTACATGGAATTCCTCTTCATGCGGTGGCGCACTAAGAAACAGGCTCCAGAAAGA 660
1220 gagaatcagcagtgatgaagccaatgacaaatgtctctactcaatcttcagagaacc 1279
661 ACATGCGATCGCAGAGCGGAGCGCCACCGGACGCTGCCATTCCTCCATCCCAAAACC 720
1280 caccgctgcccgaagagatgagcgcctgtgaacctgtcgtcgcgcgc 1329
721 ACCGACGCGCCAGAGGAGGAGAGCCGCCGAGACCGGACCGGACCGGACCGGACCG 770

RESULT 2
LOCUS AI818109/c 591 bp mRNA
DEFINITION W427605.x1 NCI_CGAP_Brnz5 Homo sapiens cDNA clone IMAGE:2413544 3',
similar to TR:088566 O88566 CONDUCTIN.; mRNA sequence.
ACCESSION AI818109
VERSION AI818109.1 GI:5437188
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 591)

Db 313 AAGGAATTATAGTATTACTTCAAAAAAGCAAGCATGATTGGCTGTGAGGGCTG 372

Qy 2657 tttagagagatctggagacgagacagatgctcccatgtaagagagatcctgggc 2716
|||||

Db 373 TTTGAGAGATCTGGAGAGATGAGAGCGTGCTCCCATGTATGAGAGCCGATTTCTGGC 432

Qy 2717 aaatgagagatgagctgagctgagctgctc 2748
|||||

Db 433 AAGTGAGCGGATGATGATGAGCCCTGGGCTC 464

RESULT 7

BF521997 427 bp mRNA EST 11-DEC-2000
LOCUS
DEFINITION UI-R-Y0-acc-b-09-0-UI.r1 UI-R-Y0 Rattus norvegicus cDNA clone
ACCESSION BF521997
VERSION BF521997.1 GI:11629964
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 427)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
cDNA library preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LNLN (info@image.lnl.gov). IMAGE ID- 1791410
Seq primer: M13 forward.
Location/Qualifiers
1.427
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-Y0-acc-b-09-0-UI"
/clone_1lb="UI-R-Y0"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pTZ193D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; The UI-R-Y0
library is a subtracted library derived from an
individually-tagged normalized whole-eye (minus the lens)
library. The driver for the subtraction consisted of a
pool of all previous libraries (UI-R-A0, UI-R-A1, UI-R-E0,
UI-R-E1, UI-R-C0, and UI-R-C1). The tag is a string of
3-5 nucleotides present between the Not I site and the
oligo-dr track which allows identification of the library
of origin of a clone within the mixture. The subtracted
library (UI-R-Y0) was constructed as follows: PCR
amplified cDNA inserts from previous library clones from
which 3' ESTs had been derived were used as a driver in a
hybridization with the normalized whole-eye library in
the form of single-stranded circles. The remaining
single-stranded circles (subtracted library) was purified
by hydroxyapatite column chromatography, converted to
double-stranded circles and electroporated into DH10B
bacteria (Life Technologies) to generate the UI-R-Y0
library. This procedure has been previously described
(Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
1996)."

BASE COUNT 118 a 126 c 113 g 70 t
ORIGIN

Query Match 13.1%; Score 370.4; DB 149; Length 427;
Best Local Similarity 92.6%; Pred. No. 2.1e-84;
Matches 389; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 2234 caccacattaccagagacccatgcatgctcccttaaccaccaccacttggcacag 2293
|||||

Db 8 CACCCATTATCCAGAGACCCCTGCTATGCTCCCTTAACCCACCAACACCTTGGCCAG 67

Qy 2294 ctgagagaaagcctgctgagagagagagagagagagagagagagagagagagagag 2253
|||||

Db 68 CTAGAGAGAGAGCTGCGCGAGAGCTGCGAGAGTGTCAAGGCCAGAAACAGAGAGCTGTC 127

Qy 2354 gtggcagctcagcag 2413
|||||

Db 128 GTGGCAGATGAGCAG 187

Qy 2414 ttgcgcaaccagagcctgctgctcagaagatcacagaagcagaagagagagagagag 2473
|||||

Db 188 TTCTCCAAACCCGAGCGCTGCTCAGAGATCAGAAAGAGAGAGAGAGAGAGAGAGAGAG 247

Qy 2474 cagcgctccagcagcagctgagctgctgctgctgctgctgctgctgctgctgctgct 2533
|||||

Db 248 CACGACTCCAAACCCAG 307

Qy 2534 tacagagagatgctgag 2593
|||||

Db 308 TACAGAGAGATGCTGAG 367

Qy 2594 aaaaaggaaattacagagatatttcaagaaggcagagagagagagagagagagagag 2653
|||||

Db 368 AAAAAGGAATTACAGAGATTTACTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 427

RESULT 8

BF812711 471 bp mRNA EST 12-JAN-2001
LOCUS
DEFINITION RC3-C10195-221100-021-a10 C10195 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF812711
VERSION BF812711.1 GI:12142597
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 471)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, R.F.,
Goldman, G.H., Carvalho, A.F., Matsushima, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LIRC Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=RC3&t=RC3-C10195-
221100-021-a10&t3=2000-11-22&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 4

FEATURES High quality sequence stop: 471.
Location/Qualifiers
1. 471
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="C10195"
/dev_stage="Adult"
/note="Organ: colon lns; Vector: puc18; Site.1: Sma1;
Site.2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 114 a 116 c 136 g 105 t
ORIGIN

Query Match 13.0%; Score 367.6; DB 169; Length 471;
Best Local Similarity 90.0%; Pred. No. 1.1e-83;
Matches 394; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 851 ggggagctggggagcctaaagtcttatgtgctacctcccaacttgataagaagag 910
DB 34 gggggagctggggagcctaaagtctgtgtgctatctccacattgaatgaagaag 93
QY 911 gaggagctgtgctgagcctcaagtgaactctcaaccacggtgtgtgtccagc 970
DB 94 gaggagctgtgctgagcctcaagtgaactctcaaccacggtgtgtgtccagc 153
QY 971 aaactcttcgggacagcgagctgtgagatccacgaagaaacagctgaacagatcag 1030
DB 154 aaactcttcgggacagcgagctgtgagatccacgaagaaacagctgaacagatcag 213
QY 1031 tccctcaagagagagagcaccacatcaatccttcaagtgatgttcgggctgttgca 1090
DB 214 tccctcaagagagagagcaccacatccttcaagtgatgttcgggctgttgca 273
QY 1091 ccagccacagcgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1150
DB 274 ccagccacagcgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 333
QY 1151 tccatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1210
DB 334 tccatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 393
QY 1211 ctcagagagagagatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcat 1270
DB 394 ctcagagagagagatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcat 453
QY 1271 ccgagagacccacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1288
DB 454 ccgagagacccacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 471

RESULT 9
LOCUS BF757617 521 bp mRNA EST 12-JAN-2001
DEFINITION MR2-CT0596-091100-001-f12 CT0596 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF757617
VERSION BF757617.1 GI:12105621
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 521)
Dias Neto, E., Garcia Corra, R., Verjovski-Almeida, S., Brites, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l1=MR2at2-MR2-CT0596-
091100-001-f12&t3=2000-11-09&t4=1)

BASE COUNT 135 a 107 c 161 g 118 t
ORIGIN

Query Match 12.8%; Score 363; DB 168; Length 521;
Best Local Similarity 84.1%; Pred. No. 1.7e-82;
Matches 433; Conservative 0; Mismatches 80; Indels 2; Gaps 2;

QY 731 caggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 789
DB 7 caggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 66
QY 790 tctgacatctaaccttgagatctgagagctggggggaagaaacagcctacatgagtaa 849
DB 67 tctgacatctaaccttgagatctgagagctggggggaagaaacagcctacatgagtaa 126
QY 850 cggggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 909
DB 127 cggggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 186
QY 910 ggaatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 969
DB 187 ggaatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 246
QY 970 caaaactcttcgggacagcgagctgtgagatccagcaggaacagcagcagcagcagcagcagc 1029
DB 247 caaaactcttcgggacagcgagctgtgagatccagcaggaacagcagcagcagcagcagcagc 306
QY 1030 gtccctcaagagagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1088
DB 307 gtccctcaagagagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 366
QY 1089 caccagc 1148
DB 367 caccagc 426
QY 1149 tctcatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1208
DB 427 tctcatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 486
QY 1209 agctccagagagagatgcatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1243

```

Db 487 AGCTCCAGAGAAATGCTTGCAGTGTCAAGCC 521
|||||
RESULT 10
AI912345 463 bp mRNA EST 16-DEC-1999
LOCUS t234c04.x1 NCI CGAP ut2 Homo sapiens cDNA clone IMAGE:2289510 3'
DEFINITION similar to TR:070240 070240 AXIL.; mRNA sequence.
ACCESSION AI912345
VERSION AI912345.1 GI:56322200
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 463)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
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Seq primer: -400P from Gibco
High quality sequence stop: 414.
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adenocarcinoma, 3 pooled tumors"
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VERSION AL266841.1
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SOURCE Tetradon nigroviridis.
ORGANISM Tetradon nigroviridis.
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Holacanthopterygii; Acanthopterygii; Percormorpha;
Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetradon.
1 (bases 1 to 1068)
Roest-Crollius,H., Jallou,O., Dasilva,C., Fizames,C., Fisher,C.,
Bonneau,L., Billault,A., Queller,F., Saurin,W., Bernot,A. and
Weissenbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetradon nigroviridis
Unpublished
2 (bases 1 to 1068)
Roest-Crollius,H., Jallou,O., Dasilva,C., Bonneau,L., Fisher,C.,
Bernot,A., Fizames,C., Mincker,P., Brothier,P., Queller,F.,
Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using
Tetradon nigroviridis DNA sequence
Unpublished
3 (bases 1 to 1068)
Genoscope.
Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetradon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetradon.
Location/Qualifiers
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 sequence.

ACCESSION AL172875.1 GI:7810932
 VERSION AL172875
 KEYWORDS GSS: genome survey sequence.
 SOURCE Tetraodon nigroviridis.

ORGANISM Tetraodon nigroviridis

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 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Eurypterygii; Ctenosquamata; Acanthomorpha; Eucanthomorpha;
 Holacanthopterygii; Acanthopterygii; Percomorpha;

Tetraodontiformes; Tetraodontidae; Tetraodon.
 1 (bases 1 to 830)

REFERENCE 1 Roest-Crolius,H., Jallion,O., Dasilva,C., Fitzames,C., Fisher,C.,
 Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and

TITLE Weissbach,J.
 CHARACTERIZATION AND REPEAT ANALYSIS OF THE COMPACT GENOME OF THE
 FRESHWATER PUFFERFISH TETRAODON NIGROVIRIDIS
 REFERENCE 2 (bases 1 to 830)
 AUTHORS Roest-Crolius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C.,
 Bernot,A., Fitzames,C., Wincker,P., Brothier,P., Quetier,F.,
 Saurin,W. and Weissbach,J.
 TITLE Human gene number estimate provided by genome wide analysis using
 Tetraodon nigroviridis DNA sequence
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 830)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
 COMMENT This sequence is a single read and was generated as part of a large
 scale clone-end sequencing project of the Tetraodon nigroviridis
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 http://www.genoscope.cns.fr/Tetraodon.
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 7373929652 residues
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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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7	308.2	83.5	2538 88	AF205888 Homo sapi
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9	308.2	83.5	184263 85	AC004805 Homo sapi
10	227.2	61.6	3485 8	AB032263 Dando rer
11	163.4	44.3	3156 8	AF009012 Gallus ga

12 161.2 43.7 3411 88 AF009674 Homo sapi
c 13 161.2 43.7 23786 91 HS415C1
c 14 161.2 43.7 35054 91 HS33810
c 15 161.2 43.7 39170 85 AC005202
c 16 161.2 43.7 133069 70 AC026836
c 17 161.2 43.7 187272 74 AC069076
18 150 40.7 2329 8 AF097313
19 149 40.4 3460 9 AF017756
20 148.8 40.3 3066 8 AB032652
21 147.4 39.9 3761 94 AF009011
22 119 32.2 2121 8 AF140243
23 64.8 17.6 910 7 AF011361
24 56.8 15.4 2638 93 HS027655
25 35.2 15.0 606 9 AR035823
26 35.2 15.0 606 9 AR035850
27 2132 93 HS094829
28 55.2 15.0 2383 10 165400
29 55.2 15.0 2383 93 HS070426
30 55.2 15.0 2406 9 AR035805
31 55.2 15.0 2406 9 AR035832
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34 52 14.1 606 94 MMU07427
35 52 14.1 2272 9 AR064044
36 50.4 13.7 838 94 MMU07281
37 50.4 13.7 995 94 MMU067189
38 50.4 13.7 2250 94 MMU094828
39 48.4 13.1 1587 92 HSPAIR
40 47.2 12.8 3494 94 AB060613
41 47 12.7 147048 89 AL353778
42 47 12.7 186051 64 AC015683
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44 45.6 12.4 543 88 AF300649
45 45.6 12.4 765 88 AF297015S1

ALIGNMENTS

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LOCUS Sequence 7 from Patent WO911780.
ACCESSION A98522
VERSION A98522.1 GI:6781608
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 369)
AUTHORS Birchmeier, W. and Behrens, J.
TITLE CONDUCTIVE PROTEIN AND A RELATED AGENT FOR DIAGNOSING AND TREATING
TUMOR ILLNESSES
JOURNAL Patient: WO 9911780-A 7 11-MAR-1999;
BIRCHMEIER WALTER (DE); BEHRENS JUERGEN (DE)
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RESULT 2
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LOCUS Sequence 6 from Patent WO911780.
ACCESSION A98521
VERSION A98521.1 GI:6781607
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2825)
AUTHORS Birchmeier, W. and Behrens, J.
TITLE CONDUCTIVE PROTEIN AND A RELATED AGENT FOR DIAGNOSING AND TREATING
TUMOR ILLNESSES
JOURNAL Patient: WO 9911780-A 6 11-MAR-1999;
BIRCHMEIER WALTER (DE); BEHRENS JUERGEN (DE)
FEATURES
source Location/Qualifiers
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 4.4e-94;
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DB 301 ATCCAGCAGATGATGAGAAATGCTTACCAAGATGTTGACTTGTGACATTTACCTG 360

Db 746 ATCCAGCAGTGTGAGGAGGAAATGCTTACACAGTGTCTTGACTTCTGACATTACTG 805
QY 361 gaataatgtg 369
Db 806 GAATATGTG 814

RESULT 3
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LOCUS Mus musculus conductin mRNA, complete cds.
DEFINITION AF073788
ACCESSION AF073788
VERSION AF073788.1 GI:3309246
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2825)
Behrens, J., Jerchow, B.-A., Wurttele, M., Grimm, J., Ashbrand, C.,
Wirtz, R., Kuhl, M., Wedlich, D. and Birchmeier, W.
Functional interaction of an axin homolog, conductin, with
beta-catenin, APC, and GSK3beta
Science 280 (5363), 596-599 (1998)
9821239
2 (bases 1 to 2825)
Behrens, J., Jerchow, B.-A. and Birchmeier, W.
Direct Submission
Submitted (22-JUN-1998) Cellular Biology, Max Delbrueck Center for
Molecular Medicine, Robert-Rössle 10, Berlin 13122, Germany

FEATURES
Source
Location/Qualifiers
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BASE COUNT 703 a 815 c 813 g 494 t
ORIGIN

Query Match 100.0%; Score 369; DB 94; Length 2825;
Best Local Similarity 100.0%; Pred. No. 4.4e-94;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 446 TGGACCAAGTCTTTACACCTCTGTGGTGAGACAGATGCTGCATACCTTCGCGAG 505
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QY 61 ttccttgagagaggaatggtgtgatacgcctggaacttctgttcttgtaatgggttc 120
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Db 506 TTCCTTGAGAGGAGAAATGTGTGATACGCTGACCTTCTGTGTAATGGGTTCC 565
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QY 121 aggcagagtgaaacttgagagataccaaaacttggcagtgaggccaaagaactctataagag 180
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Db 566 AGGCAGATGACCTGAAGATACCAAACTTTGCGATGGGCCAAAGCAATCTATAAGAG 625
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Db 626 TACATTGAGAACACACAGCGCTTGTCTCCAAAGCAGCTGAAGCCGCCACCAAGACTACATA 685
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QY 241 cgaagatgcatcaagaagaacacagatcgctggtatgtttgacaggacagaccagag 300
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Db 686 CGAGATGATCAAGAAAGCAACAGATCGCTCGCTATGTTTACCAAGCACAGACCGAG 745
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QY 301 atccagcagtgatgaggaagaatgcctaccagtgcttcttgactctgacattacctg 360
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Db 746 ATCCAGCAGTGTGAGGAGGAAATGCTTACACAGTGTCTTGACTTCTGACATTACTG 805
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QY 361 gaataatgtg 369
Db 806 GAATATGTG 814

RESULT 4
AC024114 191041 bp DNA HTG 06-NOV-2000
LOCUS AC024114/C
DEFINITION Mus musculus chromosome 11 clone RP23-278J12, WORKING DRAFT
SEQUENCE, 30 unordered pieces.
AC024114
AC024114.8 GI:11094615
VERSION AC024114.8 GI:11094615
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 191041)
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Meizker, M.L., Lewis, L.R., Hume, J., Edwards, C., Harris, C.,
Dederich, D., Thomas, S., Okwuonu, G., Carllock, C., Garner, T.,
Addison, S., Pace, A., Williams, G., Bonnin, D., Brooks, A., Brown, J.,
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Cox, C., Davis, C., Delgado, O., Ding, Y., Dugan-Rocha, S.,
Fernandez, C., Ferraguto, D., Forcum-Tansey, J., Gill, R.,
Gorrell, J.H., Gunaratne, P., Haller, G., Hernandez, J., Hogues, M.,
Hosack, H., Hou, X., Huber, J., Jackson, L., Jia, Y., Kelly, J., Kelly, S.,
Kovar, C., Liu, J., Liu, W., Louisedge, H., Lozada, R.J., Martin, R.,
Massey, E., McLeod, M.P., Mei, G., Moore, S., Morgan, M., Morris, S.,
Neal, D., Nelson, A., Nguyen, R., Nguyen, N., Ogun, M., Parish, B.,
Perez, L., Relfer, D., Say, J., Shen, H., Vasquez, L., Watlington, S.,
Williamson, A., Wrensford, G., Zhou, X., Bouck, J., Hodgson, A.,
Muzny, D.M., Rives, M., Scherer, S., Sodergren, E., Weinstock, G.,
Worley, K. and Gibbs, R.
Direct Submission
Unpublished
2 (bases 1 to 191041)
Worley, K.C.
Direct Submission
Submitted (24-FEB-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 4, 2000 this sequence version replaced gi:9929587.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: MACA
Center clone name: RP23-278J12
----- Summary Statistics
Sequencing vector: M13: 108821
Chemistry: dye-primer Bodipy: 95% of reads
Chemistry: dye-terminator Big Dye: 5% of reads
Assembly program: Phrap: version 0.990329
Consensus quality: 158769 bases at least Q40
Consensus quality: 172780 bases at least Q30
Consensus quality: 179030 bases at least Q20
Estimated insert size: 180377; sum-of-ctrls estimation

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BASE COUNT	766 a 858 c 837 g 555 t
ORIGIN	
Query Match	99.1%; Score 365.8; DB 94; Length 3016;
Best Local Similarity	99.5%; Pred. No. 3.6e-93;
Matches 367; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
Oy	1 tggaccaagctcttaacacccctgtgttggtgagcagaatgagcatatcccttcgcgact 60
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Oy	61 ttccctggagaaggagaatgctgtgatacgtctgactcttgcttgtaatgggttc 120
Db	346 TTCCTGGAAGAAGAAATGTGTGATACGCTGACCTTGCTGTTGCTGTATGGGTTG 405
Oy	121 aggcagatgaacctgagaatataccaaacttgcgagtgagccaaagcaatcttaagagg 180
Db	406 AGGCAGATGAACTTGAAGATATACCAAACTTGGCGAGTGCCAAACCAATCTTAAGAGG 465
Oy	181 tacattgagaacaacagcgttgtctccaagcagctgaagccgcacccaagactcata 240
Db	466 TACATTGAGAACACACGCGTGTCTCCAAAGCACTGAAGCCGCCCAACAGACTTACATA 525
Oy	241 cgaagatgacatacaagaacagatcgcgtcgtcatgtttgacacagcagacagcag 300
Db	526 CGAGATGGCATCAAGAAGCAAGATCGGCTCGTCAATGTTTACCAAGCAGACGCGAG 585
Oy	301 atccagagcagtgatgaggaataatgcttaccaggtgttcttgactctgacattacgtg 360
Db	586 ATCCAGGCAAGTGTGAGGAAATGCTTACCAAGTGTCTTGACTTGTGACATTTACTG 645
Oy	361 gaatatgtg 369
Db	646 GAATATGTG 654
RESULT 6	
AF017757	3216 bp mRNA
LOCUS	AF017757 Rattus norvegicus GSK-3beta Interacting protein Axin mRNA, complete cds.
DEFINITION	Rattus norvegicus GSK-3beta Interacting protein Axin mRNA, complete cds.
ACCESSION	AF017757
VERSION	AF017757.1 GI:3080758
KEYWORDS	
SOURCE	Norway rat.
ORGANISM	Rattus norvegicus
REFERENCE	Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
AUTHORS	1 (bases 1 to 3216) Yamamoto,H., Kishida,S., Uochi,T., Ikeda,S., Koyama,S., Asashima,M.

TITLE	and Kikuchi,A. Axin, a member of the Axin family, interacts with both glycogen synthase kinase 3beta and beta-catenin and inhibits axis formation of Xenopus embryos
JOURNAL	Mol. Cell. Biol. 18 (5), 2867-2875 (1998)
MEDLINE	98226558
REFERENCE	2 (bases 1 to 3216)
AUTHORS	Yamamoto,H., Ikeda,S., Mural,H., Kishida,S. and Kikuchi,A.
TITLE	Direct Submission
JOURNAL	Submitted (08-Aug-1997) Biochemistry, Hiroshima University, School of Medicine, 1-2-3 Kasumi, Minami-ku, Hiroshima 734, Japan
FEATURES	
source	Location/Qualifiers 1..3216 /organism="Rattus norvegicus" /db_xref="taxon:10116" 85..2601 /note="GSK-3beta Interacting protein; Axin like protein" /codon_start=1 /product="Axin" /protein_id="AAC40089.1" /db_xref="GI:3080759" /translation="MSSAVLVTLPLDPSSSFREDAPRPVPEEGEETPPCPSGVKQV STKPMVSSNARNEDGLGEPGRASPDSPLTRMTKSLHSLIGDDGAVLFTPLERE KCVDTLDFWFCNCRFQNMNLKDTKTLRAKAIYKRIENNSVSKOLKPATYIIRDG IKKQOIGSVMPDOAQTEIQAVMEENAYOVFLSDIYLYEVRSRGENTAYMSNGLGSL IKLCGYLPTLNEEEMTCADLCKLSPTVYGLSKTLRATASVSTETAENGFRSKFR SDPVYHVGSGVFAFAPATSAANDSELSDALTDSDMSMTDSSVDGIPPMKSKLOL REMRSVKANGOVSLPHFPRTHRLPKEMTPVPAFAELISRLKLELSRSLLE ERLQOIRDEEEKESQALSRDGA PVQHPALPLSGSYEDPOTILDDHLSRVLTPT GCOSPGVRSFSPRSRPHHHOYHHCOTHTLPTGKLPVACPLGKSSLYKTOTK TKHHNHYIHHNAVPTKEEIEAETORVRCJPGDYCYCKSKSRKAEPLDGE OFCGSRGCTLPKRNKGTPEGLALSRDGSMSAGAPOLPEEGDSODVOMWMLSE EROSKSPHSAOSIRKSYPLESARAPEVRSRHHLLGASGHSVRAHAPPTODPAM PLTPPMTLQLEACRILAEVSKPOKORCCVSAQOORNNHSAAGACAGSPANSLA PDHKEPKKLASVHALQASLIVYTFPGCEIEIPYRMILKAQSLTIGHREQLSKGNVY YFKKASDERACGAVFEIWDDEVLPMEYGRILGKVERID"
CDS	
BASE COUNT	860 a 914 c 872 g 570 t
ORIGIN	
Query Match	91.3%; Score 337; DB 94; Length 3216;
Best Local Similarity	94.6%; Pred. No. 5.3e-85;
Matches 349; Conservative	0; Mismatches 20; Indels 0; Gaps 0;
Oy	1 tggaccaagctcttaacacccctgtgttggtgagcagaatgagcatatcccttcgcgact 60
Db	316 TGGACCAAGCTCTTTGACACTCTCTTGGGGGACCAAGATGTCATACCTTCCGCGACT 375
Oy	61 ttccctggagaaggagaatgctgtgatacgtctgactcttgcttgtaatgggttc 120
Db	376 TTCCTGGAAGAAGAAATGTGTGATACGCTGACCTTGCTGTTGCTGTATGGGTTG 425
Oy	121 aggcagatgaacctgagaatataccaaacttgcgagtgagccaaagcaatcttaagagg 180
Db	436 AGGCAGATGAACTTGAAGATATACCAAACTTGGCGAGTGCCAAACCAATCTTAAGAGG 495
Oy	181 tacattgagaacaacagcgttgtctccaagcagctgaagccgcacccaagactcata 240
Db	496 TACATTGAGAACAAAGTGTCTCCAAAGCACTGAAGCCGCCCAACAGACTTACATA 555
Oy	241 cgaagatgacatacaagaacagatcgcgtcgtcatgtttgacacagcagacagcag 300
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Oy	301 atccagagcagtgatgaggaataatgcttaccaggtgttcttgactctgacattacgtg 360
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Oy	361 gaatatgtg 369
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RESULT 7
AF205888 2538 bp mRNA PRI 03-JAN-2000
LOCUS Homo sapiens AXIN2 (AXIN2) mRNA, complete cds.
DEFINITION AF205888
ACCESSION AF205888.1 GI:6653583
VERSION
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2538)
AUTHORS Zhang,T., Fagotto,F., Hsu,W., Zeng,L., Gilbert,D., Copeland,N.G.,
Jenkins,N.A., Warburton,D. and Costantini,F.
Properties of mouse Axin2 and human AXIN2: chromosomal location,
expression pattern, interaction with Axin and effects on embryonic
axis formation
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2538)
AUTHORS Zhang,T. and Costantini,F.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-1999) Genetics & Development, Columbia
University, 701 W168th St. HNSC 1416, New York, NY 10032, USA
LOCATION/Qualifiers
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EPKTLGVHAQASAEIVYVTFPGCEETPYRMLKAOSLTIGHFKEOLSKKNYNYEK
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BASE COUNT 617 a 724 c 724 g 473 t
ORIGIN
Query Match 83.5%; Score 308.2; DB 88; Length 2538;
Best Local Similarity 89.7%; Pred. No. 7.6e-77;
Matches 331; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 1 ttgaccagcttctacacccctgttggtgaccagagatgtagcatctctccgagact 60
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DB 338 TGGACCAAGTCTTTACACCTTATTGGCGCATCAAGACGGTGCTTACTGTTCCGAAT 397
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QY 61 ttccctggagagagaaatgtagatgtagatgtagatgtagatgtagatgtagatg 120
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DB 398 TTCCCTGGAGAGGAGAAATGCTGATACCTTAGACTTCTGTTGGCCGCAATGATTC 457
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QY 121 aggcagatggaactgaagatggaactgtagatgtagatgtagatgtagatgtagatg 180
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DB 458 AGGCAGATGAACCTTGAAGATACCAAACTTTACGAGTACGCAAAAGCGATACCAAAAG 517
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QY 181 tacattgagaacacagcgtgtgtctccaaagcagctgaagcccgcccaagaacctacata 240
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QY 301 atccagagcagtgatgagagaaatgagctaccagagtgcttctgactctgacattaccctg 360
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DB 638 ATCCAGTCGCTGATGAGAGAAATGCTTACCAAGATGTTTGTGACTTCTGATATATACCTC 697
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QY 361 gaatatgtg 369
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DB 698 GAATATGTG 706
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RESULT 8
AF078165 3072 bp mRNA PRI 21-MAR-1999
LOCUS AF078165 Homo sapiens conductin mRNA, complete cds.
DEFINITION AF078165
ACCESSION AF078165
VERSION AF078165.1 GI:4454790
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 3072)
AUTHORS Mai,M., Qian,C., Yokomizo,A., Smith,D.I. and Liu,W.
TITLE Cloning of the human homolog of conductin (AXIN2), a gene mapping
to chromosome 17q23-q24
JOURNAL Genomics 55 (3), 341-344 (1999)
MEDLINE 99168905
REFERENCE 2 (bases 1 to 3072)
AUTHORS Mai,M., Qian,C., Smith,D.I. and Liu,W.
TITLE Direct Submission
JOURNAL Submitted (15-JUL-1998) Lab Medicine and Pathology, Mayo clinic,
200 First Street SW, Rochester, MN 55905, USA
LOCATION/Qualifiers
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RLQOIRDEDEREGSELTINSREGAPTDHPLSLSGSTEEDPOTLDDHLSVLTGK
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EPKTLGVHAQASAEIVYVTFPGCEETPYRMLKAOSLTIGHFKEOLSKKNYNYEK
KASDFRACGAFEEIWEDEVLPMTREGTILKVERID"

BASE COUNT 769 a 838 c 883 g 582 t
ORIGIN
Query Match 83.5%; Score 308.2; DB 88; Length 3072;
Best Local Similarity 89.7%; Pred. No. 7.7e-77;

Matches	331;	Conservative	0;	Mismatches	38;	Indels	0;	Gaps	0;
Qy	1	tggaccacaaattcttaaccctctgttggtgaccagatggtgcatactcttcgcgact	60						
Db	321	tggaccacaaattcttaaccctctgttggtgaccagatggtgcatactcttcgcgact	360						
Qy	61	ttccctggaggaggaagaatgtgtgatacagctgactctctgtgttctgttaatggttc	120						
Db	381	ttccctggaggaggaagaatgtgtgatacagctgactctctgtgttctgttaatggttc	440						
Qy	121	aggcagaatgaacctggaaggatataccaactttgcgagtgagccaaagaacatctaagaag	180						
Db	441	aggcagaatgaacctggaaggatataccaactttgcgagtgagccaaagaacatctaagaag	500						
Qy	181	tacatgtgaagaacacagcgcttctcccaagcagctgaagccgcacccaagaacctacata	240						
Db	501	tacatgtgaagaacacagcgcttctcccaagcagctgaagccgcacccaagaacctacata	560						
Qy	241	cgagatgagcatcaagaagaacacagatcgctcgatcatgtttgaccagagcacagaccag	300						
Db	561	cgagatgagcatcaagaagaacacagatcgctcgatcatgtttgaccagagcacagaccag	620						
Qy	301	atccagagcagtgatggaaggaaaaatgcctaccaggtgtctctgactctgacatctactg	360						
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Qy	361	gaataatgtg 369							
Db	681	gaataatgtg 689							

RESULT 9

AC004805 184263 bp DNA PRI 07-OCT-1998
 LOCUS Homo sapiens xp22 bins 16-17 BAC GSHB-531117 (Genome Systems Human
 DEFINITION BAC Library) complete sequence.
 AC004805
 AC004805.1 GI:3687201
 HG.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 AUTHORS 1 (bases 1 to 184263)

Muzny, P., Arenson, A.D., Adams, C., Brundage, E., Bunac, C.,
 Carvelli, K., Chacko, J., Chen, J., Di, W., Ding, Y., Dugan, S.,
 Durbin, J., Forcum, J., Ganes, R., Garcia, C., Goodman, M.,
 Gorelli, J., H., Haywood, M., Hernandez, J., Jackson, L., Jin, S.,
 Kampal, R., Karpathy, S., Kovar, C., Leal, B., Li, Y., Lichteberg, O.,
 Liu, W., Logan, O., Lu, J., Ly, T., Martinez, C., Oswal, G., Perez, L.,
 Rashid, N.D., Rowland, K., Savage, L., Scherer, S.E., Shen, H.,
 Simon, M., Stovall, K., Timms, K.M., Todd, J., Vo, O., Williamson, A.,
 Worley, K.C., Yu, W., Chinnault, C., Nelson, D. and Gibbs, R.A.
 Direct Submission

TITLE Unpublished
 JOURNAL 2 (bases 1 to 184263)
 REFERENCE

AUTHORS Worley, K.C.
 TITLE Direct Submission
 JOURNAL Submitted (06-JUN-1998) Molecular and Human Genetics, Baylor
 College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 184263)

REFERENCE Worley, K.C.
 TITLE Direct Submission
 JOURNAL Submitted (01-OCT-1998) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 4 (bases 1 to 184263)

REFERENCE Worley, K.C.
 TITLE Direct Submission
 JOURNAL Submitted (07-OCT-1998) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Oct 1, 1998 this sequence version replaced gi:3482897.

Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality does not meet this standard, it will be indicated in the annotation.

The repeat regions shown were identified using RepeatMasker by Adrian Smit.

Sequence similarities were identified using Powerblast by Jinghui Zhang.

Exon/Intron boundaries of identified genes were chosen if there were canonical splice junctions that maintained sequence continuity across the splice junctions.

FEATURES

source
 1. 184263
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 /db_xref="taxon:9606"
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26971..27250
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33755..34015
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complement(35781..35902)
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/rpt_family="L2"
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repeat_region complement(46499..46811)
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repeat_region complement(46812..47117)

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Query Match 83.5%; Score 308.2; DB 85; Length 184263;
 Best Local Similarity 89.7%; Pred. No. 1.2e-76;
 Matches 331; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

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QY 1 tggaccagttcttacactcctgttgggtagacagatggtgcatacctctcgagc 60
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DB 2327 TGGACCAAGTCCTTACACTCCTTATGGCGCATCAAGCGTCTTACCTTCCGAACT 2268
|||
QY 61 ttcttgagagagggaatggtgtatagcgtgactctgttgccttgatgggttc 120
|||
DB 2267 TTCTGGAGAGGAGAAATGCTGATACCTTAGACTTCTGTTGCTCGAATGATTC 2208
|||
QY 121 aggcagatgaacccggaagatatacaaaacttgcgagtgacgaagaatctataagag 180
|||
DB 2207 AGGCAGATGAACTCGAAGATACCAAACTTAGAGTAGCCAAAGGATACAAAAG 2148
|||
QY 181 tacattggaacaaacagcgtgtctcaagacgtgaagccgcacaaagactata 240
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DB 2147 TACATTGGAACAAACAGATGTCTCCAAAGCAGCTGAGCCTGCCACCAACCTTACATA 2088
|||
QY 241 cgaatggacatcaagaagaacacagatgcgcgtcatgtttgacagagacagccag 300
|||
DB 2087 AGAGTGGCATCAAGAACACAGATGATTCATCATGTTTGACACAGGCCACAGCCAG 2028
|||
QY 301 atccagcagatgatggaagaaatgactacacagtggtcttgaactctgacattacctg 360
|||
DB 2027 ATCCAGTCGGGATGAGAGGAAATGCCATCACAGATGTTTGATTCGATATATACCTC 1968
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QY 361 gaatatgtg 369
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DB 1967 GAATATGTG 1959
|||

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RESULT 10
 AB032263 3485 bp mRNA VRT 01-AUG-2000
 LOCUS
 DEFINITION Danio rerio mRNA for axln2, complete cds.
 ACCESSION AB032263
 VERSION AB032263.1 GI:7229079
 KEYWORDS
 SOURCE Danio rerio cDNA to mRNA.
 ORGANISM Danio rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Rasbora; Danio.

REFERENCE
 1 (sites)
 Shimizu,T., Yamanaka,Y., Ryu,S.L., Hashimoto,H., Yabe,T.,
 Hirata,T., Bae,Y.K., Hibli,M. and Hirano,T.
 Cooperative roles of Bozozok/Dharma and Nodal-related proteins in
 the formation of the dorsal organizer in zebrafish
 Mech. Dev. 91 (1-2), 293-303 (2000)

JOURNAL MEDLINE
 REFERENCE 2 (bases 1 to 3485)
 Hirano,T., Hibli,M. and Shimizu,T.
 Direct Submission
 TITLE Submitted (09-SEP-1999) to the DDBJ/EMBL/Genbank databases. Toshio
 Hirano, Biomedical research center, Osaka Univ. Med. school,
 Department of Molecular Oncology, 2-2, Yamadaoka, Suita, Osaka

565-0871, Japan (E-mail: hirano@molonc.med.osaka-u.ac.jp,
URL: http://www.med.osaka-u.ac.jp/pub/molonc/www/index.html,
Tel: 81-6-879-3880, Fax: 81-6-879-3889)

FEATURES

source

Location/Qualifiers
1. 3485

gene

/organism="Danio rerio"
/db_xref="taxon:7955"

CDS

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PVKTIADLRCTARDEDGLDEPGSASPDPRLAWTSLSHFLGLDDGADLFRAYL
EERKCVDTLDFWFCNCFROMDKDTRKRAKATYKRIENNSIVAKSLPATKFI
RNIRKROOISAMPQAOEIQTAMEENAYOMFLSDILEYVRTGCEHSPVNGSL
GGLKIVCGYLPITNEEESKCDKAKALATVGLSATSRLRPVPALEKGRSY
KRSDFGNPRTSGTSFAPATSANDSEVSDALTDMSMTDSVDALPPTKLSKRO
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LEERLQOIOEERDESESSASHSLPLPGTCEDDPAQLIDELHSLVLTGCGC
SPGLRHSRSPRSPORPLPRGGLSTRSSSMNGVPAKTFISROSTKHINHTIH
HAGPKSKOIEVEATROVOCICHTSECTATYRSRISGRDCAAPAVAIHGSSTL
SKRLCKSGEVMEGLNSLLOLPADSTDRSONWOMILESROTKRKHSTONKKS
HSLPRTHTWGGSSGHLRAHOPAHNPVODPAMPPLPPNPLAOLEARRLLEVS
KPSKORHSTSLQKRDKSHRPVONGSSAPMDERDPPKMGSHSLGSETVYVFFC
GEIPIYRRMKHTSLTGHFKBQLRRKKGNRYFRFRASDEFCAGVFEVMDCVLP
MYEGKILGVDMND"

BASE COUNT 986 a 839 c 864 g 796 t
ORIGIN

Query Match 61.6%; Score 227.2; DB 8; Length 3485;
Best Local Similarity 76.1%; Pred. No. 7.3e-54;
Matches 280; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

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QY 61 ttcctgagagaggaatgtgtgtaagcctgactctgtgtgtgtaagcttc 120
DB 597 TACCTTGAACGCGCAAAATGTGTGACACTTTTGATTTTGGTTTGGCTGCAATGCTTC 656
QY 121 aggcagatgaacctgaaggaatacacaactttgcagatggcacaagaacatcataagag 180
DB 657 AGCAAAATGGAAGCTCAAGATACCAAAAGCAGACAGATTGCCAAAGCAATTTCAACGG 716
QY 181 tacattgagaacaacagcggtgtctccaagagcctgaagccgcacacaaacctacata 240
DB 717 TATATTGAGAACACAGCAATTTGTGGCCAAAGCACTTAACCTTCAAGACCTTTATT 776
QY 241 cggatggagcacaagaagacagatcggctggtgcatatgtttgacaagagcagacagag 300
DB 777 AGGGAATTAATTTAAGCGTTCAGCAATTTGACTCTGCATGTTTGTCAAGGCTCAATGGAG 836
QY 301 atccagagcagtgatgaggaagaaatgctcacaagtgcttctgactctgacattacatg 360
DB 837 ATCCAGACGCGCTATGGAGGAGATGCTTATCAGATGTTTGTGACCTCGGACATATACCTC 896
QY 361 gaataatgt 368
DB 897 GACTATGT 904

RESULT 11
AF009012 AF009012 3156 bp mRNA VRT 15-JUL-1997
LOCUS gallus gallus Axin mRNA, complete cds.
DEFINITION
ACCESSION AF009012
VERSION AF009012.1 GI:2252817

KEYWORDS

SOURCE

chicken.

ORGANISM

Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

1 (bases 1 to 3156)

AUTHORS

Zeng, L., Fagotto, F., Zhang, T., Hsu, W., Vasilek, T.J., Perry, W.L.

TITLE

3rd, Lee, J.J., Tilghman, S.M., Gumbiner, B.M. and Costantini, F.

JOURNAL

The mouse fused locus encodes Axin, an inhibitor of the Wnt

MEDLINE

signaling pathway that regulates embryonic axis formation

REFERENCE

Cell 90 (1), 181-192 (1997)

AUTHORS

Zeng, L., Zhang, T., Perry, W.L. III, Lee, J.J. and Costantini, F.

TITLE

Direct Submision

JOURNAL

Submitted (13-JUN-1997) Genetics and Development, Columbia

FEATURES

University, 701 W. 168th Street, New York, NY 10032, USA

source

Location/Qualifiers

gene

1. 3156
/organism="Gallus gallus"
/db_xref="taxon:9031"

CDS

1. 3156
/gene="Axin"
/note="Fused is the classical dominant mouse tail kink
mutation due to an lap insertion in the Axin gene"
258..2783
/gene="Axin"
/function="may inhibit embryonic axis formation"
/codon_start=1
/product="Axin"
/protein_id="AAC60245.1"
/db_xref="GI:2252818"

BASE COUNT 875 a 825 c 858 g 598 t
ORIGIN

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Best Local Similarity 68.7%; Pred. No. 9e-36;
Matches 259; Conservative 0; Mismatches 106; Indels 12; Gaps 2;

QY 1 tggaccaagctcttacactcctgtgtggtgaccaggaatggtcatcactcctccgact 60
DB 510 TGGCCCGAGTGGCTGCTCTTCTGAGACATCAACGCTATCAATCTTTAGGACT 569
QY 61 ttcctgagagaggaatgtgtgtaagcctgactctgtgtgtgtaagcttc 120
DB 570 TTCTTGAACAGAGACTGTGCGGATCTGCTGACTTTTGTTTGGCTGACAGGCTTC 629
QY 121 aggcagatgaacctg-----aaagatacaaaaacttgcagatggcacaagaacatc 171
DB 630 AGGAAGCTGAGCGGTGTGTGTCATGAGAGAAAAAGACTCAAACTGCGCAAAAGCCATT 689
QY 172 tataagagtgacatt---ggaacaacaacagctgtctccaagcagcgaagccgcacc 228
DB 690 TACAAAAAGTACATTTCTGCGAACACACGAGCATTTGTGTCGCGGAGATCAACCGCCACA 749
QY 229 aagaccatacagatgcatcaagaagaacagatcggtcgtgcacatgttgacag 288

Db 750 AAAAGCTTCAATAAAAGACTGTGTCATGAACTGACGATGACCTGACATGCTTGACAG 809
 QY 289 gcaagacccagatccagcagcagtgatgagagaaatcctccagtgcttcttactct 348
 Db 810 GCCCAACTGAGATTCGATGATGAGACAACTACTCCCTTGCTTCTTAAGTCG 869
 QY 349 gacattaccctgaata 365
 Db 870 GATATTATTGGAATA 886

RESULT 12
 AF009674 3411 bp mRNA PRI 15-JUL-1997
 LOCUS Homo sapiens axin (AXIN) mRNA, partial cds.
 DEFINITION AF009674
 VERSION AF009674.1 GI:2252819
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 3411)
 AUTHORS Vasicsek,T.J., Zeng,L., Guan,X.-J., Zhang,T., Costantini,F. and Tilghman,S.M.
 TITLE Two dominant mutations in the mouse Fused gene are the result of transposon insertions
 JOURNAL Genetics (1997) in press
 REFERENCE 2 (bases 1 to 3411)
 AUTHORS Zeng,L., Fagotto,F., Zhang,T., Hsu,W., Vasicsek,T.J., Perry,W.L., 3rd, Lee,J.J., Tilghman,S.M., Gumbiner,B.M. and Costantini,F.
 TITLE The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling pathway that regulates embryonic axis formation
 JOURNAL Cell 90 (1), 181-192 (1997)
 MEDLINE 97373830
 REFERENCE 3 (bases 1 to 3411)
 AUTHORS Vasicsek,T.J., Tilghman,S.M., Costantini,F., Zeng,L., Perry,W.L. III and Zhang,T.
 TITLE Direct Submission
 JOURNAL Submitted (22-JUN-1997) Biological Technology, Millennium Pharmaceuticals, Inc., 640 Memorial Drive, Cambridge, MA 02139, USA
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 /note="contains RGS domain and Daugherless similarity; may inhibit embryonic axis formation"
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 TLNDEEMKCDMDDEDGRDAPGRPKLLETAPRVSRRSSRRSGREPRFGSM
 REPAPRYVNGGYALAPATNSDSEOSISDADLTISDVSVCIGIPRYRKRHRE
 MOESAQVNGRVPPLHPIRTYRVKVEKPEPKFAELIHLREAVORTREAEKLEERL
 KRVMEEGEDGDPSSGPGCHKLPAPAMHPPRLCWTWACAGLDAHEENPEST
 LDEHVORVLTGTGROSPPGHRSPDSGHVAMPVYALGGAAGHGKPKSGAKLDAAG

BASE COUNT 752 a 1010 c 1066 g 582 t 1 others
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 PLTQLEEARRRRLIEEKERASRAPSKORVQVEVRRRACVAPCAVLHVPAVSOME
 LSETREARORVGGSGSAOPCDSIVVAIVCGEIPYRTLVGRVAVLGGFKELLTKRG
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Query Match 43.7%; Score 161.2; DB 88; Length 3411;
 Best Local Similarity 68.3%; Pred. No. 3.8e-35;
 Matches 258; Conservative 0; Mismatches 108; Indels 12; Gaps 2;

QY 1 tgaaccaagcttcttaccctcctgttggtgagcaagatgtgcatccttccagact 60
 Db 365 TGGGCTGATCAGTCACTTCCTGCTGATGATGACCAAGATGAGATGATGAGACT 424
 QY 61 ttcttgagagaggaatgtgtgtatagctgtgacttctgtgttcttgtaaggttc 120
 Db 425 TTCCGTGAAGCAGAGAGGCGTGCAGCTTCCTGACTTCCTGCTGCTGCTGCTTC 484
 QY 121 agcgagatg-----aacctgaagataccaaacttcgcagatgagcaagaacatc 171
 Db 485 AGGAGCTGGAGCCCTGTGACTCGACAGAGAGAGAGAGCTGAGCTGGAGAGCCATC 544
 QY 172 tataagaggtaca---ttgaacaacacagcgttcttccaagcagctgaagccgcaac 228
 Db 545 TACCGAAGTACATCTTGATTAACATGCAATCGTCCCGACAGACCAACGACGCC 604
 QY 229 aagactcatacagatgagatgaagaagaacagatcgctgtgtatcttggaccag 288
 Db 605 AAGAGCTTCATTAAGGGCTGATCATGAGCAAGCTGATGATCTGCAATTTGACCA 664
 QY 289 gcaagaccgagatccagcagtgatgagagaaatcctccagtgcttcttactct 348
 Db 665 GCCCAGACCGAATTCAGCCACATGAGGAGAAACACTTCCCTCTTCTTAAGTCT 724
 QY 349 gacattaccctgaata 366
 Db 725 GATATTATTGGAATA 742

RESULT 13
 HS415C1 23786 bp DNA PRI 23-NOV-1999
 LOCUS Human DNA sequence from cosmid 415C1 from a contig from the tip of
 DEFINITION the short arm of chromosome 16, spanning 2mb of 16p13.3. Contains
 EST and Cpg Islands.
 ACCESSION Z98272
 VERSION Z98272.1 GI:3036780
 KEYWORDS 16p13.3; Cpg.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 23786)
 AUTHORS Smye,R. and Lightning,J.
 TITLE Direct Submission
 JOURNAL Submitted (23-OCT-1997) Chromosome 16 Project Group
 (http://www.sanger.ac.uk/HGP/chr16/) Sanger Institute, Wellcome Trust
 Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail
 enquiries: humquery@sanger.ac.uk; Clone requests:
 clonerequest@sanger.ac.uk
 On Apr 8, 1998 this sequence version replaced gi:2578104.
 IMPORTANT: This sequence is the entire insert of clone 415C1. The
 true left end of clone 415C1 is at 1 in this sequence. The true
 right end of clone C33B10 is at 8634.
 The true left end of clone C36768 is at 23683.
 415C1 is from a 400kb clone contig on 16p.
 Higgs D.R., Flint J. unpublished. MRC Molecular Haematology Unit,
 Institute of Molecular Medicine, Oxford.
 415C1 came from the Los Alamos flow sorted human Chromosome 16

COMMENT


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/note="AluJb repeat: matches 193. .1 of consensus;
incomplete repeat"
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/note="AluSg repeat: matches 294. .1 of consensus"
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repeat_region 5808. .5917
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/note="AluY repeat: matches 1. .300 of consensus"
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/note="AluSg repeat: matches 1. .302 of consensus"
repeat_region 10596. .10635
/note="20 copies of 2 mer 85 & conserved"
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/note="AluJb repeat: matches 134. .206 of consensus;
incomplete repeat"
repeat_region 17990. .19134
/note="A,C rich region"
prim_transcript complement(<17999. .20054)
/note="match: 5' EST AA007530 clone 429378; paired with
EST AA007531 matching this clone; contains 11 repeat"
prim_transcript 19202. .>19484
/note="match: 3' EST AA007531 clone 429378; match:
15755. .>16037; Paired with EST AA007530 matching this
clone"
repeat_region 19546. .19936
/note="A,C rich region"
repeat_region 20174. .20467
/note="AluSg repeat: matches 1. .294 of consensus"
repeat_region 20762. .21055
/note="AluSg repeat: matches 2. .298 of consensus"
repeat_region 21089. .21390
/note="AluY repeat: matches 1. .301 of consensus"
repeat_region 21713. .21738
/note="13 copies of 2 mer 92 & conserved"
repeat_region 22862. .23161
/note="AluSg repeat: matches 1. .300 of consensus"
repeat_region 23220. .23259
/note="AluY repeat: matches 41. .1 of consensus; incomplete
repeat"
repeat_region 23226. .23280
/note="AluSp/q repeat: matches 169. .121 of consensus;
incomplete repeat"
repeat_region 23317. .23434
/note="FLAM C repeat: matches 1. .133 of consensus"
repeat_region 23443. .23751
/note="AluY repeat: matches 1. .301 of consensus"
repeat_region 23752. .23914
/note="AluSx repeat: matches 132. .296 of consensus;
incomplete repeat"
repeat_region 24246. .24281
/note="12 copies of 3 mer 86 & conserved"
repeat_region 25305. .26209
/note="PTR5 repeat: matches 743. .1641 of consensus"
repeat_region 25932. .26608
/note="PTR5 repeat: matches 1533. .2438 of consensus"
repeat_region 27641. .27943
/note="AluSx repeat: matches 1. .302 of consensus"
repeat_region 27954. .28248
/note="AluSx repeat: matches 2. .302 of consensus"
repeat_region 28372. .28666
/note="AluY repeat: matches 1. .297 of consensus"
repeat_region 28586. .28587
/note="AluY repeat: matches 1. .297 of consensus"
repeat_region 28605. .28608
/note="AluSg repeat: matches 1. .303 of consensus"
repeat_region 28699. .29009
/note="AluSp repeat: matches 303. .1 of consensus"
repeat_region 29654. .29955
/note="AluSp repeat: matches 1. .303 of consensus"
repeat_region 32740. .33035
/note="AluJo repeat: matches 2. .293 of consensus"
repeat_region 33038. .33342
/note="AluY repeat: matches 1. .301 of consensus"
repeat_region 34019. .34290
/note="AluJb repeat: matches 301. .21 of consensus;
incomplete repeat"
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ORIGIN
Query Match 43.7%; Score 161.2; DB 91; Length 35054;
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repeat_t_region      complement(24537. .25018)  

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repeat_t_region      complement(27430. .27745)  

/rpt_family="Alu"  

repeat_t_region      27770. .28773  

/rpt_family="Alu"  

repeat_t_region      29024. .29305  

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repeat_t_region      29315. .29628  

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repeat_t_region      30394. .30851  

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repeat_t_region      complement(336989. .37594)  

/rpt_family="Alu"  

repeat_t_region      complement(337579. .37894)  

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/rpt_family="Alu"  

BASE COUNT      9832 a 11267 c 10484 g 7587 t  

ORIGIN

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					Gaps 2
QY 1	tygaccaagctcttaccactcctctgttcttggtgagccagatggtgtacacctcttcgagact	60			
Db 18602	TGGCGTGTGACTACTCATTCCTCCGTGGATGCACCAAGATGGATTAAGCCTGTTCCAGAACT	18543			
QY 61	ttccctggagagggagaatggtgtgatatgcgtggagactctgtgttctgtatgagtttc	120			
Db 18542	TTCCTGAAGCAGAGAGGGCGTGTCCCACTTGTCTGGAGCTTGTGTGTGCTGTGCACCTGGCTTC	18483			
QY 121	aggcagatc-----aacctgaagatatacacaacttctcgatggtggccaaagaatlc	171			
Db 18482	AGGAAGCTGTGAGCCCTGTGACTGTCAACGAGGAGAAAGAGGCTGAAGCTGGCGAGAGCAATC	18423			
QY 172	tataagaggtaca---ttgagaaacaacagcgttctctcaagcagatcgaagccgcaccc	228			
Db 18422	TACCGAAGTATCATTTCTGTGATTAACATGGCAATCGTGTCCCGGCAAGCCAGCCAGCCACC	18363			
QY 229	aagacctacatcacgatatggtcatcaagaagacaacagatcgggtctgtcatgtttgacag	288			
Db 18362	AAGACCTTCATTAAGGGGCTGATTCATGAAGCAGCTGATGATCTCTGCCATGTTTGAACAG	18303			
QY 289	gacacagaccagatccaaagcagtgatgtaggaanaatgacctacaaagtgttcttgactct	348			
Db 18302	GCCCGAGACCGGAATTCAGGCGCACTATGTGAGGAGAAACACCTATTCCTCCCTTAAGTCT	18243			
QY 349	gacattctaccgtgaatat 366				
Db 18242	GATATTATTGGAAAT 18225				

Search completed: June 7, 2001, 00:35:26
Job time: 20940 sec

XX Claim 18; Fig 3; 22pp; German.
PS
XX
CC This invention describes a novel human conductin protein which has
CC anti-tumour activity. Detecting the presence or amount of conductin,
CC at protein or nucleic acid levels, is used to diagnose tumours, while
CC agents that (re)activate conductin are used for tumour therapy.
CC Conductin binds to beta-catenin and induces its cytoplasmic degradation,
CC resulting in blockade of the Wnt/Mingless signalling pathway in
CC vertebrates. Conductin also binds to Adenomatous Polyposis Coil (APC)
CC fragments and, in conjunction with APC, acts as a tumour suppressor.
XX
SQ Sequence 2523 BP; 620 A; 728 C; 723 G; 452 T; 0 other;

Query Match 100.0%; Score 369; DB 20; Length 2523;
Best Local Similarity 100.0%; Pred. No. 1.1e-110; Indels 0; Gaps 0;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tggaccaagcttactactctctgtgtgggtgacacagatgtgtacatctctccgact 60
Db 232 tggaccaagcttactactctctgtgtgggtgacacagatgtgtacatctctccgact 291
QY 61 ttcttgagagaggagaaatgtgtgatacgtgacatctctgtgtgtgtgtgtgtgtc 120
Db 232 ttcttgagagaggagaaatgtgtgatacgtgacatctctgtgtgtgtgtgtgtgtc 351
QY 121 aggcagatgaacctgaagatacacaactttgagagtgccaaagacatctataagag 180
Db 352 aggcagatgaacctgaagatacacaactttgagagtgccaaagacatctataagag 411
QY 181 tacattggaacaacagcgtgtgtctcccaagcagctgaagccgcacacaagactata 240
Db 412 tacattggaacaacagcgtgtgtctcccaagcagctgaagccgcacacaagactata 471
QY 241 cgaatgcatcaagaagaacacagatcgctcgatcatgtttgaccagagacacagcag 300
Db 472 cgaatgcatcaagaagaacacagatcgctcgatcatgtttgaccagagacacagcag 531
QY 301 atccagcagatgatgaggaataatccctacagatgtgtcttgacttgacatttactg 360
Db 532 atccagcagatgatgaggaataatccctacagatgtgtcttgacttgacatttactg 591
QY 361 gaatatgtg 369
Db 592 gaatatgtg 600

RESULT 2
X23369 X23369 standard; cDNA; 2825 BP.
XX
AC X23369;
XX
DT 17-JUN-1999 (first entry)
XX
DE Human conductin DNA.
XX
KW Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour;
KW therapy; cytoplasmic degradation; blockade; Wnt signalling pathway;
KW Mingless signalling pathway; Adenomatous Polyposis Coil; APC;
KW tumour suppressor; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 215..2737
FT /*tag= a
FT /*product= "Conductin"
FT misc_signal 446..814
FT /*tag= b
FT /*note= "regulator of G-protein signalling region as
FT described in Claim 19"

FT protein_bind 1241..1402
FT /*tag= c
FT /bound_moiety= GSK-3beta
FT /note= "as described in Claim 20"
FT 1403..1609
FT /*tag= d
FT /bound_moiety= beta-catenin
FT /note= "as described in Claim 21"
FT misc_feature 2561..2713
FT /*tag= e
FT /note= "Dishevelled homology region as described in
FT Claim 22"
XX
SQ W09911780-A2.
XX
PN 11-MAR-1999.
XX
PD 01-SEP-1998; 98WO-DE02621.
XX
PF 02-SEP-1997; 97DE-1038205.
XX
PR (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI Behrens J, Birchmeier W;
XX
PI WPI: 1999-214706/18.
XX
DR P-PSDB: W93569.
XX
PT Tumor-suppressing protein conductin - used for treatment and
PT diagnosis of tumors
XX
PS Claim 18; Fig 2; 22pp; German.
XX
CC This invention describes a novel human conductin protein which has
CC anti-tumour activity. Detecting the presence or amount of conductin,
CC at protein or nucleic acid levels, is used to diagnose tumours, while
CC agents that (re)activate conductin are used for tumour therapy.
CC Conductin binds to beta-catenin and induces its cytoplasmic degradation,
CC resulting in blockade of the Wnt/Mingless signalling pathway in
CC vertebrates. Conductin also binds to Adenomatous Polyposis Coil (APC)
CC fragments and, in conjunction with APC, acts as a tumour suppressor.
XX
SQ Sequence 2825 BP; 703 A; 815 C; 813 G; 494 T; 0 other;

Query Match 100.0%; Score 369; DB 20; Length 2825;
Best Local Similarity 100.0%; Pred. No. 1.1e-110; Indels 0; Gaps 0;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tggaccaagcttactactctctgtgtgggtgacacagatgtgtacatctctccgact 60
Db 446 tggaccaagcttactactctctgtgtgggtgacacagatgtgtacatctctccgact 505
QY 61 ttcttgagagaggagaaatgtgtgatacgtgacatctctgtgtgtgtgtgtgtgtc 120
Db 506 ttcttgagagaggagaaatgtgtgatacgtgacatctctgtgtgtgtgtgtgtgtc 565
QY 121 aggcagatgaacctgaagatacacaactttgagagtgccaaagacatctataagag 180
Db 566 aggcagatgaacctgaagatacacaactttgagagtgccaaagacatctataagag 625
QY 181 tacattggaacaacagcgtgtgtctcccaagcagctgaagccgcacacaagactata 240
Db 626 tacattggaacaacagcgtgtgtctcccaagcagctgaagccgcacacaagactata 685
QY 241 cgaatgcatcaagaagaacacagatcgctcgatcatgtttgaccagagacacagcag 300
Db 686 cgaatgcatcaagaagaacacagatcgctcgatcatgtttgaccagagacacagcag 745
QY 301 atccagcagatgatgaggaataatccctacagatgtgtcttgacttgacatttactg 360
Db 746 atccagcagatgatgaggaataatccctacagatgtgtcttgacttgacatttactg 805

Oy	361	gaatcatctg	369	
Db	806	gaatcatctg	814	
RESULT 3				
ID	X09012	standard; DNA: 3411 BP.		
XX	AC	X09012;		
XX	DT	14-JUN-1999	(first entry)	
XX	DE	Human axin gene.		
XX	KM	Axin; cancer; breast cancer; colorectal cancer;		
XX	KM	gastrointestinal cancer; esophageal cancer; melanoma;		
XX	KM	diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;		
XX	KM	beta-catenin; se.		
XX	OS	Homo sapiens.		
XX	FT	Key	Location/Qualifiers	
XX	FT	CDS	2..2704	
XX	FT		/*tag= a	
XX	FT		/product= Axin	
XX	PN	M09902179-A1.		
XX	PD	21-JAN-1999.		
XX	PE	09-JUL-1998;	98MO-US14414.	
XX	PR	10-JUL-1997;	97US-0890865.	
XX	PA	(UYCO) UNIV COLUMBIA NEW YORK.		
XX	PI	Constantini F, Zeng L;		
XX	DR	WPI: 1999-120510/10.		
XX	DR	P-PSDB: W96264.		
XX	PT	Newly isolated nucleic acid encoding "axis inhibition" protein (Axin) - useful for detecting, diagnosing and treating cancer		
XX	PS	Disclosure: Figure 10A-10B; 95pp; English.		
XX	CC	Nucleic acids encoding mutant and wild type Axin and		
XX	CC	oligonucleotides derived from them are useful for detecting		
XX	CC	mutations in the Axin gene and for determining whether a subject is		
XX	CC	likely to develop cancer (including breast, colorectal,		
XX	CC	gastrointestinal, esophageal, carcinomas or melanomas). The wild		
XX	CC	type Axin and homologues of Axin are useful for treating subjects		
XX	CC	who are likely to develop cancer (thyroid carcinomas). The nucleic		
XX	CC	acids are also useful for diagnosing cancer and for detecting		
XX	CC	mutations in cancerous cells. Wild type Axin, its antisense		
XX	CC	molecule and identified compounds form pharmaceutical compositions		
XX	CC	in the treatment of cancer. The compositions are also useful for		
XX	CC	treating cancer by inhibiting tumorigenesis (by inducing degradation		
XX	CC	of beta-catenin). The nucleic acid encoding Axin acts through		
XX	CC	negative regulation of the Wnt pathway in the Nieuwkoop Center.		
XX	SO	Sequence 3411 BP; 752 A; 1010 C; 1066 G; 582 T; 1 other;		
Oy	Query Match	43.7%;	Score 161.2;	DB 20; Length 3411;
Oy	Best Local Similarity	68.3%;	Pred. No. 1.3e-42;	
Oy	Matches 258; Conservative	0;	Mismatches 108;	Indels 12; Gaps 2;
Db	1	tgaccacagctcttaccactctctgtgtggtgacccagatgagtcatactcttcggact	60	
Db	365	tgggctgtgctacctccctcctgctgatatgaccacagatggatgaacctgttcggact	424	

OY	61	ttctcgtgagaggagaatagtgtggatacgcgtggacttcgttgcttgaatggctc	120
Db	425	tctccgaagcgaggaaggctgtgccgacctgtgactctgttgcctgcacgtgcttc	480
OY	121	aggccgcatg-----aacctgaagatatccaaaactttgcgtagtggccaagcaatc	171
Db	485	aggaaagctcgggaagccccgtgacctcgacaacgaagaagagcgtgaagctggcgaaggccatc	544
OY	172	tataaagagtgta--tctgagaacaacacagcgttcttccaaagcagcgtgaagcccgcacc	228
Db	545	taccgaagaagtacattctctgtataacaatgycatcgtgtcccgccagaccaagccagccacc	604
OY	229	aagaccatacatacgaatgycatcctaagaagaacagacatcggtctgcgtcatgtttgaccag	288
Db	605	aagagcttcataaagagcgtgatcatgaatgaagcagctgatacctcctgcacatgtttgaccag	664
OY	289	gcacagaccggagatcccaagcgcgtgatgtgaaagaaatgctctcacacaggtgtcttgacttc	348
Db	665	gccccagaccgaatcccaagcgcacatctggaagaaacacataccctccttccttaagctc	724
OY	349	gacattaccctggaatat 366	
Db	725	gatatttatcttggaaatc 742	
RESULT	4		
XO9013			
ID	XO9013	standard; DNA; 3761 BP.	
XX			
AC	XO9013;		
XX			
DT	14-JUN-1999	(first entry)	
XX			
DE	Murine axin gene.		
XX			
KW	Axin; cancer; breast cancer; colorectal cancer;		
KM	gastrointestinal cancer; esophageal cancer; carcinoma; melanoma;		
KW	diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;		
KM	beta-catenin; ss.		
XX			
OS	Mus musculus.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	1..2981	
FT		/*tag= a	
FT		/product= Axin	
XX			
PA	WO9902179-A1.		
XX			
PN	21-JAN-1999.		
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PD			
XX	09-JUL-1998; 98WO-US14414.		
PE			
XX			
PR	10-JUL-1997; 97US-0890865.		
XX			
PA	(UYCO) UNIV COLUMBIA NEW YORK.		
XX			
PI	Constantini F, Zeng L;		
XX			
DR	WPI; 1999-120510/10.		
XX			
DR	P-PsDB; W96265.		
XX			
PT	Newly isolated nucleic acid encoding "axis inhibition" protein		
XX	(Axin) - useful for detecting, diagnosing and treating cancer		
PS	Claim 7; Figure 9A-9B; 95pp; English.		
XX			
CC	Nucleic acids encoding mutant and wild type Axin and		
CC	oligonucleotides derived from them are useful for detecting		
CC	mutations in the Axin gene and for determining whether a subject is		
CC	likely to develop cancer (including breast, colorectal, esoph-		
CC	ageo-intestinal, esophageal), carcinomas or melanomas). The wild		
CC	type Axin and homologues of Axin are useful for treating subjects		

Db 567 acacgtaccctgatgagagaagaccctaccacagcttccctgaagtgcgcgtcttaaccgg 626
 QY 361 ga 362
 Db 627 ga 628

RESULT 8
 T43376
 ID T43376 standard; cDNA; 2406 BP.
 AC T43376;
 XX 11-MAR-1997 (first entry)
 DE Human cytokine response gene CRI.
 XX Cytokine response gene; CRI; interleukin-2; IL-2;
 KW ligand-stimulated gene expression; diagnosis; therapy; ss.
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT CDS 116..724
 FT /*tag= a

XX PN W09639427-A1.
 XX PD 12-DEC-1996.
 XX PF 05-JUN-1996; 96W0-US09194.
 XX PR 05-JUN-1995; 95US-0465585.
 XX PR 05-JUN-1995; 95US-0461379.
 XX PR 05-JUN-1995; 95US-0462337.
 XX PR 05-JUN-1995; 95US-0462390.
 XX PR 05-JUN-1995; 95US-0463074.
 XX PR 05-JUN-1995; 95US-0463081.
 XX PA (DART-) DARTMOUTH COLLEGE.
 XX PI Beadling C, Smith KA;
 XX DR WPI: 1997-043062/04.
 XX DR P-PSDB; W08133.
 XX FT Cytokine response proteins and genes - used in the detection and
 FT therapy of diseases caused by a mutation in the CR coding region
 XX
 PS Disclosure; Page 11-12; 81pp; English.
 XX
 CC 8 Clones (T43376-83) contg. interleukin-2 (IL-2)-induced genes were
 CC isolated from a human IL2 receptor-positive T blast cell cDNA
 CC library following IL-2 stimulation. 6 Of these ligand-induced genes
 CC (CRI, 2, 3, 5, 6, 8) are novel. CRI expression is rapidly and
 CC transiently induced by IL-2, and mRNA expression is suppressed by
 CC elevated intracellular cAMP. It encodes an intracellular protein
 CC (W08133) that shows homology to GOS8 and BL-34. CR genes and
 CC polypeptides (W08133-40) can be used as diagnostic or therapeutic
 CC agents; CR gene sequences can be used to detect and treat allelic
 CC mutations.
 CC
 SO Sequence 2406 BP; 565 A; 621 C; 656 G; 564 T; 0 other;

Query Match 15.08; Score 55.2; DB 18; Length 2406;
 Best Local Similarity 51.14; Pred. No. 5.7e-08;
 Matches 185; Conservative 0; Mismatches 168; Indels 9; Gaps 2;
 QY 1 tggaccagcttaccctctgtgtggagacagatggtgcatcctcttcgcgact 60
 DB 299 tggagagatcgttcgacctgctgtagcagtaaatgagtgctgcttccacgct 358

QY 61 ttctcgagagagagaatgtgtgatctacgtgactctgtgttctgttaatgggttc 120
 Db 359 ttccggaagacagagtltaagtgaagagaacctggaattctgtgcctgaggaagttc 418
 QY 121 aggcagatgaacctggaagatcaccaaaacttgcgagtgagccaaagaacatcataaagg 180
 Db 419 a--agaagatcgcatacgaactacaaagctgctcccaagggcacaccagatctttgaggag 475
 QY 181 tacattggaacaacagcgttgtctccaagcagctgaagccgcaccacaagactacata 240
 Db 476 ttcatltg-----cagtgaagccccaataaaggltcaacattgacatgaagaccgcgag 529
 QY 241 cgagatggcatcaagaagacaacagatcgctcggtcatgtttgacagagcacagaccgag 300
 Db 530 ctgaagagatgaacctgcgacctgcacagccacacagcttgaatgcgctcaagggaag 589
 QY 301 atccagagcagtgatgaggaatgacctaccaggtgttcttgactctgaattactctg 360
 Db 590 acacgtaccctgatgagagaagactctaccaccagcttccctgaagtgccctgcttaaccg 649

QY 361 ga 362
 Db 650 ga 651

RESULT 9
 A39660
 ID A39660 standard; cDNA; 2406 BP.
 AC A39660;
 XX
 XX DT 18-SEP-2000 (first entry)
 DE Human CRI cDNA.
 XX
 XX CR2; human; antibody; cytokine response gene; cytostatic; anti-allergic;
 KW immunosuppressive; antimicrobial; therapy; cell proliferation; treatment;
 KW cell differentiation; cancer; immune disease; rheumatologic disease;
 KW transplant rejection; anti-infective; CRI; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 116..724
 FT /*tag= a
 FT /product= "CRI"

XX PN US6057427-A.
 XX PD 02-MAY-2000.
 XX PF 05-JUN-1996; 96US-0652446.
 XX PR 20-NOV-1991; 91US-0796066.
 XX PR 10-AUG-1993; 93US-0104736.
 XX PR 27-OCT-1994; 94US-0330108.
 XX PR 05-JUN-1996; 96W0-US08992.
 XX PA (DART-) DARTMOUTH COLLEGE.
 XX PI Beadling C, Smith KA;
 XX DR WPI: 2000-338623/29.
 XX DR P-PSDB; Y87952.
 XX
 PT Novel antibody or antibody fragment which selectively binds to a
 PT polypeptide encoded by cytokine response gene 2
 PS Example IV; Column 75-78; 66pp; English.
 CC
 CC This invention describes a novel isolated antibody or antibody fragment
 CC (I) which selectively binds to a polypeptide encoded by cytokine response

OS Homo sapiens.
 XX Key Location/Qualifiers
 FH 70..615
 FT /*tag= a
 FT CDS /product= "regulator of G-protein signalling"
 XX
 PN M09820128-A1.
 XX
 PD 14-MAY-1998.
 XX
 PD 06-NOV-1997; 97MO-US18476.
 XX
 PR 08-NOV-1996; 96US-0748483.
 XX
 PA (INCY-) INCYTE PHARM INC.
 PI Goli SK, Hillman JL;
 DR WPI: 1998-286944/25.
 DR P-PSDB: W62075.
 XX
 PT Regulator of G-protein signalling - used to develop products for
 PT treating e.g. cancer, inflammation, hypertension, cardiovascular
 PT shock, arrhythmias or asthma
 XX
 PS Claim 5; Fig 1; 66pp; English.
 CC The present sequence encodes human regulator of G-protein signalling
 CC (HRGS). The HRGS regulates G-protein signalling in cancer cells and
 CC may be useful in the treatment of any cancer, especially cancers of the
 CC brain and thyroid. Products of the present invention can also be used
 CC for treating other conditions associated with uncontrolled cell
 CC signalling such as inflammation. The products can also be used to
 CC modulate HRGS activity in response to disorders involving the
 CC sympathetic nervous system including hypertension, cardiovascular shock,
 CC arrhythmias and asthma. The products can also be used for detection,
 CC diagnosis and drug screening.
 XX
 SQ Sequence 745 BP; 221 A; 174 C; 169 G; 179 T; 2 other;

Query Match 10.3%; Score 38; DB 19; Length 745;
 Best Local Similarity 48.1%; Pred. No. 0.014;
 Matches 175; Conservative 0; Mismatches 180; Indels 9; Gaps 2;

QY 1 tggaccaggtcttaactcctgtgtgtgagcagagatgtgcatccttcgcgact 60
 DB 250 tggcgtgattcccttgacaacactcctgcagacaactatgtgacttgcagttcaaaagt 309
 QY 61 ttccctggagggaggaatgtgtgatacgcgtgactctgtgttctgtgaatggttc 120
 DB 310 ttccctgaagcttgatcaagtgaagaaaccttgagcttcgtgattgctgtgagattac 369
 QY 121 aggcagatgaacctgaagatacacaacatttgcagatggcccaagcaatctataagagg 180
 DB 370 aagaagatcaaa--gtccctgcgcaagatgtgtgagaagcaagcaaatattatgaagaa 426
 QY 181 tacattggaacaacacagcgtgtctccaagcagctgaagccgcgccaagaagactacata 240
 DB 427 ttcatcacaacgagagcctccctaagaaggtgaattgaccacttcaactaaggacataca 486
 QY 241 cgaagtgcacacaagaacagatcgctgcgtgcatgattgaccagcagaagccgag 300
 DB 487 atgaagaacctggttgaac-----cttccttgagcagccttgaatgcccagaagaa 540
 QY 301 atccagagagatgatggaataatgctcactacagagtgcttctgacttgacatttactc 360
 DB 541 atccatgcccctgatggaagaaagattctctgcctcgtcttggtgcgtctgagtttatacag 600
 QY 361 gaat 364
 DB 601 gagt 604

RESULT 12
 A52090
 ID A52090 standard; cDNA; 1164 BP.
 XX
 AC A52090;
 XX
 DT 04-DEC-2000 (first entry)
 XX
 DE Murine RGS protein coding sequence.
 XX
 KW RGS; regulators of G-protein signalling; GTPase activating protein; GAP;
 KW G-alpha protein; cell adhesion; chemotaxis; vulnery; immunosuppressor;
 KW anti-rheumatic; anti-arthritis; anti-diabetic; anti-inflammatory;
 KW cyostatic; hepatotropic; anti-anaemic; modulator; gene therapy; ss.
 XX
 OS Mus sp.
 XX
 FH Location/Qualifiers
 FT 134..841
 FT CDS /*tag= a
 FT /product= RGS_protein
 XX
 PN M0200046236-A2.
 XX
 PD 10-AUG-2000.
 XX
 PF 04-FEB-2000; 2000MO-US02977.
 XX
 PR 04-FEB-1999; 99US-0244314.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 PI Hodge MR, Yowe D;
 DR WPI: 2000-532893/48.
 DR P-PSDB: Y97154.
 XX
 PT Novel regulator of G-protein signalling nucleic acids and polypeptides,
 PT useful as diagnostic and investigative tools and to treat G-protein
 PT signalling disorders
 XX
 PS Claim 1; Page 102-104; 105pp; English.
 CC The RGS (regulators of G-protein signaling) protein genes, clones h16395
 CC and m1975, were identified in human and murine spleen cDNA libraries. The
 CC C-terminal location of the RGS domain is consistent with RGS known to
 CC act as GTPase activating proteins (GAPs) for G-alpha proteins. G-alpha-1
 CC linked receptors support rapid adhesion and directed migration of
 CC leukocytes and other cell types. The novel RGS proteins may be used to
 CC modulate cell adhesion and chemotaxis, e.g. for aiding wound repair.
 CC The RGS proteins, related cDNAs and anti-RGS antibodies are useful for
 CC modulation, diagnosis and treatment of immune and respiratory disorders.
 XX
 SQ Sequence 1164 BP; 406 A; 202 C; 222 G; 334 T; 0 other;

Query Match 10.3%; Score 38; DB 21; Length 1164;
 Best Local Similarity 48.1%; Pred. No. 0.017;
 Matches 175; Conservative 0; Mismatches 180; Indels 9; Gaps 2;

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 QY 61 ttccctggagggaggaatgtgtgatacgcgtgactctgtgttctgtgaatggttc 120
 DB 440 ttcttaaacatgaattcagtgaggaacattgatttggctgcgtctggaagacttc 499
 QY 121 aggcagatgaacctgaagatacacaacatttgcagatggcccaagcaatctataagagg 180

Db 500 a---agaaatgcagaagacacccaatacatccttaaaagcaagcatatgagaa 556
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Db 557 ttaattcaagaatga-----tgccccaagaagtgtaaacattgatttcatactaaagaa 610
QY 241 cgaagatgagcacaagaagacagatcgctcgtgtcatgtttgacagagacagcgag 300
Db 611 gtaattgctaaagacatcgccaccagccactctccacagtttgaatacgacaagaagaga 670
QY 301 atccagagcagtgatgaggaagaatgacctaccaggtgtcttctgactctgcattacctg 360
Db 671 gttgaccagctcatgtgacaatgacagtataaacgcttttgaatcctgagactactta 730
QY 361 gaat 364
Db 731 caat 734

RESULT 13
Z36910 ID Z36910 standard; cDNA, 1691 BP.
XX AC Z36910;
XX 13-MAR-2000 (first entry)
XX DE cDNA encoding a regulator of G protein signalling RGS5.
XX KM Activator of G protein signalling; AGS; ras-related G protein;
KM GTP hydrolysis; G protein activity; pheromone response pathway;
KM G protein-coupled signal transduction; G-gamma selectivity;
KM cellular signal transduction; regulator of G protein signalling;
KM RGS5; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT CDS 45..590
FT /tag= a
FT /product= "regulator of G-protein signalling"
XX PN MO958670-A1.
XX 18-NOV-1999.
XX PD 07-MAY-1999; 99MO-US10151.
XX PF 08-MAY-1998; 98US-0084842.
XX PR 07-OCT-1998; 98US-0103355.
XX PA (CADU-) CADUS PHARM CORP.
XX PI Cismowski M, Duzic E;
XX WPI; 2000-072337/06.
XX DR P-PSDB; Y53931.
XX PT A new activator of G protein signalling used to treat disorders
XX characterized by an aberrant AGS protein activity -
XX Claim 73; Page 139-140; 162pp; English.

XX The present sequence encodes a regulator of G protein signalling (AGS)
XX protein, RGS5. The specification also describes an activator of G
XX protein signalling (AGS) protein. The AGS cDNA sequence was isolated
XX from a human liver cDNA library. The AGS protein exhibits homology to
XX ras-related G proteins, and contains alterations in conserved amino
XX acids consistent with a deficiency in GTP hydrolysis activity. AGS
XX stimulates G protein activity, G protein-coupled signal transduction
XX and the pheromone response pathway in a receptor-independent manner.
XX The AGS protein also shows G-gamma selectivity, as measured by growth
XX assays in yeast expressing various mammalian G-gamma constructs, and

CC tissue-specific expression, as measured by Northern blot analysis.
CC The AGS protein can be used to screen for compounds that modulate
CC cellular signal transduction. The protein is used to treat disorders
CC characterized by an aberrant AGS protein activity or AGS nucleic acid
CC expression.
SQ Sequence 1691 BP; 548 A; 343 C; 305 G; 495 T; 0 other;
Query Match 10.3%; Score 38; DB 21; Length 1691;
Best Local Similarity 48.1%; Pred. No. 0.02;
Matches 175; Conservative 0; Mismatches 180; Indels 9; Gaps 2;
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Db 225 tggcgtgattccctgcgaacaactctctgcagaacaatactgacttgcgaatgtaaaagt 284
QY 61 ttccctgagagggagaatgtgtgatacgtctgactctcgttctgttgtaatgggttc 120
Db 285 ttctctgaagcttgatcattcagtgaggaagaaccttgatcttgatctgctgtgagattac 344
QY 121 aggcagatgaacctgaagataccacaaccttgcgagtgagccaaagaacatcataagagg 180
Db 345 aagaagatcaaa---gtccctgcagaagatgctgagaaggaagcaaatltaagaagaa 401
QY 181 tacattgagaacaacacagctgtgtctccaagcagctgaagccgcaccagactacata 240
Db 402 ttcatltaaaaggaggtctccctaaagagtgatattgaccacttccatlaagagatca 461
QY 241 cgagatgcatcaagaagacaagacagatcgctcgtgtcatgtttgaccagagacagcgag 300
Db 462 atgaagaacctggtggaac-----cttccttgacgcgcttggacatgagccagaagaa 515
QY 301 atccagcagtgatgaggaagaatgcbtaccaggtgttctgactctgacatttacctg 360
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QY 361 gaat 364
Db 576 gaat 579

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XX AC X51745;
XX 17-JUN-1999 (first entry)
XX DE DNA encoding a human secreted protein.
XX KM Human secreted protein; cancer; immune disorder; infection;
KM inflammatory disorder; skin disorder; tumour; atherosclerosis;
KM restenosis; autoimmune disorder; Alzheimer's disease;
KM peripheral neuropathy; trauma; spinal cord injury; allergy;
KM hematopoietic disorder; skeletal disorder; neurological disorder;
KM arthritic disorder; asthma; immunodeficiency disease; AIDS;
XX transplamt rejection; ss.
XX OS Homo sapiens.
XX PN WO9911293-A1.
XX PD 11-MAR-1999.
XX PF 03-SEP-1998; 98MO-US18360.
XX PR 12-SEP-1997; 97US-0058974.
XX PR 05-SEP-1997; 97US-0057626.
XX PR 05-SEP-1997; 97US-0057663.
XX PR 05-SEP-1997; 97US-0057669.
XX PR 12-SEP-1997; 97US-0058666.

PR 12-SEP-1997; 97US-0058667.
PR 12-SEP-1997; 97US-0058973.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Brewer LA, Ebner R, Lafleur DW, Moore PA, Olsen HS;
PI Rosen GA, Ruben SM, Shi Y;
XX
XX WPI; 1999-204988/17.
DR P-PSDB; Y12958.
XX
XX New isolated human genes and the secreted polypeptides they encode
PT - useful for diagnosis and treatment of e.g. neurological disorders,
PT tumours, immune disorders, inflammation or haematological disorders
XX
XX
PS Claim 1; Page 175-176; 215pp; English.
XX
XX X51701-55 encode human secreted proteins. The polynucleotides and
CC their corresponding secreted polypeptides are useful for preventing,
CC treating or ameliorating medical conditions, e.g. by protein or gene
CC therapy. Pathological conditions can also be diagnosed by determining
CC the amount of the new polypeptides in a sample or by determining the
CC presence of mutations in the new polynucleotides. Specific uses are
CC described for each polynucleotide, based on which tissues they are
CC most highly expressed in, and include developing products for the
CC diagnosis or treatment of cancer, immune disorders, infection,
CC inflammatory disorders, skin disorders, tumours, atherosclerosis,
CC restenosis, autoimmune disorders, Alzheimer's disease, peripheral
CC neuropathies, trauma, spinal cord injuries, allergy, hematopoietic
CC disorders, skeletal disorders, neurological disorders, arthritic
CC disorders, asthma, immunodeficiency diseases, AIDS and transplant
CC rejection. The polypeptides are also useful for identifying their
CC binding partners.
XX
XX Sequence 1923 BP; 604 A; 400 C; 363 G; 553 T; 3 other:
SQ
Query Match 10.3%; Score 38; DB 20; Length 1923;
Best Local Similarity 48.1%; Pred. No. 0.022;
Matches 175; Conservative 0; Mismatches 180; Indels 9; Gaps 2;
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QY 61 tttccgtgagggaggaatgtgtgatacgcgtgactctgttctgttgaatggttc 120
DB 505 ttcctgaggtctgaattcagtgaggaacacctgagttctgtgattgctgtgagattac 564
QY 121 aggcagatgaactgaagatcaccaaaacttgcgagtggtgccaagaatctataagag 180
DB 565 aagaagatcaa---gtccctgcgaagatgctgtagaagcgaaagcaattatgaagaa 621
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DB 622 ttcatctcaacgagagcctccaaagagtgatattgacaccttactactaagacataca 681
QY 241 cgaggtgcatcaagaagaacagatcgctgcgtcatgatttgaccagagcagccgag 300
DB 682 atgaagaacctggtggaac-----cttccctgagcagcttggatattgcccagaaga 735
QY 301 atccagcagtgatgaggaatgctcactacagagtgcttcttacttgcatttactctg 360
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QY 361 gaat 364
DB 796 gagt 799
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C41294
ID C41294 standard; DNA; 477 BP.

XX
AC C41294;
XX
DT 17-OCT-2000 (first entry)
XX
DE Zea mays DNA fragment SEQ ID NO: 31364.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic;
KW pathway; promoter; termination sequence; corn; ss.
XX
XX Zea mays subsp. mays.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
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PR 18-MAY-1999; 99US-0134370.
PR 19-MAY-1999; 99US-0134768.
PR 20-MAY-1999; 99US-0134941.
PR 21-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
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PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.

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GenCore version 4.5
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and is derived by analysis of the total score distribution.

SUMMARIES

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3	55.2	15.0	606	2	US-08-462-390B-27
4	55.2	15.0	606	3	US-08-463-074B-27
5	55.2	15.0	606	3	US-08-465-585C-27
6	55.2	15.0	606	3	US-08-652-446-27
7	55.2	15.0	746	4	US-08-870-815-3
8	55.2	15.0	746	4	US-08-949-004-3
9	55.2	15.0	2383	2	US-08-274-318-1
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22	33	8.9	5057	2	US-08-365-486A-12
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26	29.8	8.1	3632	1	US-08-424-788-4
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c 33	29.2	7.9	1690	1	US-08-798-744-24	Sequence 24, Appl
c 34	29.2	7.9	8878	1	US-08-759-444-2	Sequence 2, Appl1
c 35	29.2	7.9	9880	3	US-08-680-897-1	Sequence 1, Appl1
c 36	29	7.9	1605	2	US-09-000-846-1	Sequence 1, Appl1
c 37	28.6	7.8	1244	2	US-08-755-728-1	Sequence 1, Appl1
c 38	28.6	7.8	1244	2	US-08-974-653-1	Sequence 1, Appl1
c 39	28.6	7.8	1244	4	US-09-283-011-1	Sequence 1, Appl1
c 40	28.6	7.8	1281	2	US-09-016-000-7	Sequence 7, Appl1
c 41	28.6	7.8	2242	1	US-08-641-627A-37	Sequence 37, Appl
c 42	28.6	7.8	2427	2	US-08-678-039A-39	Sequence 39, Appl
c 43	28.6	7.8	246240	2	US-08-724-394A-20	Sequence 20, Appl
c 44	28.6	7.8	246240	2	US-08-724-394A-21	Sequence 21, Appl
c 45	28.6	7.8	246240	2	US-08-724-394A-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-08-463-081B-27
Sequence 27, Application US/08463081B
Patent No. 5871960 5837487
GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
TITLE OR INVENTION: Vector and Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
STREET: 444 South Flower St. - Suite 1900
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,081B
FILING DATE: 5-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/104,736
FILING DATE: 10-AUG-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Vytiana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38150 (DART-060)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 606 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-463-081B-27
Query Match 15.0%; Score 55.2; DB 2; Length 606;

REFERENCE/DOCKET NUMBER: DART-040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)407-0700
TELEFAX: (610)407-0701
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 606 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-462-390B-27

Query Match 15.0%; Score 55.2; DB 2; Length 606;
Best Local Similarity 51.1%; Pred. No. 8.4e-09;
Matches 185; Conservative 0; Mismatches 168; Indels 9; Gaps 2;

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184 tggacagagctcttgcacctgctgctgacagcagtaaaatgagtgctctccacgct 243
OY 61 ttcctgagagggagaaatgltgtgatacgtctgactctgtgtgtgtaattggttc 120
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DB 244 TTCCTGAAGACAGAGTTCAGTAGAGGAGAACCTGAGATTCTGCTGCGCTGTGAGGATTTC 303
OY 121 aggcagatgaacctgaagataccaaacttgcgagtgtgccaagaactcataagag 180
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OY 361 ga 362
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DB 535 GA 536
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RESULT 4
US-08-463-074B-27
Sequence 27, Application US/08463074B
Patent No. 6020155
GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CRI Fusion Protein, Vector an
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
CITY: Los Angeles (B) STREET:
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463.074B
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/104,736

FILING DATE: 10-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38143 (DART-020)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 606 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-463-074B-27

Query Match 15.0%; Score 55.2; DB 3; Length 606;
Best Local Similarity 51.1%; Pred. No. 8.4e-09;
Matches 185; Conservative 0; Mismatches 168; Indels 9; Gaps 2;

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DB 244 TTCCTGAAGACAGAGTTCAGTAGAGGAGAACCTGAGATTCTGCTGCGCTGTGAGGATTTC 303
OY 121 aggcagatgaacctgaagataccaaacttgcgagtgtgccaagaactcataagag 180
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DB 304 A---AGAAATCCGATCAGCTACCAAGCTGCGCTCCAGGGCAGACAGATCTTTGAGGAG 360
OY 181 tcatatgagaacaacagcgtgtgttccaaagcagctgaagcccgccacagaacctcata 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 361 TTCATTG-----CAGTAGAGGCCCTTAAGAGGTCAACATTGACCATGAGACCCCGGAG 414
OY 241 cgaagatgcatcaagaagaacagatcggctcgtcatgtttgaccaggcacaagaccgag 300
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 415 CTGACGAGATGAACTGCGAGCTGCACAGCCACATGCTTGTATGATCGGCTCAGGGGAG 474
OY 301 atccagcagtgatgaggaagaaatgctctaccagtggttcttgactctgacattaccctg 360
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 475 ACACGTACCCCTGATGAGAGAGACTCTTACCCACAGCTTCTCTGAAAGTCGCTTACCGG 534
OY 361 ga 362
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DB 535 GA 536
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RESULT 5
US-08-465-585C-27
Sequence 27, Application US/08465585C
Patent No. 6027914
GENERAL INFORMATION:
APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR6 Polypeptide, Vecto
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
CITY: Los Angeles (B) STREET:
STATE: California
COUNTRY: USA
ZIP: 900071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,585C
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/330,108
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 20-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38149 (DART-050)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 4894210
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 606 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-465-585C-27

Query Match 15.0%; Score 55.2; DB 3; Length 606;
Best Local Similarity 51.1%; Pred. No. 8.4e-09;
Matches 185; Conservative 0; Mismatches 168; Indels 9; Gaps 2;

QY 1 tggaccgaagtttcaactccttctgttggtgacccagatggtgacatcttccgagact 60
DB 184 TGGAGAGAGTGTTCGACCTGCTGCTGAGCAGTAAATGAGTGGCTGCTTCACGCT 243
QY 61 ttccctggagaggaatgtgtgatacagctgagacttctgttcttgaatggttc 120
DB 244 TTCCTGAAGACAGAGTTTACGTAGAGAGAACTGGAGTTCTGGCTGGCCCTGAGAGATTG 303
QY 121 aggcagatgaacctgaagatacacaacttgcagatgagcgaagaacataaagag 180
DB 304 A---AGAGATCCGATCGATCAAGCTGACCTCCAGGACACACAGATCTTTGAGAG 360
QY 181 tacattggaacacacaggtgttctccaagcagctgaaagcccgccacaagaactacata 240
DB 361 TTCAATTG-----CAGTGAAGCCCTTAAGAGGTCAACATTGACCATGAGACCGCGAG 414
QY 241 cgaagatgcatcaagaacacacagatcgctcgatcatttgaccagacacagacgag 300
DB 415 CTGAGAGAGATGAACCTTCAGACAGCTCCACAGGCACATGCTTTGATCGCGCTCAGGGAG 474
QY 301 atccagcagctgataggagaaatgacctaccaggtgttcttgaacttctgaacttacctg 360
DB 475 ACAGGTACCTGATGAGAGAGAGACTCTACCCACGCTTCTGCTGAGAGTCCCTGCTTACCG 534
QY 361 ga 362
DB 535 GA 536

RESULT 6
US-08-652-446-27
Sequence 27, Application US/08652446
Patent No. 6057427
GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CRS
TITLE OF INVENTION: Polypeptide, Vector and Transformed Cell Thereof, and
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:

ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
ADDRESSEE: (B) STREET:
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,446
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP App. # 96921319.8
FILING DATE: 5-JAN-1998
APPLICATION NUMBER: PCT/US/96/09194
FILING DATE: 5-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,108
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/463,074
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,337
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,390
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,585
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/463,081
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/461,379
FILING DATE: 5-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/739,523
FILING DATE: 29-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 40035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 606 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-652-446-27

Query Match 15.0%; Score 55.2; DB 3; Length 606;
Best Local Similarity 51.1%; Pred. No. 8.4e-09;
Matches 185; Conservative 0; Mismatches 168; Indels 9; Gaps 2;

QY 1 tggaccgaagtttcaactccttctgttggtgacccagatggtgacatcttccgagact 60
DB 184 TGGAGAGAGTGTTCGACCTGCTGCTGAGCAGTAAATGAGTGGCTGCTTCACGCT 243
QY 61 ttccctggagaggaatgtgtgatacagctgagacttctgttcttgaatggttc 120
DB 244 TTCCTGAAGACAGAGTTTACGTAGAGAGAACTGGAGTTCTGGCTGGCCCTGAGAGATTG 303

Db 276 TGAGAGAGTCGTCGACCGTCGTCGAGAGAGTAAATGAGCTGGCTTCCACGCT 335
Qy 61 ttcctggagaggaagaatgtgtgatacgcgtgacttctgttctgttaatgggttc 120
Db 336 TTCCTGAAGACAGAGTTCAGTGAAGAGAACCTGAGTTCGTGGCTGGCTTGAGGAGTTC 395
Qy 121 aggcagatgaacctgaagatgacaaacttgcgagtggtgcacaaacatactaaagag 180
Db 396 A--AGAAATCCGATCCATCAGTACCAAGCTGGCTCCAGGGGACACAGATCTTTGAGGAG 452
Qy 181 tacatgagagaacaacagctgtctccaagcagctgaagccgcccaagacctacata 240
Db 453 TTCATTG-----CAGTAGGCCCCCTAAAGAGTCAACATTGACCATGAGACCCGCGAG 506
Qy 241 cgaagatgcatcaagaagaacagatcgctcgatcatgtttgacagagacagaccag 300
Db 507 CTGACGAGATGAACCTGACGACTGCCACAGCCACATGCTTTGATGGGCTCAGGGGAG 566
Qy 301 atccagagcagtgatgagagaataatgcctaccaggtgttcttgacttgcacattactg 360
Db 567 ACACGTACCTGATGAGAGAGAGACTCTACCCAGCTTCTGTAAGTCGCTGCTTACCGG 626
Qy 361 ga 362
Db 627 GA 628

RESULT 11
US-08-463-081B-1
; Sequence 1, Application US/08463081B
; Patent No. 5871960 5837487
; GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A. & Beadling, Carol
; TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
; TITLE OF INVENTION: Vector and Transformed Cell Thereof, and Expression Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
; STREET: 444 South Flower St. - Suite 1900
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0,
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,081B
; FILING DATE: 5-JUN-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/104,736
; FILING DATE: 10-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,066
; FILING DATE: 20-NOV-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel, Ph. D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38150 (DART-060)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 632-7700
; TELEFAX: (213) 489-4210
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2406 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 116..722
US-08-463-081B-1

Query Match 15.0%; Score 55.2; DB 2; Length 2406;
Best Local Similarity 51.1%; Pred. No. 1.6e-08;
Matches 185; Conservative 0; Mismatches 168; Indels 9; Gaps 2;

Qy 1 tggacaagctcttaacctcttctgtgtggtgacagatgtgtcacaacctccagact 60
Db 299 TGAGAGAGTCGTCGACCTGCTGCTGAGAGAGTAAATGAGAGTGGCTTCCACGCT 358
Qy 61 ttcctggagaggaagaatgtgtgatacgcgtgacttctgttctgttgaatgggttc 120
Db 359 TTCCTGAAGACAGAGTTCAGTGAAGAGAACCTGAGTTCGTGGCTGGCTTGAGGAGTTC 418
Qy 121 aggcagatgaacctgaagatgacaaacttgcgagtggtgcacaaacatactaaagag 180
Db 419 A--AGAAATCCGATCCATCAGTACCAAGCTGGCTCCAGGGGACACAGATCTTTGAGGAG 475
Qy 181 tacatgagagaacaacagctgtctccaagcagctgaagccgcccaagacctacata 240
Db 476 TTCATTG-----CAGTAGGCCCCCTAAAGAGTCAACATTGACCATGAGACCCGCGAG 529
Qy 241 cgaagatgcatcaagaagaacagatcgctcgatcatgtttgacagagacagaccag 300
Db 530 CTGACGAGATGAACCTGACGACTGCCACAGCCACATGCTTTGATGGGCTCAGGGGAG 589
Qy 301 atccagagcagtgatgagagaataatgcctaccaggtgttcttgacttgcacattactg 360
Db 590 ACACGTACCTGATGAGAGAGAGACTCTACCCAGCTTCTGTAAGTCGCTGCTTACCGG 649
Qy 361 ga 362
Db 650 GA 651

RESULT 12
US-08-461-379A-1
; Sequence 1, Application US/08461379A
; Patent No. 5871961
; GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A. & Beadling, Carol
; TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
; TITLE OF INVENTION: Vector and Transformed Cell Thereof, and
; TITLE OF INVENTION: Expression Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; CITY: Valley Forge
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0,
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,379A
; FILING DATE: 5-JUNE-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/330,108; 08/104,736
; FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel, Ph. D.
; REGISTRATION NUMBER: 30,930

STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,074B
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/104,736
FILING DATE: 10-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/96,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38143 (DART-020)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2406 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 116..722
US-08-463-074B-1

Query Match 15.0%; Score 55.2; DB 3; Length 2406;
Best Local Similarity 51.1%; Pred. No. 1.6e-08;
Matches 185; Conservative 0; Mismatches 168; Indels 9; Gaps 2;

QY 1 tggaccagcttctacacccctgttgggtgaccagatgagtcatactcttcggact 60
DB 299 tggagagatcgttcgacctgctgacgacgataaaatggatggcttccacgct 358
QY 61 ttcctggaaggagaaatgtgtgatacgtcgtgacttggcttggctgtaagtgtc 120
DB 359 ttccgtaagacagacttgcgtgaggaagaaacttgagtttgcctgctgtagagattc 418
QY 121 aggcagatgaacctgaagataccaacttgcaggtgagccaaagcaactataagagg 180
DB 419 a---AGAAAGATCCGATCAGCTACCAAGCTGGCCTCCAGGGCACACAGATCTTGGAGAG 475
QY 181 tacattggaagaacaagcgtgtgtcccaagcagctgaagcccgcccaagacctacata 240
DB 476 ttcatTTG-----CAGTAGGCCCCCTAAAGGTCAACATTGACCATGACCCCGAG 529
QY 241 cgaagatgcatcaagaagaacacagatcgctcgatcatgtttgaccagacagaccgag 300
DB 530 ctgacagagatgaacctgcagacgtccacagccacatgcttttgatgctgctcaggggaag 589
QY 301 atccagcagatgagtgaggaanaatgcctacacagctgttcttgactctgacattactc 360
DB 590 ACACGTACCCCTGATGAGAAAGACTCTACCCAGCCTTCTCTGAAGTCGCTCTTACCG 649
QY 361 ga 362
DB 650 GA 651

RESULT 15
US-08-465-585C-1

Sequence 1, Application US/08465585C
Patent No. 6027914
GENERAL INFORMATION:
APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR6 Polypeptide, Vector
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
ADDRESS: (B) STREET:
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 900071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,585C
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/330,108
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/96,066
FILING DATE: 20-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38149 (DART-050)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 4894210
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2406 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 116..722
US-08-465-585C-1

Query Match 15.0%; Score 55.2; DB 3; Length 2406;
Best Local Similarity 51.1%; Pred. No. 1.6e-08;
Matches 185; Conservative 0; Mismatches 168; Indels 9; Gaps 2;

QY 1 tggaccagcttctacacccctgttgggtgaccagatgagtcatactcttcggact 60
DB 299 tggagagatcgttcgacctgctgacgacgataaaatggatggcttccacgct 358
QY 61 ttcctggaaggagaaatgtgtgatacgtcgtgacttggcttggctgtaagtgtc 120
DB 359 ttccgtaagacagacttgcgtgaggaagaaacttgagtttgcctgctgtagagattc 418
QY 121 aggcagatgaacctgaagataccaacttgcaggtgagccaaagcaactataagagg 180
DB 419 a---AGAAAGATCCGATCAGCTACCAAGCTGGCCTCCAGGGCACACAGATCTTGGAGAG 475
QY 181 tacattggaagaacaagcgtgtgtcccaagcagctgaagcccgcccaagacctacata 240
DB 476 ttcatTTG-----CAGTAGGCCCCCTAAAGGTCAACATTGACCATGACCCCGAG 529
QY 241 cgaagatgcatcaagaagaacacagatcgctcgatcatgtttgaccagacagaccgag 300
DB 530 ctgacagagatgaacctgcagacgtccacagccacatgcttttgatgctgctcaggggaag 589

QY 301 atccaggcagtgatggaggaaatgcctaccaggatgttcttgacttctgacatttacctg 360
 Db 590 ACACGTACCTGTGATGAGAGGACTCCTACCCACGCTTCTGAAGTCGCGCTGCTTACCGG 649
 QY 361 ga 362
 Db 650 GA 651

Search completed: June 7, 2001, 00:26:30
 Job time: 19733 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 6, 2001, 23:00:39 ; Search time 3054.04 Seconds
(without alignments)
1055.527 Million cell updates/sec

Title: US-09-587-574-7

Perfect score: 369

Sequence: 1 tgaaccacagctcttacac...acattaccctggaatatgtg 369

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 4368049070 residues

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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 189: em-gss-hum21:*

190: em-gss-pln1:*
 191: em-gss-pln2:*
 192: em-gss-pro:*
 193: em-gss-rod1:*
 194: em-gss-rod2:*
 195: em-gss-rod3:*
 196: em-gss-rod4:*
 197: em-gss-rod5:*
 198: em-gss-rod6:*
 199: em-gss-rod7:*
 200: em-gss-rod8:*
 201: em-gss-rod9:*
 202: em-gss-rod10:*
 203: em-gss-rod11:*
 204: em-gss-rod12:*
 205: em-gss-rod13:*
 206: em-gss-rod14:*
 207: em-gss-rod15:*
 208: em-gss-rod16:*
 209: em-gss-rod17:*
 210: em-gss-rod18:*
 211: em-gss-rod19:*
 212: em-gss-rod20:*
 213: em-gss-rod21:*
 214: em-gss-rod22:*
 215: em-gss-rod23:*
 216: em-gss-rod24:*
 217: em-gss-rod25:*
 218: em-gss-rod26:*
 219: em-gss-rod27:*
 220: em-gss-rod28:*
 221: em-gss-rod29:*
 222: em-gss-rod30:*
 223: em-gss-rod31:*
 224: em-gss-rod32:*
 225: em-gss-rod33:*
 226: em-gss-rod34:*
 227: em-gss-rod35:*
 228: em-gss-rod36:*
 229: em-gss-rod37:*
 230: em-gss-rod38:*
 231: em-gss-rod39:*
 232: em-gss-rod40:*
 233: em-gss-rod41:*
 234: em-gss-rod42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	247.4	67.0	1068	231	CNS03YWO
2	237.4	64.3	830	230	CNS01YDU
3	218.6	59.2	902	231	CNS03GZD
4	207.2	56.2	798	140	BE872155
5	162	43.9	975	230	CNS03J34
6	161.2	43.7	651	141	BE894571
7	147.4	39.9	585	140	BE854108
8	147.4	39.9	556	150	BE582324
9	143.6	38.9	539	3	AA198606
10	126.8	34.4	475	147	BF406997
11	120.2	32.6	406	169	BF802488
12	114.8	31.1	935	106	AL526136
13	109.6	29.7	491	105	AL045145
14	108.6	29.4	364	140	AL044979
15	103.8	28.1	217	150	BF559312
16	99.2	26.9	1029	232	CNS051XC
17	94.6	25.6	303	109	AV138493
18	86.4	23.4	565	170	BF892872

19	84.4	22.9	646	136	BE545269	BE545269	601074872
20	74.8	20.3	228	143	BF091963	BF091963	RC6-TR007
21	74	20.1	709	113	BF04757	BF04757	DB7808.Y
22	73.2	19.8	617	118	AM64465	AM64465	CM43901.W
23	71	19.2	393	168	BF763535	BF763535	IL2-CS004
24	57.4	15.6	474	141	BE932286	BE932286	IL3-TR061
25	55.8	15.1	552	102	AT196489	AT196489	WH46A01.X
26	55.2	15.0	552	172	BG058803	BG058803	NAF1008.
27	55.2	15.0	582	19	AT339304	AT339304	Q101D10.X
28	55.2	15.0	593	24	AT176848	AT176848	WH22A05.X
29	55.2	15.0	613	103	AT1885075	AT1885075	W189A01.X
30	55.2	15.0	654	24	AT1769888	AT1769888	W130A08.X
31	55.2	15.0	772	146	BF304996	BF304996	601888511
32	55.2	15.0	918	139	BE795291	BE795291	601592385
33	53.2	14.4	693	107	AU122006	AU122006	AU122006
34	52.6	14.3	294	170	BF896301	BF896301	RC1-MT014
35	52.6	14.3	752	111	AM193671	AM193671	XM29B11.X
36	52.2	14.1	550	111	AM172334	AM172334	XJ37A04.X
37	51	13.8	505	102	AT1794576	AT1794576	FC6B01.Y
38	50.8	13.8	552	8	AA497296	AA497296	FA03E12.Y
39	50.8	13.8	947	147	BF384062	BF384062	602045593
40	49.4	13.4	431	2	AA139095	AA139095	mq95C11.Y
41	49.2	13.3	400	169	BF802233	BF802233	CM1-CI009
42	48.8	13.2	451	130	AM828213	AM828213	rs67h12.Y
43	48.8	13.2	931	139	BE798461	BE798461	601583325
44	48.6	13.2	338	169	BF843143	BF843143	MR2-HI104
45	48.6	13.2	339	120	AM849747	AM849747	IL3-CT021

ALIGNMENTS

RESULT 1
LOCUS CNS03YMO 1068 bp DNA GSS 18-MAY-2000
DEFINITION Tetraodon nigroviridis genome survey sequence PUC-Or1 end of clone
069C20 of library G from Tetraodon nigroviridis, genomic survey
sequence.

ACCESSION AL268841.1 GI:7988628
VERSION AL268841.1
KEYWORDS GSS: genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Eurypterygii; Ctenosquamata; Acanthomorpha; Eucanthomorpha;
Holacanthopterygii; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE 1 (bases 1 to 1068)
AUTHORS Roest-Crollius, H., Jallion, O., Dasilva, C., Fizames, C., Fisher, C.,
Bonneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1068)
AUTHORS Roest-Crollius, H., Jallion, O., Dasilva, C., Fizames, C., Fisher, C.,
Bonneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
TITLE Human gene number estimate provided by genome wide analysts using
Tetraodon nigroviridis DNA sequence

JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1068)
AUTHORS Roest-Crollius, H., Jallion, O., Dasilva, C., Fizames, C., Fisher, C.,
Bonneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
TITLE Direct Submision
JOURNAL Submitted (12-APR-2000) to the EMBL/Genbank/DBJ databases
COMMENT This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.

FEATURES
source 1..1068
/organism="Tetraodon nigroviridis"

/db_xref="taxon:99883"
/clone="069C20"
/clone_lib="G"
/note="Genoscope sequence ID : C0BG069BBI0SP1-end :
PUC-Or1"

BASE COUNT 255 a 294 c 313 g 199 t 7 others
ORIGIN

Query Match 67.0%; Score 247.4; DB 231; Length 1068;
Best Local Similarity 79.4%; Pred. No. 8.7e-63;
Matches 293; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

1 tggaccagatcttaccatccctgtgtgtgacacagatgagatgacatcttcggact 60
|||||
407 tggacaaatcttcttgcaccccttgcgggacacagacacgacgacgacgacgac 466
|||||
61 ttcctgagagagagagagagatgagatgagatgagatgagatgagatgagatgag 120
|||||
467 ttcctgagagagagagagagatgagatgagatgagatgagatgagatgagatgag 526
|||||
121 aggcagatgac 180
|||||
527 cggacatgac 586
|||||
181 tacatgagac 240
|||||
587 ttcacatgagac 646
|||||
241 cagatgac 300
|||||
647 cggacatgac 706
|||||
301 atccagcagatgag 360
|||||
707 atccagcagatgag 766
|||||
361 gaatatgtg 369
|||||
767 gaatatgtg 775

RESULT 2
LOCUS CNS01YDU 830 bp DNA GSS 12-MAY-2000
DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone
218017 of library G from Tetraodon nigroviridis, genomic survey
sequence.

ACCESSION AL172875.1 GI:7810932
VERSION AL172875.1
KEYWORDS GSS: genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Eurypterygii; Ctenosquamata; Acanthomorpha; Eucanthomorpha;
Holacanthopterygii; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE 1 (bases 1 to 830)
AUTHORS Roest-Crollius, H., Jallion, O., Dasilva, C., Fizames, C., Fisher, C.,
Bonneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 830)
AUTHORS Roest-Crollius, H., Jallion, O., Dasilva, C., Fizames, C., Fisher, C.,
Bonneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
TITLE Human gene number estimate provided by genome wide analysts using
Tetraodon nigroviridis DNA sequence

JOURNAL Unpublished
REFERENCE 3 (bases 1 to 830)
AUTHORS Roest-Crollius, H., Jallion, O., Dasilva, C., Fizames, C., Fisher, C.,
Bonneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
TITLE Direct Submision
JOURNAL Submitted (12-APR-2000) to the EMBL/Genbank/DBJ databases
COMMENT This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.

FEATURES
source 1..1068
/organism="Tetraodon nigroviridis"

COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LAM9569 row: k column: 15
High quality sequence stop: 544.

FEATURES
source location/Qualifiers
1..798
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3850502"
/clone_1lb="NIH_MGC_65"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site: 1; Ncti; Site_2: Salt; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.8 kb. Library constructed by Life Technologies."

BASE COUNT 218 a 229 c 207 g 144 t

ORIGIN

Query Match 56.2%; Score 207.2; DB 140; Length 798;
Best Local Similarity 90.6%; Pred. No. 7e-51;
Matches 221; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 126 gatgaacctgaagataccaacattcgagtgccaaagcaactataaggtacat 185
DB 1 GATGAACCTGAAGATACCAAACTTACGATGACCAAGCATCAAAAGTACAT 60
186 tggaaacaaagctgtgtcccaagagctgaagccgcacaaagcaactaagaga 245
DB 61 TGAAGAACAGCAGCTGTCTCCAGAGCTGAAGCCTGCACCAAGCATCAATGAAGA 120
246 tggatcaagaagaacagatcgctcgatcatgttgacaaagcagacagacatcca 305
DB 121 TGGCATCAAGAAGACAGACAGATTGATTCATCATGTTGACAGCGGAGAGACAGATCCA 180
QY 306 ggcagtgatgaggaagaatgctaccagtgcttcgaacttcgaacttaactggaata 365
DB 181 GTGGGTGATGAGAGAAATGCTTACCAAGATGTTTGACTTGTATATATACCTCGAATA 240
QY 366 tgtg 369
DB 241 TGTG 244

RESULT 5
LOCUS CNS03334 975 bp DNA GSS 15-MAY-2000
DEFINITION Tetradon nlgroviridis genome survey sequence PUC-ori end of clone 209617 of library G from Tetradon nlgroviridis, genomic survey sequence.

ACCESSION AL226201 GI:7885113
VERSION AL226201
KEYWORDS GSS: genome survey sequence.
SOURCE Tetradon nlgroviridis
ORGANISM Tetradon nlgroviridis

REFERENCE 1 (bases 1 to 975)
AUTHORS Roest-Crolius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Ballault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.

TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradon nlgroviridis

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 975)
AUTHORS Roest-Crolius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Winkler,P., Brotlier,P., Quetier,F., Saurin,W. and Weissenbach,J.
TITLE Human gene number estimate provided by genome wide analysis using Tetradon nlgroviridis DNA sequence

JOURNAL Unpublished
REFERENCE 3 (bases 1 to 975)
AUTHORS Genoscope.
TITLE Direct Submission

JOURNAL Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetradon nlgroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetradon>.

FEATURES
source location/Qualifiers
1..975
/organism="Tetradon nlgroviridis"
/db_xref="taxon:99883"
/clone="209617"
/clone_1lb="G"
/note="Genoscope sequence ID : C0AG209AD09SP1-end : PUC-ori"

BASE COUNT 201 a 276 c 316 g 145 t 37 others

ORIGIN

Query Match 43.9%; Score 162; DB 230; Length 975;
Best Local Similarity 68.8%; Pred. No. 2e-37;
Matches 249; Conservative 11; Mismatches 95; Indels 7; Gaps 3;

QY 1 tggacaagctcttacacatctctgtgttgagacagatgtgcatacctctccgact 60
DB 621 TGGACCAAGTCCCTGCACCTTCGTGCTGGGACGACGAGCGGCTCGCTTCAGAGCT 680
QY 61 tctctgagagggagaaatgtgtgatacgtgacttcgtgttctgttaatgggtc 120
DB 681 TTCTGTGAGCGGGACGACGCCGCGACACCTGTGACTTGTGCTGCGCTCAACGGCTTC 740
QY 121 aggcagatgaactgaaggtatccaacttcgagtgccaaagcaactaagagg 180
DB 741 AGGCAGATGAGACCTGAAGATGCCAANAACCTTGCGCTGGCCAAAGCATTTCAAGCGC 800
QY 181 tacattgagaacaacagatgtgtctccaagcagctgaagccgcacaaagactacata 240
DB 801 TACGTGACAGCAAGACAGCGTGTCTCCAGGAMMMAMMMNNNCAMCADACTTCATC 860
QY 241 cgaatgcatcaagaagaacagatcgctcgatcatgttgacacagacagaccgag 300
DB 861 AGGAGAMAGSTTMA--GAGAGAGAGATGATTCGG-CATGTTCCACAGCGCCVKGAGGT 917
QY 301 atccagcagtgatgagaggaatgctaccagtgcttcgacttcgacttaactactg 360
DB 918 TCAGAGGACATGAGAGGGA---GCTACACAGCTTCCTGACCTCGACATATATCTG 973
QY 361 ga 362
DB 974 GA 975

RESULT 6
LOCUS BE894571 651 bp mRNA EST 20-OCT-2000
DEFINITION 601433182F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918285 5', mRNA sequence.

ACCESSION BE894571
VERSION BE894571
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

RESULT	8
LOCUS	BF582324
DEFINITION	BF582324 956 bp mRNA EST 12-DEC-2000
ACCESSION	602101153F1 NC1_CGAP_Co24 Mus musculus cDNA clone IMAGE:4224469 5'
VERSION	BF582324
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus.
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE	1 (bases 1 to 956)
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/ .
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert.Strausberg@nih.gov Tissue Procurement: Jeffrey E. Green, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LHAM9814 row: 1 column: 14 High quality sequence start: 5 High quality sequence stop: 668.

FEATURES	
source	Location/Qualifiers
	1. .956

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/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_image:4224469"
/clone_11b="NCI-CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: colon; Vector: pCMV-SpORf6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
technologies. Note: this is a NCI-CGAP library."

```

Query Match	39.98;	Score 147.4;	DB 150;	Length 956;
Best Local Similarity	66.08;	Pred. No. 4.3e-33;		
Matches 249; Conservative	0;	Mismatches 116;	Indels 12;	Gaps 2

Qy	1	tgagccaaagctcttacaacccctcttgaggagcaagaatgtagaacctctccgaat	60
Db	86	tgggcctagatcactgcgacttctcttactgcatgaccaaagatgggactcgtttcagagact	145
Qy	61	tctcctgagagagagaaatgtagtagacgctggaactctggtcttgcttlaatggttc	120
Db	146	tttcctgaagcagagggcgctgctgacactgctggacttctggtttgctgcagatggccttc	205
Qy	121	agcagat-----gaacctgaaagataccaacacttgcgagtggccaagaacat	171
Db	206	aggaagcttgcagccctgtgactcaaaagagaaagagcctggaagctggcagacagcattc	265
Qy	172	tataaaggttaca---cttgagaaacaaaggtgtgtctccaagaagcctgaagccgcgcacc	228
Db	266	taccgaaagatcactccttgatagcaaatggcattgtgtctcagacaaaccaaagccagccact	325
Qy	229	aagacctacatacagagaatggcatcaagaagacaacagatactgcgtctgcatgcttgaccag	288
Db	326	aagagcttcatpaaagagactgctgcatcatgaacagacagatagatcctgcacatgcttgaaccag	385
Qy	289	gcacagaccgagatccacagcgatgtagaggaataatgcctaccagtgctcttgaaetct	348

Db	386	GCAAGACAGAAATCCAGTCACCATGAGAGAGAAATACCTACCTTCCTTTTAAGTC	445
Qy	349	gacatttacctgata	365
Db	446	GACATTTATTTGGAGTA	462

RESULT	9
AA198606/c	
LOCUS	539 bp mRNA EST 19-FEB-1997
DEFINITION	m153d4.r1 Soares thymus_2NbMt Mus musculus cDNA clone IMAGE:639463 cds=1; utm=00709 gb=1; protein=000 prom=0; p22

ACCESSION	AA198606
VERSION	AA198606.1
KEYWORDS	GI:1794333
SOURCE	EST.
ORGANISM	house mouse. <i>Mus musculus</i>

REFERENCE
AUTHORS
1 (bases 1 to 539)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gessel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,B.,
Schellenberg,K., Stepec,M., Tan,F., Underwood,K., Moore-B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE
The Mashu-HMM Mouse EST Project
JOURNAL
Unpublished (1996)
COMMENT
Contact: Marra M/Mouse EST Project

TITLE	JOURNAL	COMMENT
The Mashu-HHMI Mouse EST Project	Unpublished (1996)	Contact: Marra M/Mouse EST Project Mashu-HHMI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information. MGI:391455
Possible reversed clone: similarity on wrong strand		Seq primer: -28ml3 rev2 from Amersham High quality sequence stop: 496

FEATURES
SOURCE

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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_image="639463"
/clone_lib="Soares-thymus_2NBMT"
/sex="male"
/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dt) primer [5',
TGTATCCCAATCTGAAGTGGAGCGGCCGCGCTTTTTTTTTTTTTTTT
3']; Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M. Palina Bonaïdo."

```

	Query Match	38.9%	Score 143.6	DB: 3	Length 539;
	Best Local Similarity	65.4%	Pred. No. 4	gc=32;	
	Matches 246;	Conservative	0;	Mismatches 119;	Indels 11; Gaps 2;
Oy	1	tggaccaagctcttaactcctgtgtggtgacgaagtatgataaccttcgcgact	60		
b	533	tggcgtagtgcacgtgcattccctttacgtgatgccacaagaatggcatcaggctgttgtaggact	474		

/note="Vector: pT773D-Pac (Pharmacia) with a modified polylinker: Site_1: Not I; Site_2: Eco RI; The UI-R-E1 library is a subtracted library derived from the UI-R-E0 library. The UI-R-E0 library consisted of a mixture of individually tagged normalized libraries constructed from 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dt track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-E1) was constructed as follows: PCR amplified cDNA inserts from a pool of UI-R-E0 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the UI-R-E0 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-E1 library. This procedure has been previously described (Ronald, Lennon and Soares, Genome Research 6: 791-806, 1996).

BASE COUNT 47 a 70 c 42 g 58 t
ORIGIN

Query Match 28.1%; Score 103.8; DB 150; Length 217;
Best Local Similarity 90.2%; Pred. No. 2.5e-20;

Matches 11; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY	247	ggcatcaagaagcaacagatcggtcgtatgtttgaccagcacagaccgagatcag	306
Db	217	ggcatcaagaagcaacagatcggtcgtatgtttgaccagcacagaccgagatcag	158
QY	307	gcagtgatgaggaagaaatgctaccaggtgttcttgaccttgacattacctggaat	366
Db	157	gcagtgatgaggaagaaatgctaccaggtgttcttgaccttgacattacctggaat	98
QY	367	gttg 369	
Db	97	gttg 95	

Search completed: June 6, 2001, 23:00:43
Job time: 13527 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 7, 2001, 00:35:26 ; Search time 4956.99 Seconds
(without alignments)
481.977 Million cell updates/sec

Title: us-09-587-574-8
Perfect score: 162
Sequence: 1 gcccaatggccaagtctctc.....gtctggagagcgagctgcag 162

Scoring table: IDENTITY-MUC
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 7373929652 residues
Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba1:*
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89: gb_pr5:*
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92: gb_pr8:*
93: gb_pr9:*
94: gb_ro1:*
95: gb_ro2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	162	100.0	162	9 A98523	A98523 Sequence 8
2	162	100.0	2825	9 A98521	A98521 Sequence 6
3	162	100.0	2825	9 AF073788	AF073788 Mus muscu
4	162	100.0	3016	94 AF205889	AF205889 Mus muscu
5	147.6	91.1	3216	94 AF017757	AF017757 Rattus no
6	133.4	82.3	191041	69 AC024114	AC024114 Mus muscu
7	131.6	81.2	2104	89 AK025718	AK025718 Homo sapi
8	131.6	81.2	3072	88 AF078165	AF078165 Homo sapi
9	128.4	79.3	2538	88 AF205888	AF205888 Homo sapi
10	82.8	51.1	3485	8 AB032263	AB032263 Dantio rer
11	56.4	34.8	3411	88 AF009674	AF009674 Homo sapi

12 54.8 21.21 8 AF140243 Xenopus 1
13 51.8 30.66 8 AB032262 Danio rer
14 42.8 31.56 8 AF009012 Gallus ga
15 39.8 24.6 8 HS419C1
16 39.8 24.6 8 AC004652
17 39.8 24.6 8 AC028836
18 39.8 24.6 8 AC069076
19 39.8 24.6 8 AC074322
20 38.8 24.0 8 AF017756
21 38.8 24.0 8 AF009011
22 35.2 21.7 8 AC025531
23 35.2 21.7 8 AC024049
24 35.2 21.7 8 AC040933
25 34.8 21.5 8 AF097313
26 34.8 21.5 8 AF002999
27 34.4 21.2 8 AF276758
28 33.8 20.9 8 AB030253
29 33.6 20.7 8 AF032387
30 33.4 20.6 8 MM001103
31 33.4 20.6 8 HS998C11
32 33.4 20.6 8 AC009412
33 33 20.4 8 AC002554
34 33 20.4 8 AL139096
35 33 20.4 8 AL139643
36 32.8 20.2 8 AC026758
37 32.8 20.2 8 AC019122
38 32.4 20.0 8 AF064873
39 32.4 20.0 8 MM122512
40 32.4 20.0 8 AC073957
41 32.4 20.0 8 AC073759
42 32.2 19.9 8 AL450307
43 32.2 19.9 8 AC034122
44 32 19.8 8 LMFL7836
45 31.8 19.6 8 RNCROW2

ALIGNMENTS

RESULT 1
LOCUS A98523 162 bp DNA PAT 26-JAN-2000
DEFINITION Sequence 8 from Patent WO9911780.
ACCESSION A98523
VERSION A98523.1 GI:6781609
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 162)
AUTHORS Birchmeier,W. and Behrens,J.
TITLE CONDUCTIVE PROTEIN AND A RELATED AGENT FOR DIAGNOSING AND TREATING
TUMOR ILLNESSES
JOURNAL Patent: WO 9911780-A 8 11-MAR-1999;
BIRCHMEIER WALTER (DE); BEHRENS JUERGEN (DE)
FEATURES
source 1..162
BASE COUNT 36 a 51 c 46 g 29 t
ORIGIN

Query Match 100.0%; Score 162; DB 9; Length 162;
Best Local Similarity 100.0%; Pred. NO.1,1e-31;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gccaatggccaagtgtctctacatcttcacgaacccacgcgtcgccaagagatg 60
DB 1 gccaatggccaagtgtctctacatcttcacgaacccacgcgtcgccaagagatg 60
QY 61 acgcctgtggaacctgtccttcgacgcgcgagatcattccaggcttgagaactgaa 120

Db 61 ACGCCTGTGGAACCTGTCTCCCTCCGCCGACGCTCATCTCCAGGCTGGAGAACTGAAA 120
QY 121 ctgagcttggaagccgcacatagtcttgaggagcgcgtcgag 162
Db 121 CTGAGCTTGGAAGCCGCCATAGTCTGGAGAGAGCGGCTGGCAG 162

RESULT 2
LOCUS A98521 2825 bp DNA PAT 26-JAN-2000
DEFINITION Sequence 6 from Patent WO9911780.
ACCESSION A98521
VERSION A98521.1 GI:6781607
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2825)
AUTHORS Birchmeier,W. and Behrens,J.
TITLE CONDUCTIVE PROTEIN AND A RELATED AGENT FOR DIAGNOSING AND TREATING
TUMOR ILLNESSES
JOURNAL Patent: WO 9911780-A 6 11-MAR-1999;
BIRCHMEIER WALTER (DE); BEHRENS JUERGEN (DE)
FEATURES
source 1..2825
BASE COUNT 703 a 815 c 813 g 494 t
ORIGIN

Query Match 100.0%; Score 162; DB 9; Length 2825;
Best Local Similarity 100.0%; Pred. NO.6,3e-32;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1241 gccaatggccaagtgtctctacatcttcacgaacccacgcgtcgccaagagatg 1300
QY 61 acgcctgtggaacctgtccttcgacgcgcgagatcattccaggcttgagaactgaa 120
DB 1301 ACGCCTGTGGAACCTGTCTCCCTCCGCCGACGCTCATCTCCAGGCTGGAGAACTGAAA 1360
QY 121 ctgagcttggaagccgcacatagtcttgaggagcgcgtcgag 162
Db 1361 CTGAGCTTGGAAGCCGCCATAGTCTGGAGAGAGCGGCTGGCAG 1402

RESULT 3
LOCUS AF073788 2825 bp mRNA ROD 13-JUL-1998
DEFINITION Mus musculus conductin mRNA, complete cds.
ACCESSION AF073788
VERSION AF073788.1 GI:3309246
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 2825)
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Behrens,J., Jerchow,B.-A., Wurttele,M., Grimm,J., Asbrand,C.,
Wirtz,R., Kuhl,M., Wedlich,D. and Birchmeier,W.
TITLE Functional interaction of an axin homolog, conductin, with
beta-catenin, APC, and GSK3beta
JOURNAL Science 280 (5363), 596-599 (1998)
MEDLINE 98221239
REFERENCE 2 (bases 1 to 2825)
AUTHORS Behrens,J., Jerchow,B.-A. and Birchmeier,W.
TITLE Direct Submission
JOURNAL Submitted (22-JUN-1998) Cellular Biology, Max Delbrueck Center for
Molecular Medicine, Robert-Rössle 10, Berlin 13122, Germany
FEATURES
source 1..2825

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215. .2737
CDS

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 TKKOOLGVMFACQDQFTEILOAVMEENAYQVLTSTIYLEYVRSGEENYANNGGLSGI
 KVLCSYILPTLNBEERWPCADLKCKLSTPVVGLSKTILATASVSTSTAEENGPSFKRK
 SDVNPVTHVSGYVFAPATISANDSELSDLTLDTSMMTDSVDGVPPTLRGSKKQQLQ
 RENDHRSYKANGQVSLPHFPTATHRLPKMTEVPEAPFAEELISLEKLTLEHSHSLSE
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Best Local Similarity 100.0% Pred. No. 6.3e-32;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 gccaatggccaaatgctctactcatttccgagaaaccacgcgcctccccaagaatg 60
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QY 61 acgcctgtggaacctgcctgccttcgcgcgcgaatcattccaaagctgagaactgaa 120
DB 1301 ACGCCTGTGGAAACCTGCTGCCTTCGCCGCCGAGCTCATCTCCAGGCTGGAGAAACTGAAA 1360

QY 121 ctggaagctggaagaccgcacatagctcggagagagcgagctgagcag 162
DB 1361 CTGGAGCTGGAAAGCCGCAATGCTGGAGAGAGCGGCTGGACG 1402

RESULT 4
AF205889
LOCUS AF205889 3016 bp mRNA ROD 03-JAN-2000
DEFINITION Mus musculus Ax1n2 (Ax1n2) mRNA, complete cds.
ACCESSION AF205889
VERSION AF205889.1 GI:6653585
KEYWORDS
SOURCE .
ORGANISM house mouse.
MUS musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (Bases 1 to 3016)
Zhang,T., Fagotto,F., Hsu,W., Zeng,L., Gilbert,D., Copeland,N.G.,
Jenkins,N.A., Warburton,D. and Costantini,F.
Properties of mouse Ax1n2 and human AXIN2: Chromosomal location,
expression pattern, interaction with Axin and effects on embryonic
axis formation
Unpublished
2 (Bases 1 to 3016)
Zhang,T. and Costantini,F.
Direct Submisson
Submitted (16-NOV-1999) Genetics & Development, Columbia
University, 701 W168th St. HSC 1416, New York, NY 10032, USA
Location/Qualifiers
1. 3016
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="11"
/map="between Wnt3 and Pkca"

FEATURES
SOURCE

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CDS	55. .2577

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IKKQOIGSVMEADQOTILOAEMENAVOFTSLIYLEYRSGSENPATYNGSLGSL
KYLQGLPTLNEEBEWCADLKCLSPVNGLSKTLRATASVSTETANGSPSPER
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Best Local Similarity		100.0%	Pred. NO. 6.2e-32:		
Matches 162:	Conservative	0:	Mismatches	0:	Gaps 0:
Oy	1	gccaatgacgaagtgtccttaccatatttcocagaaacccacgccttgcccagaagagata	60		
Db	1081	GCCAATGGCCAAAGTGTCTCTACCTATTTCGGAACAACCACCGCCTGCCCAAGAAGATG	1140		
Oy	61	acggcctgtgaaacctgtccttcgcgcgcgcagactcatctccaggcttgagaactgtaa	120		
Db	1141	ACGCCTGTGGAAACCTGCTGCTTGCCGCCGCCGACTCATCTCCAGCCTGAGAAACTGAAA	1200		
Oy	121	ctggagcctgaaaagccgcgatagtttgagaagagcgctgcgac	162		
Db	1201	CTGGAGCTGGAAAGCCGCCATAGTGTGGAGAGACGCGCTGCAG	1242		
RESULT	5				
AF017757					
LOCUS	AF017757	3216 bp	mRNA	ROD	24-Apr-1998
DEFINITION	Rattus norvegicus GSK-3beta Interacting protein Axil mRNA, complete cds.				
ACCESSION	AF017757				
VERSION	AF017757.1	GI:3080758			
KEYWORDS					
SOURCE	Norway rat.				
ORGANISM	Rattus norvegicus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;				
	Rattus.				
REFERENCE	1 (bases 1 to 3216)				
AUTHORS	Yamamoto,H., Kishida,S., Uochi,T., Ikeda,S., Koyama,S., Asashima,M.				
	and Kikuchi,A.				
TITLE	Axil, a member of the Axin family, interacts with both glycogen synthase kinase 3beta and beta-catenin and inhibits axis formation of Xenopus embryos				
JOURNAL	Mol. Cell. Biol. 18 (5), 2867-2875 (1998)				
MEDLINE	98226558				
REFERENCE	2 (bases 1 to 3216)				
AUTHORS	Yamamoto,H., Ikeda,S., Murai,H., Kishida,S. and Kikuchi,A.				
TITLE	Direct Submission				
JOURNAL	Submitted (08-AUG-1997) Biochemistry, Hiroshima University, School of Medicine, 1-2-3 Kasumi, Minami-ku, Hiroshima, Hiroshima 734,				
	Japan				
FEATURES	Location/Qualifiers				
source	1..3216				

CDS

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CGSRGCTLPKRTKGTPEGLALPAREGMSAAGAPQLPGEGRGSDQVWMLSEK
OSKSPHSTOSIRKSYPLESARAPGERVSRHHLGASGHPRARAPFTODPAMP
LTPPTLQLEACRRLAEVSPKRCVAVSQOORHNPATGAGPFSFNSLASE
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BASE COUNT

860 a 914 c 872 g 570 t

ORIGIN

Query Match 91.1%; Score 147.6; DB 94; Length 3216;
Best Local Similarity 94.4%; Pred. No. 3.1e-28;
Matches 153; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 gccaatgccaagtgtctctacatcttccgagaaccaccgcctgccaagaagatg 60

Db 1111 GCCATGGCCAGTGTCTTACTCTACCTCCGAGAACCCGCTGCCCAAGAGATG 1170

OY 61 acgcctgtggaacctgtgctctcgcgcgagctatctcgaagcttgagaactgaa 120

Db 1171 AGCCCGTGGACCTGCTCTCCGCCGAGACCTCATCTCCAGGCTGAGAACTGAAA 1230

OY 121 ctgagagctggaagccgcatagtctgagagcgagctgcaag 162

Db 1231 CTGAGCTGGAGCGCCGACGCTGAGAACTGCTGAG 1272

LOCUS

AC024114 191041 bp DNA HTG 06-NOV-2000

DEFINITION Mus musculus chromosome 11 clone RP23-278J12, WORKING DRAFT

ACCESSION AC024114

VERSION AC024114.8 GI:11094615

KEYWORDS HTG; PHASE1; HTGS_DRAFT.

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 191041)
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Mus musculus.
house mouse.
Metzker, M.L., Lewis, L.R., Hume, J., Edwards, C., Harris, C.,
Dederich, D., Thomas, S., Okumura, G., Carlock, C., Garner, T.,
Addison, S., Pace, A., Williams, G., Bonin, D., Brooks, A., Brown, J.,
Bunay, C., Bunac, C., Burkett, C., Chacko, J., Chen, G., Chen, Z.,
Cox, C., Davis, C., Delgado, O., Ding, Y., Dugan-Rocha, S.,
Fernandez, C., Ferraguto, D., Forcum-Tansey, J., Gil, R.,
Gorell, J.H., Gunaratne, P., Haller, G., Hernandez, J., Hogues, M.,
Hosaki, H., Hou, X., Huber, J., Jackson, U., Jia, Y., Kelly, J., Kelly, S.,
Kovari, C., Liu, J., Liu, J., Louised, H., Lozano, R., J., Martin, R.,
Massey, E., McLeod, M.P., Mei, G., Moore, S., Morgan, M., Morris, S.,
Neel, D., Nelson, A., Nguyen, R., Nguyen, N., Ogih, M., Parish, B.,
Perez, L., Reiter, D., Say, J., Shen, H., Vasquez, L., Watlington, S.,
Williams, A., Wrensford, G., Zhou, X., Bouck, J., Hodgson, A.,
Muzny, D.M., Rives, M., Scherer, S., Sodergren, E., Weinstock, G.,
Wolfe, K. and Gibbs, R.
Direct Submission

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

Unpublished
2 (bases 1 to 191041)
Worley, K.C.
Direct Submission
Submitted (24-FEB-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 4, 2000 this sequence version replaced gi:9929587.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: MACA
Center clone name: RP23-278J12
----- Summary Statistics
Sequencing vector: M13; L08821
Chemistry: Dye-terminator Big Dye 5% of reads
Chemistry: Dye-terminator Big Dye 5% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 158769 bases at least Q40
Consensus quality: 172780 bases at least Q30
Consensus quality: 179030 bases at least Q20
Estimated insert size: 180377; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-gel estimation
Quality coverage: 3.2x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_dirft_data.html).
* NOTE: This is a "working draft" sequence. It currently
* consists of 30 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 19344: contig of 19344 bp in length
* 19345 19444: gap of unknown length
* 19445 33763: contig of 14319 bp in length
* 33764 33863: gap of unknown length
* 33864 47738: contig of 13875 bp in length
* 47739 47838: gap of unknown length
* 47839 59611: contig of 11773 bp in length
* 59612 59711: gap of unknown length
* 59712 67897: contig of 8186 bp in length
* 67898 67997: gap of unknown length
* 67998 77929: contig of 9932 bp in length
* 77930 78029: gap of unknown length
* 78030 86605: contig of 8576 bp in length
* 86606 86705: gap of unknown length
* 86706 93904: contig of 7199 bp in length
* 93905 94004: gap of unknown length
* 94005 104236: contig of 10232 bp in length
* 104237 104337: gap of unknown length
* 104338 113241: contig of 8905 bp in length
* 113242 113341: gap of unknown length
* 113342 120171: contig of 6830 bp in length
* 120172 120271: gap of unknown length
* 120272 125989: contig of 5718 bp in length
* 125990 126089: gap of unknown length
* 126090 131869: contig of 5780 bp in length
* 131870 131969: gap of unknown length
* 131970 132994: contig of 7325 bp in length
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* 133995 146006: contig of 6612 bp in length
* 146007 146106: gap of unknown length
* 146107 150788: contig of 4682 bp in length
* 150789 150888: gap of unknown length
* 150889 156925: contig of 6037 bp in length
* 156926 157025: gap of unknown length
* 157026 161170: contig of 4145 bp in length

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* 161171 161270: gap of unknown length
* 1643271 164311: contig of 3041 bp in length
* 164312 164411: gap of unknown length
* 164412 167354: contig of 2943 bp in length
* 167355 167454: gap of unknown length
* 167455 171291: contig of 3837 bp in length
* 171292 171391: gap of unknown length
* 171392 174233: contig of 2842 bp in length
* 174234 174333: gap of unknown length
* 174334 177744: contig of 3411 bp in length
* 177745 177844: gap of unknown length
* 177845 179402: contig of 1558 bp in length
* 179403 179502: gap of unknown length
* 179503 182420: contig of 2918 bp in length
* 182421 182520: gap of unknown length
* 182521 184923: contig of 2403 bp in length
* 184924 185023: gap of unknown length
* 185024 187054: contig of 2031 bp in length
* 187055 187154: gap of unknown length
* 187155 188272: contig of 1118 bp in length
* 188273 188372: gap of unknown length
* 188373 189634: contig of 1262 bp in length
* 189635 189734: gap of unknown length
* 189735 191041: contig of 1307 bp in length.

FEATURES
    source
        1. 191041
            /organism="Mus musculus"
            /db_xref="taxon:10090"
            /chromosome="11"
            /clone="RP23-278J12"

BASE COUNT  49790 a 43523 c 42989 g 51816 t 2923 others
ORIGIN

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Query Match
Best Local Similarity 95.8%; Pred. No. 6.7e-25;
Matches 137; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 20 tacctcatttcgagaaacacacgcgcctgcgaagagatgagcctgtggaacctgctg 79
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 30765 TCCACACCCCTCAGAGAACCCACCCCTGCCAAGAGATGAGCGCTGTGGAACCTGCTG 30824

OY 80 ccttcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 139
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 30825 CCTTGGCCGCCAGCTCACTCTCAGCGTGAGAACTGGAAGTGAAGTGAAGAAAGCCGCC 30884

OY 140 atagctcgagagagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 162
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 30885 ATAGCTGTGAGAGAGCGCGCTGCAG 30907

RESULT 7
LOCUS AK025718 2104 bp mRNA PRI 29-SEP-2000
DEFINITION Homo sapiens cDNA: FLJ22065 fis, clone HEP10566, highly similar to
ACCESSION AK025718
VERSION AK025718.1 GI:10438327
KEYWORDS oligo capping: fis (full insert sequence).
SOURCE Homo sapiens hepatoma cell_line:hepg2 cDNA to mRNA, clone_11b:HEP
    Clone:HEP10566.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
    1 (sites)
TITLE Kanabara, A., Hiji, J., Kobatake, N., Inagaki, H., Ikema, Y.,
JOURNAL Okamoto, S., Okitani, R., Ota, T., Suzuki, Y., Obayashi, M., Nishi, T.,
REFERENCE Shihabara, T., Tanaka, T., Nakamura, Y., Isogai, T. and Sugano, S.
AUTHORS NEDO human cDNA sequencing project
TITLE Unpublished (2000)
JOURNAL 2 (bases 1 to 2104)
REFERENCE Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T.,
AUTHORS Shihabara, T., Tanaka, T. and Nakamura, Y.

```

```

TITLE Direct Submission
JOURNAL Submitted (29-AUG-2000) to the DDBJ/EMBL/GenBank databases. Sumio
Sugano, Institute of Medical Science, University of Tokyo,
Laboratory of Genome Structure Analysis, Human Genome Center;
Shirokane-dai, 4-6-1, Minato-Ku, Tokyo 108-8639, Japan
(E-mail:cdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing: Department of
Virology and Human Genome Center, Institute of Medical Science,
University of Tokyo (partly supported by Science and Technology
Agency).

FEATURES
    source
        1. 2104
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /cell_line="hepg2"
            /cell_type="hepatoma"
            /clone="HEP10566"
            /clone_11b="HEP"
            /note="Cloning vector pME18SFL3"
            /note="highly similar to AF078165 Homo sapiens conductin
            mRNA"

BASE COUNT  506 a 610 c 619 g 369 t
ORIGIN

Query Match
Best Local Similarity 81.2%; Pred. No. 4.4e-24;
Matches 143; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 1 gccaatggccaagtgtctactcatttcgcgagaaacacacgcgcctgcgaagagatg 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 338 GCCAATGGCAAGTGTCTACTCTATTTCGAGAAACCCACCGCTGCCAAGAGATG 397

OY 61 agcgcctggaacctgctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 398 ACCCCCGTGAACCCCGCCACCTTTCGACGCTGATCTCGAGCTGGAAAGCTGAAG 457

OY 121 cggagctggaagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 162
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 458 CTGGAGTTGAGAGCGCGCCACAGCTGAGAGAGCGCTGCAG 499

RESULT 8
LOCUS AF078165 3072 bp mRNA PRI 21-MAR-1999
DEFINITION Homo sapiens conductin mRNA, complete cds.
ACCESSION AF078165
VERSION AF078165.1 GI:4454790
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
    1 (bases 1 to 3072)
TITLE Mai, M., Qian, C., Yokomizo, A., Smith, D.I. and Liu, W.
JOURNAL Cloning of the human homolog of conductin (XXIN2), a gene mapping
REFERENCE to chromosome 17q23-q24
AUTHORS Genomics 55 (3), 341-344 (1999)
TITLE 2 (bases 1 to 3072)
JOURNAL Mai, M., Qian, C., Smith, D.I. and Liu, W.
REFERENCE Direct Submission
AUTHORS Submitted (15-JUL-1998) Lab Medicine and Pathology, Mayo Clinic,
JOURNAL 200 First Street SW, Rochester, MN 55905, USA
FEATURES
    source
        1. 3072
            /organism="Homo sapiens"
            /db_xref="taxon:9606"

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/chr="17"
/map="17q23-q24"
90.2621
CDS

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BASE COUNT	ORIGIN
769 a	GNRYRYFKKASDEFACGAVFEIIMEDETIVLPMYEGRILGVERID"
838 c	
883 g	
582 t	

Query Match	81.2%;	Score 131.6;	DB 88;	Length 3072;
Best Local Similarity	88.3%;	Pred. NO. 4.1e-24;		
Matches 143; Conservative	0;	Mismatches 19;	Indels 0;	Gaps 0;

QY	1	gcaatgagccaatgctctcaactcatcttcgcgaagaccacacgcgtcgccaaagaagt	60
Db	1116	GCCAATGGCCAAAGTCTCACTACCTCAATTCGCCGAGAACCAACGGCTGCCAAGGATG	1175
QY	61	acgcctctggaacctgctgcttcgcgcgcgcagctatcttcaggtctggaagaactgaa	120
Db	1176	ACCCCGCTGGAAACCCCGCACACTTTCGACGCTGACGACTATCTCCAGGCTGGAAAAGCTGAG	1235
QY	121	cttgagactggaagaagccgcaatgctctggaagagcagatcgag	162
Db	1236	CTTGAGATTGGAGAGCCGCCACACACTCTGGAGAGAGCCGCTTCGAC	1277

RESULT AF205888	9	AF205888
LOCUS		AF205888
DEFINITION	2538 bp	mRNA
ACCSSION	Homo sapiens AXI2 (AXIN2), complete cds.	PRTS
VERSION	AF205888	
KEYWORDS	AF205888.1 GI:6653583	
SOURCE	human.	

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 2538)	Zhang, T., Fagotto, F., Hsu, W., Zeng, L., Gilbert, D., Copeland, N. G., Jenkinson, N. A., Warburton, D. and Costantini, F.	Properties of mouse Axin2 and human AXIN2: chromosomal location, expression pattern, interaction with Axin and effects on embryonic axis formation
unpublished		
2 (bases 1 to 2538)	Zhang, T. and Costantini, F.	Direct Submision
Submitted (16-NOV-1999)		
Genetics & Development, Columbia University, 701 W168th St. HHSC 1416, New York, NY 10032, USA		
Location/Qualifiers		

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1. 2538
location/Vadaillets
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="17"
/map="17q24"
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/tissue_type="brain; lymphoblast"
/notes="similar to ESTs 823683 and 446378
1..2538
/gene="AXIN2"
110..2443
CDS

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BASE COUNT	617 a	724 c	724 g	473 t
ORIGIN				

Query Match	79.3%;	Score 128.4;	DB 88;	Length 2538;
Best Local Similarity	87.0%;	Pred. No. 2.9e-23;		
Matches 141; Conservative	0;	Mismatches 21;	Indels 0;	Gaps 0;

QY	1	gcacatgccaacatgactctactcaatttcgcgagaccacacgcctgcccagaagatg	60
Db	1133	GCACATGGCAGAGTGTCTCTACTCATTTTCCGAGAACCCACGCGCTGCCCAAGAGATG	1199
QY	61	acgcctctggaacctctgctgccttcgcgcgcgcagcctatctccagctgagaaactgaa	120
Db	1193	ACCCCGCTGGAAACCCGCGCACCTTTGAGAGCTGACGTATCTCAGAGCGTGGAAAAAGCTGAAG	1255
QY	121	ctggaagctggaagaacgcgcatagtctggagagagcgcctgcag	162
Db	1253	CTGGAGTTGGAGAGACGCCACACACCTCTGGAGAGACGCCCTTCAG	1294

RESULT	10			
AB032263		AB032263	3485 bp	mRNA
LOCUS		Danio rerio	mRNA for axin2,	VFT
DEFINITION		AB032263	complete cds.	
ACCESSION		AB032263.1	GI:7229079	
VERSION				
KEYWORDS				
SOURCE		Danio rerio	cDNA to mRNA.	

REFERENCE	
AUTHORS	Shimizu,T., Yamanaka,Y., Ryu,S.L., Hashimoto,H., Yabe,T., Hirata,T., Bae,Y.K., Hibli,M. and Hirano,T.
TITLE	Cooperative roles of Borzok/Dharma and Nodal-related proteins in the formation of the dorsal organizer in zebrafish
JOURNAL	Mech. Dev. 91 (1-2), 293-303 (2000)
MEDLINE	20171051
AUTHORS	2 (bases 1 to 3485)
REFERENCE	Hirano,T., Hibli,M. and Shimizu,T.
TITLE	Direct Submission
JOURNAL	Submitted (09-SEP-1999) to the DDBJ/EMBL/Genbank databases. Toshio

Submitted (09-SEP-1999) to the DDBJ/EMBL/GenBank databases. Toshio Hirano, Biomedical research center, Osaka Univ. Med. school, Department of Molecular Oncology, 2-2, Yamadaoka, Suita, Osaka 565-0871, Japan (E-mail: hirano@molonc.med.osaka-u.ac.jp, URL: <http://www.med.osaka-u.ac.jp/pub/molonc.med.osaka-u.ac.jp>, Tel:81-6-879-3880, Fax:81-6-879-3889)

REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE	AUTHORS	TITLE	JOURNAL
1	(bases 1 to 3156)	Archosauria: Aves: Neognathae: Galliformes: Phasianidae: Gallus	Phasianidae: Gallus	2	(bases 1 to 3156)	Zeng, L., Zhang, T., Hsu, W., Vasicek, T. J., Perry, W. L., 3rd, Lee, J. J., Tillingham, S. M., Gumbler, B. M. and Costantini, F.	The mouse fused locus encodes Axlin, an inhibitor of the Wnt signaling pathway that regulates embryonic axis formation
3	Cell 90 (1), 181-192 (1997)			4	97373830		
5	Submitted (13-JUN-1997)	Genetics and Development, Columbia University, 701 W. 168th Street, New York, NY 10032, USA		6	Location/Qualifiers		
7	1. 3156	/organism="Gallus gallus"		8	/db_xref="taxon:9031"		
9	1. 3156	/gene="Axlin"		10	/note="Fused is the classical dominant mouse tail kink mutation due to an 1ap insertion in the Axlin gene"		
11	258. 2783	/gene="Axlin"		12	/function="may inhibit embryonic axis formation"		
13	/product="Axlin"			14	/codon_start=1		
15	/protein_id="AAC60245.1"			16	/db_xref="GI:2252818"		
17	/translation="MTIOGKRGPLDILGRSPEDAPRPVPGEGELVTDROPVSHGF			18	YSSSDAVNRETSTATPRRSDDLDGCPREGASAPPTPYLKAEBSHLDODDINFL		
19	RTFLKEDCADLDFWTFACSGFKLEPCVSNEEKRLAKATYKYLIDNNGIVSRDI			20	KIPAKSPFKDCVMKLGIDPMDQAEQICMDINDYPLFKSDIYLEYRTGEGSP		
21	KIAPDPSGSGGTGGLGYLPTLNEDEMKCDQDTEPEASDASPSRLQKILETFA			22	TQRTSTIRRYSEGREPRHGSWREPVNPLYVNTGYAMA.PATSANSEDOSSDADTMS		
23	LTDSITGIPRYRLRKORHRRMOBSAKANGVPLPHI.PRYRMPKDIHVEPEKRAEL			24	INRLIEYOKEREAEKLEBRKRYRAEEGEDADISSPSYISKMSAOPFFHFAFRP		
25	YSESGCAGMOMRDHHEENPESITDEHVQVWKVTKGSCSPGGRHSPPRSESGHLK			26	LSGRLCTIPGCHGHTTNSQMKLDAANLYHKHYHIIHHSNMKPEQIEAETORL		
27	ONSAPMNVDSHNYATKSRNYSENLGMA.PVPSDLSYGKASLKRNIKTDSKSDGS			28	ANYMSPDEPVERNOKILWIIEGKEIKSHKKTNGSSGVKKLSDHWVRSTIEPE		
29	PVNAVPRVSAQLRVNVPSPHFIDDPMPMPAPRPLVQLLEARRRLIEEERKGLPL			30	LKQNLAKPKRFGSCASPCENIVAYITFCGEPIYRPLVLKGRVYTLQCFKELLTKKG		
31	YRYYKAFVSDFFDGVVFEVEREDDTLPIFEKXIKGVKID						

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SOURCE          human.
ORGANISM        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 22029)
AUTHORS        Smev, R.
TITLE          Direct Submission
JOURNAL        Submitted (27-OCT-1997) Chromosome 16 Project Group
               (http://www.sanger.ac.uk/HGP/chr16/) Sanger Centre, Wellcome Trust
               Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail
               enquiries: humquerry@sanger.ac.uk Clone requests:
               clone.requests@sanger.ac.uk
COMMENT        On Apr 8, 1998 this sequence version replaced gi:2465054.
               IMPORTANT: This sequence is not the entire insert of clone 419C1.
               It may be shorter because we only sequence overlapping sections
               once, or longer because we arrange for a small overlap between
               neighbouring submissions.
               The true left end of clone 419C1 is at 1 in this sequence. The true
               right end of clone 314G4 is at 104.
               The true left end of clone 333B10 is at 21926.
               419C1 is from a 400kb clone contig on 16p.
               Higgs D.R., Flint J. unpublished. MRC Molecular Haematology Unit,
               Institute of Molecular Medicine, Oxford.
               419C1 came from the Los Alamos, flow sorted human Chromosome 16
               libraries constructed by Norman Doggett (unpublished).

FEATURES
Source
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/db_xref="taxon:9606"
/chromosome="16"
/map="16p13.3"
/clone="LA16.419C1"
/clone_id="LA16"
43..327
/note="Alusx repeat: matches 1..302 of consensus"
345..627
/note="Alusq repeat: matches 21..303 of consensus;
incomplete repeat"
644..922
/note="Alusq repeat: matches 25..303 of consensus;
incomplete repeat"
928..1228
/note="Aluv repeat: matches 1..299 of consensus"
1244..1529
/note="Alusq repeat: matches 302..28 of consensus;
incomplete repeat"
1596..1714
/note="Aludv repeat: matches 184..299 of consensus;
incomplete repeat"
1827..2124
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2131..2294
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incomplete repeat"
4653..4914
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incomplete repeat"
4928..5213
/note="Alusq repeat: matches 286..1 of consensus"
5508..5801
/note="Alusx repeat: matches 294..1 of consensus"
5804..6101
/note="Aluv repeat: matches 298..1 of consensus"
6106..6383
/note="Alusq repeat: matches 303..6 of consensus"
6389..6642
/note="Aludv repeat: matches 247..5 of consensus;
incomplete repeat"
7150..7437
/note="Aluv repeat: matches 15..301 of consensus"
7656..7779
/note="Aludv repeat: matches 1..124 of consensus;
incomplete repeat"

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Search completed: June 7, 2001, 00:35:43
Job time: 20957 sec

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repeat_region 9042. .9307 /note="AluNb repeat: matches 267. .1 of consensus;  
incomplete repeat"  
repeat_region 9532. .9828 /note="AluSg repeat: matches 297. .1 of consensus"  
prln_transcript 9967. .10175 /note="match: 5' EST AA085320"  
prln_transcript 10450. .>16291 /note="match: mouse 5' EST AA238939"  
repeat_region 10683. .10981 /note="AluSx repeat: matches 299. .1 of consensus"  
repeat_region 11335. .11635 /note="AluNb repeat: matches 1. .295 of consensus"  
unsure 11604  
unsure 11609  
unsure 11627  
repeat_region 11689. .11990 /note="AluY repeat: matches 301. .1 of consensus"  
repeat_region 12003. .12110 /note="AluSg repeat: matches 123. .1 of consensus;  
incomplete repeat"  
repeat_region 12132. .12248 /note="MER42c repeat: matches 1536. .1414 of consensus"  
repeat_region 12361. .12508 /note="MER42c repeat: matches 1335. .1186 of consensus"  
repeat_region 12672. .12743 /note="MIR repeat: matches 111. .181 of consensus"  
repeat_region 13651. .13844 /note="MER1B repeat: matches 333. .139 of consensus"  
repeat_region 14879. .14912 /note="17 copies of 2 mer 82 & conserved"  
repeat_region 15202. .15422 /note="AluY repeat: matches 7. .227 of consensus;  
incomplete repeat"  
repeat_region 16542. .16847 /note="AluY repeat: matches 301. .1 of consensus"  
repeat_region 17178. .17476 /note="AluY repeat: matches 301. .1 of consensus"  
repeat_region 17637. .17936 /note="AluY repeat: matches 1. .300 of consensus"  
repeat_region 19054. .19163 /note="AluY repeat: matches 2. .124 of consensus;  
incomplete repeat"  
repeat_region 19179. .19468 /note="AluY repeat: matches 2. .302 of consensus"  
repeat_region 20549. .20724 /note="4 copies of 44 mer 88 & conserved"  
repeat_region 21693. .21994 /note="AluY repeat: matches 1. .301 of consensus"  
repeat_region 21999. .22028 /note="AluSx/g repeat: matches 82. .111 of consensus;  
incomplete repeat"  
BASE COUNT 5145 a 6217 c 5887 g 4780 t  
ORIGIN
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Query Match 24.6%; Score 39.8; DB 91; Length 22029;
Best Local Similarity 60.4%; Pred. No. 1.2;
Matches 84; Conservative 0; Mismatches 52; Indels 3; Gaps 1;

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QY 24 tcatttcgagaaacccgcgcctgccaagaagatgaagcctgtgaaactgtcgtcctt 83  
Db 10598 TCCCTCGAGCGCACGCTACGGCGGCTCCAGAGAGT---CCGCGTGGAGCCTCAGAA GTT 10542  
QY 84 cgcgcgcgagctcatctccagagctggaactgaactgagctgagaaagcgcgcataag 143  
Db 10541 CGCGGAGAGAGCTATTCACCGCTCGAGAGGCTGTGTGACGCGCAGCGGAGGCGCGAGAGAA 10482  
QY 144 tctgagagagcgcgtcag 162  
Db 10481 GCTGGAGAGAGCGGCTGAAG 10463
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 7, 2001, 00:31:47 ; Search time 276.75 Seconds
(without alignments)
341.726 Million cell updates/sec

Title: US-09-587-574-8

Perfect score: 162
Sequence: 1 gccatgagcccaagtgctctc.....gtctgagggagcgctgcag 162

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_0401:*

- 1: /SIDS2/gcgdata/geneseq/geneseqn/NA1980.DAT:*
- 2: /SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
- 3: /SIDS2/gcgdata/geneseq/geneseqn/NA1982.DAT:*
- 4: /SIDS2/gcgdata/geneseq/geneseqn/NA1983.DAT:*
- 5: /SIDS2/gcgdata/geneseq/geneseqn/NA1984.DAT:*
- 6: /SIDS2/gcgdata/geneseq/geneseqn/NA1985.DAT:*
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- 11: /SIDS2/gcgdata/geneseq/geneseqn/NA1990.DAT:*
- 12: /SIDS2/gcgdata/geneseq/geneseqn/NA1991.DAT:*
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- 21: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:*
- 22: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	162	100.0	2523	20	Human conductin CN
2	162	100.0	2825	20	Human conductin CD
3	56.4	34.8	3411	20	Human axin gene.
4	38.8	24.0	3761	20	Murine axin gene.
5	32.4	20.0	1584	20	Mouse brain CNG-2
6	31.2	19.3	1342	20	Human Ih ion channel
7	31.2	19.3	2029	20	Human heart tissue
8	31.2	19.3	2886	20	Human Ih ion channel
9	31.2	19.3	38186	20	Human MET1 relate
10	31.2	19.3	38186	22	AC004449 cDNA clone
11	30.8	19.0	794	20	Rat olfactory Ih 1

12	30.8	19.0	1247	14	041354	Human GDF-1 coding
13	30.8	19.0	1247	14	038862	Morphogen GDF-1 co
14	30.8	19.0	1247	15	058055	Human morphogenic
15	30.8	19.0	1247	15	067315	Human GDF-1 (fx) mo
16	30.8	19.0	1247	15	045120	Human GDF-1 (fx) mo
17	30.8	19.0	1247	15	067402	Human GDF-1 (fx) mo
18	30.8	19.0	1247	18	V10351	Human GDF-1 cDNA.
19	30.8	19.0	1247	18	V97883	CDNA sequence enco
20	30.8	19.0	1247	19	V25588	Human GDF-1 cDNA.
21	30.8	19.0	1247	19	V19538	Human GDF-1 (fx) p
22	30.8	19.0	1247	19	V19538	Mouse GDF-1 encodi
23	30.8	19.0	2510	13	Q20690	hGDF-1 and hOG-1
24	30.4	18.8	1553	21	258953	Human MIF1 protein
25	30.4	18.8	1914	21	258958	Human MIF1 protein
26	30.2	18.4	533	21	A42312	Human secreted exp
27	29.8	18.4	537	21	C56489	Eucahyptus grandis
28	29.6	18.3	372	21	C00205	Human secreted pro
29	29.6	18.3	1034	20	X87634	Human porphobilino
30	29.6	18.3	1246	22	F33247	Human porphobilino
31	29.6	18.3	1307	20	X25488	Human cyclic nucle
32	29.6	18.3	1507	20	X84446	Mouse brain CNG-3
33	29.6	18.3	1790	20	X84445	Human brain CNG-2
34	29.6	18.3	1820	20	209488	Bovine retina Ih 1
35	29.6	18.3	4751	20	209496	Human heart tissue
36	29.2	18.0	3531	21	C58368	Human PRO290 nucle
37	29.2	18.0	3531	21	Z64954	Membrane-bound pro
38	28.8	17.8	550	20	Z07225	Human lung tumour
39	28.8	17.8	751	20	C79115	Human lung tumour
40	28.8	17.8	751	20	X40107	Gastric cancer ass
41	28.8	17.8	1034	20	X87637	Human porphobilino
42	28.8	17.8	1035	20	X87638	Human porphobilino
43	28.8	17.8	1035	20	X87630	Human porphobilino
44	28.8	17.8	1035	20	X87632	Human porphobilino
45	28.8	17.8	1035	20	X87633	Human porphobilino

ALIGNMENTS

RESULT 1	
ID X23370	
ID X23370 standard; cDNA: 2523 BP.	
XX AC X23370;	
XX DT 17-JUN-1999 (first entry)	
XX DE Human conductin cDNA.	
XX KW Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour;	
KW therapy; cytoplasmic degradation; blockade; Wnt signalling pathway;	
KW Wingless signalling pathway; Adenomatous Polyposis Coll; APC;	
KW tumour suppressor; ss.	
XX OS Homo sapiens.	
XX PN W09911780-A2.	
XX PD 11-MAR-1999.	
XX PF 01-SEP-1998; 98MO-DE02621.	
XX PR 02-SEP-1997; 97DE-1038205.	
XX PA (DELB-) DELBROECK CENT MOLEKULARE MEDIZIN MAX.	
XX PI Behrens J, Birchmeier W;	
XX DR WPI; 1999-214706/18.	
XX DR P-PSDB; W93570.	
XX PT Tumor-suppressing protein conductin - used for treatment and	
PT diagnosis of tumors	

XX	Claim 18; Fig 3; 22pp; German.
PS	
CC	This invention describes a novel human conductin protein which has
CC	anti-tumour activity. Detecting the presence or amount of conductin,
CC	at protein or nucleic acid levels, is used to diagnose tumours, while
CC	agents that (re)activate conductin are used for tumour therapy.
CC	Conductin binds to beta-catenin and induces its cytoplasmic degradation,
CC	resulting in blockade of the Wnt/Wingless signalling pathway in
CC	vertebrates. Conductin also binds to Adenomatous Polypsis Coli (APC)
CC	fragments and, in conjunction with APC, acts as a tumour suppressor.
XX	
SQ	Sequence 2523 BP; 620 A; 728 C; 723 G; 452 T; 0 other;
	Query Match 100.0%; Score 162; DB 20; Length 2523;
	Best Local Similarity 100.0%; Pred. No. 1.2e-38;
	Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps
OY	1 gccaatggccaagtgctcctcatcttccgagaacaccacgcgtcgccaaggagt 60
Db	1027 gccaatggccaagtgctcctcatcttccgagaacaccacgcgtcgccaaggagt 1086
OY	61 acgcctggaacctgctgccttcgcgcgcgcagctcatctccagctcgagaactgaa 120
Db	1087 acgcctggaacctgctgccttcgcgcgcgcagctcatctccagctcgagaactgaaa 1146
OY	121 ctggaactggaagccgcgatagcttggaagagcgctgcag 162
Db	1147 ctggaactggaagccgcgatagcttggaagagcgctgcag 1188
RESULT	2
XZ3369	
ID	XZ3369 standard; CDNA; 2825 BP.
XX	
AC	XZ3369;
XX	
DT	17-JUN-1999 (first entry)
XX	
DE	Human conductin DNA.
KW	Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour;
KM	therapy; cytoplasmic degradation; blockade; Wnt signalling pathway;
KW	Wingless signalling pathway; Adenomatous Polypsis Coli; APC;
KW	tumour suppressor; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key
CDS	Location/Qualifiers
FT	215..2737
FT	/tag= "a"
FT	/product= "Conductin"
FT	446..814
FT	/tag= b
FT	/note= "regulator of G-protein signalling region as
FT	described in Claim 19"
FT	1241..1402
FT	/tag= c
FT	/bound_moiety= GSK-3beta
FT	/note= "as described in Claim 20"
FT	1403..1609
FT	/tag= d
FT	/bound_moiety= beta-catenin
FT	/note= "as described in Claim 21"
FT	2561..2713
FT	/tag= e
FT	/note= "Dishevelled homology region as described in
FT	Claim 22"
XX	
PN	W09911780-A2.
XX	
DD	11-MAR-1999.

XX	01-SEP-1998;	98WO-DE02621.	
PF			
XX	02-SEP-1997;	97DE-1038205.	
PR			
XX			
PA	(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.		
XX			
PI	Behrens J, Birchmeier W;		
XX			
XX	WPI; 1999-214706/18.		
DR	P-PSDB; W93569.		
XX			
PT	Tumour-suppressing protein conductin - used for treatment and		
PT	diagnosis of tumors		
XX			
PS	Claim 18; Fig 2; 22pp; German.		
XX			
CC	This invention describes a novel human conductin protein which has		
CC	anti-tumour activity. Detecting the presence or amount of conductin,		
CC	at protein or nucleic acid levels, is used to diagnose tumours, while		
CC	agents that (re)activate conductin are used for tumour therapy.		
CC	Conductin binds to beta-catenin and induces its cytoplasmic degradation,		
CC	resulting in blockade of the Wnt/Wingless signalling pathway in		
CC	vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC)		
CC	fragments and, in conjunction with APC, acts as a tumour suppressor.		
XX			
SQ	Sequence 2825 BP; 703 A; 815 C; 813 G; 494 T; 0 other;		
Query Match	100.0%; Score 162; DB 20; Length 2825;		
Best Local Similarity	100.0%; Pred. No. 1,2e-38;		
Matches 162; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 gccaatggccaagtgtctctactcaatttccgagaaaccacgcgctggccaagagatg 60		
DB	1241 gccaatggccaagtgtctctactcaatttccgagaaaccacgcgctggccaagagatg 1300		
QY	61 acgcctgtggaaactgctgccttgcgcgcgagcttcattccagctggagaactgaaa 120		
DB	1301 acgcctgtggaaactgctgccttgcgcgcgagcttcattccagctggagaactgaaa 1360		
QY	121 ctggagctggaaagcgcgcattgcttgagagagcgctgcag 162		
DB	1361 ctggagctggaaagcgcgcattgcttgagagagcgctgcag 1402		
RESULT 3			
X09012			
ID	X09012 standard; DNA: 3411 BP.		
AC			
XX	X09012;		
XX			
DT	14-JUN-1999 (first entry)		
XX			
DE	Human axin gene.		
XX			
KW	Axin; cancer; breast cancer; colorectal cancer;		
KW	gastrointestinal cancer; esophageal cancer; carcinoma; melanoma;		
KW	diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;		
KW	beta-catenin; ss.		
OS	Homo sapiens.		
XX			
XX			
FT	Key	Location/Qualifiers	
FT	CDS	2..2704	
FT		/*tag= a	
FT		/product= Axin	
XX			
XX	W099002179-A1.		
PN			
XX	21-JAN-1999.		
DD			
XX			
PF	09-JUL-1998;	98WO-US14414.	

XX 26-AUG-1999.
PD 12-FEB-1999; 99WO-EP00942.
XX 17-FEB-1998; 98DE-1006581.
XX (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.
XX Baumann A, Boenigk W, Gauss R, Kaupp B, Scholten A;
PI Seifert R;
XX MPI: 1999-527472/44.
XX
XX New nucleic acid encoding an Ih ion channel, used to identify
PT specific modulators, and for treatment, prevention and diagnosis of
PT e.g. cardiac disease
XX
XX Disclosure: Page 68-69; 82pp; German.
XX
XX This invention describes a novel Ih ion channel, isolated from human,
CC sea urchin, bovine, rat, and fruitfly. The ion channels of the invention
CC have analgesic and cardioactive activity. The Ih ion channel participates
CC in the pacemaker function in cardiac muscle. The Ih ion channel nucleic
CC acid and its encoding protein is used to identify substances (A) that
CC modulate activity of ion channels; to treat and/or diagnose ion
CC channel-related diseases, particularly cardiac or circulatory disorders
CC and to prevent and/or treat cardiac/circulatory disorders (especially
CC faulty regulation of the sinus ganglion), sleep disorders (particularly
CC abnormal function of cortico-thalamic neurons) and/or pain. Fragments of
CC the Ih ion channel nucleic acid are used to detect mutations e.g. for
CC differential diagnosis. This sequence encodes a human Ih channel
CC fragment isolated from heart tissue.
XX
SQ Sequence 2029 BP: 338 A; 774 C; 509 G; 356 T; 52 other;

Query Match 19.3%; Score 31.2; DB 20; Length 2029;
Best Local Similarity 58.7%; Pred. No. 3.9;
Matches 54; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

OY 39 ccacgcgcgtcccaaggagatgacgcctgtggaacctgctgcctgcgcgcgagccat 98
DB 166 CCACGCCATGCTGTGATGACATCTCTTCCCATGTGCTGCCGATGATGATGAT 107
OY 99 ctccagcctggagaagaactggaactggagctgg 130
DB 106 CCCCAGGCTGGAGACCTCAAAACGACGCTTG 75

RESULT 8
Z09491/C
ID 209491 standard; DNA; 2886 BP.
XX
AC 209491;
XX
DT 02-NOV-1999 (first entry)
XX
DE Human Ih ion channel DNA fragment #2.
XX
XX Human Ih ion channel; sea urchin; fruit fly; rat; bovine; analgesic;
KW cardioactive; pacemaker; cardiac muscle; ion channel modulator;
KW treatment; diagnosis; ion channel-related disease; cardiac disease;
KW circulatory disorder; sinus ganglion regulation; sleep disorder;
KW cortico-thalamic neuron; pain; detection; mutation; ss.
XX
OS Homo sapiens.
XX
XX MO9942574-A1.
XX
XX 26-AUG-1999.
XX
XX 12-FEB-1999; 99WO-EP00942.

XX 17-FEB-1998; 98DE-1006581.
XX (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.
XX Baumann A, Boenigk W, Gauss R, Kaupp B, Scholten A;
PI Seifert R;
XX MPI: 1999-527472/44.
XX
XX New nucleic acid encoding an Ih ion channel, used to identify
PT specific modulators, and for treatment, prevention and diagnosis of
PT e.g. cardiac disease
XX
XX Disclosure: Page 67-68; 82pp; German.
XX
XX This invention describes a novel Ih ion channel, isolated from human,
CC sea urchin, bovine, rat, and fruitfly. The ion channels of the invention
CC have analgesic and cardioactive activity. The Ih ion channel participates
CC in the pacemaker function in cardiac muscle. The Ih ion channel nucleic
CC acid and its encoding protein is used to identify substances (A) that
CC modulate activity of ion channels; to treat and/or diagnose ion
CC channel-related diseases, particularly cardiac or circulatory disorders
CC and to prevent and/or treat cardiac/circulatory disorders (especially
CC faulty regulation of the sinus ganglion), sleep disorders (particularly
CC abnormal function of cortico-thalamic neurons) and/or pain. Fragments of
CC the Ih ion channel nucleic acid are used to detect mutations e.g. for
CC differential diagnosis. This sequence encodes a human Ih channel
CC fragment isolated from human thalamus tissue.
XX
SQ Sequence 2886 BP: 605 A; 774 C; 940 G; 558 T; 9 other;

Query Match 19.3%; Score 31.2; DB 20; Length 2886;
Best Local Similarity 58.7%; Pred. No. 4.2;
Matches 54; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

OY 39 ccacgcgcgtcccaaggagatgacgcctgtggaacctgctgcctgcgcgcgagccat 98
DB 1309 CCACGCCGCTGTGATGACATCTCTTCCCGATGTGCTGCCGATGATGATGAT 1250
OY 99 ctccagcctggagaagaactggaactggagctgg 130
DB 1249 CACCCGGCTGGAGACCTCAACTGAGCTTG 1218

RESULT 9
Z32028/C
ID 232028 standard; DNA; 38186 BP.
XX
AC 232028;
XX
DT 10-JAN-2000 (first entry)
XX
DE Human METH1 related EST AC004449.
XX
XX Human; METH1; METH2; anti-angiogenic; metalloprotease thrombospondin;
KW cancer; diagnosis; hyperproliferative disorder; autoimmune disease;
KW angiogenesis inhibitor; abnormal wound healing; inflammation;
KW rheumatoid arthritis; psoriasis; endometrial bleeding disorder;
KW diabetic retinopathy; macula degeneration; hemangioma; detection;
KW arterial-venous malformation; immune deficiency; ss.
XX
OS Homo sapiens.
XX
XX MO9937660-A1.
XX
XX 29-JUL-1999.
XX
XX 22-JAN-1999; 99WO-US01313.
XX
XX 23-JAN-1998; 98US-0072298.
XX
XX 28-AUG-1998; 98US-0098539.

XX	Rat olfactory Ih ion channel DNA fragment #4.
DE	
KW	Ih ion channel; human; sea urchin; fruit fly; rat; bovine; analgesic;
KM	cardioactive; pacemaker; cardiac muscle; ion channel modulator;
KW	treatment; diagnosis; ion channel-related disease; cardiac disease;
KM	circulatory disorder; sinus ganglion regulation; sleep disorder;
KM	cortico-thalamic neuron; pain; detection; mutation; ss.
OS	Rattus sp.
XN	
PX	M09942574-A1.
PD	26-AUG-1999.
XX	
PF	12-FEB-1999; 99MO-EP00942.
XX	
PR	17-FEB-1998; 98DE-1006581.
PA	(KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.
PI	Baumann A, Boenigk W, Gauss R, Kaupp B, Scholtten A;
PI	Seifert R;
PS	
DR	WPt: 1999-527472/44.
PT	New nucleic acid encoding an Ih ion channel, used to identify
PT	specific modulators, and for treatment, prevention and diagnosis of
XX	e.g. cardiac disease
CC	
PS	Disclosure: Page 71: 82pp; German.
XX	
CC	This invention describes a novel Ih ion channel, isolated from human,
CC	see urchin, bovine, rat, and fruitfly. The ion channels of the invention
CC	have analgesic and cardioactive activity. The Ih ion channel participates
CC	in the pacemaker function in cardiac muscle. The Ih ion channel nucleic
CC	acid and its encoding protein is used to identify substances (A) that
CC	modulate activity of ion channels: to treat and/or diagnose ion
CC	channel-related diseases, particularly cardiac or circulatory disorders
CC	and to prevent and/or treat cardiac/circulatory disorders (especially
CC	a faulty regulation of the sinus ganglion), sleep disorders (particularly
CC	abnormal function of cortico-thalamic neurons) and/or pain. Fragments of
CC	the Ih ion channel nucleic acid are used to detect mutations e.g. for
CC	differential diagnosis. This sequence encodes a rat Ih channel fragment
CC	isolated from olfactory tissue.
XX	
SQ	Sequence 794 BP; 179 A; 230 C; 224 G; 161 T; 0 other:
	Query Match 19.08; Score 30.8; DB 20; Length 794; Best Local Similarity 58.98; Pred. No. 4.1; Matches 53; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
OY	39 ccacgcctgcccgaagcgtgacgcctgtggaaacctgcttcgcccgccagctcat 98 DB 618 CCACCCCCTGCGTGAATGAGTAACAATCTTCGCCGATGGTCCCTCTCGGATGATACT 559 OY 99 ctccaggctggagaacaactgtaacctgacct 128 DB 558 CTCAGCCTGGAAAGACTCAATTGTGACT 529
RESULT 12	
ID 041354	
XX Q41354 standard; cDNA: 1247 BP.	
XX Q41354;	
XX AC	
D7 15-JUL-1993 (first entry)	
XX Human GDF-1 coding sequence.	
XX KM	
XX Human brain; Growth/Differentiation factor;	

KM	morphogenic protein; developmental cascade; morphogen;
KW	inflammatory; anti-inflammatory;
KX	Transforming Growth Factor; TGF-beta super-family; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	84..1202
FT	/*tag= a
FT	726..1199
FT	/tag= b
FT	/note= "contains conserved 7 cysteine skeleton"
XX	
PN	M09304692-A.
PD	18-MAR-1993.
PF	28-AUG-1992; 92MO-US07358.
PR	30-AUG-1991; 91US-0752764.
PR	30-AUG-1991; 91US-0752861.
PR	30-AUG-1991; 91US-0753059.
PA	(CREA-) CREATIVE BIOMOLECULES INC.
PI	Cohen CM, Kuberansampath T, Oppermann H, Ozkaynak E;
PI	Pang RHL, Rueger DC, Smart JE;
DR	WPI; 1993-100652/12.
DR	P-PADB; R34582.
XX	
PT	Morphogen-induced modulation of inflammatory response - and
PT	resulting tissue damage, e.g. in autoimmune diseases, diabetes,
PT	asthma, ischemia reperfusion injury, etc.
XX	
PS	Claim 26; Page 138-140; 165pp; English.
CC	GDF-1 is a preferred morphogen for use in treating tissue
CC	damage in e.g. inflammatory disease, autoimmune disease, arthritis,
CC	psoriasis, dermatitis, diabetes and emphysema. Proteins having at
CC	least 70% homology with GDF-1 amino acid sequences can also be used.
CC	"GDF-1(1fx)" (see R33407) refers to protein sequences encoded by the
CC	human GDF-1 gene and defining the seven cysteine skeleton.
XX	
SQ	Sequence 1247 BP; 127 A; 497 C; 448 G; 175 T; 0 other;
XX	
Query Match	19.0%; Score 30.8; DB 14; Length 1247;
Best Local Similarity	52.3%; Pred. No. 4.5;
Matches 68; Conservative	0; Mismatches 62; Indels 0; Gaps 0;
OY	31 ccgaaacccaccgcctcccgaagatgaacgcgtgtgaaacctgctcgccgc 90
DB	
DB	711 ccggcgaacgttcgtgtgctgtgcgttaaggccccgggccccgtcgcgcgcc 770
OY	91 gagccatctccaggcttgagaactgaaactggaagtgtgaaaagcccatatgctgag 150
DB	
DB	771 ctgcgcgagcgctcgtctgtgtgtgacccctcgaccgccgctgtgccaaccccttggcc 830
OY	151 gaggcgctgc 160
DB	
DB	831 cggccgcgcg 840
RESULT 13	
ID	Q38862
AC	Q38862 standard; DNA: 1247 BP.
DT	13-JUL-1993 (first entry)
DE	Morphogen GDF-1 coding sequence.

```

XX Morphen; homodimer; stimulate; proliferation; progenitor cell;
KW differentiation; growth; redifferentiation; transformation; human;
KW mouse; Drosophila; Xenopus; committed cells; hippocampus;
KW growth/differentiation factor 1; GDF-1; ss.
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT CDS 84..1202
ET /tag= a
XX
XX MO9305172-A.
XX 18-MAR-1993.
XX 28-AUG-1992; 92WO-US07359.
XX 30-AUG-1991; 91US-0752861.
XX (CREA-) CREATIVE BIOMOLECULES INC.
XX Cohen CN, Kuberampath T, Oppermann H, Ozkaynak E, Pang RHL;
XX Rueger DC, Smart JE;
XX WPI; 1993-100993/12.
XX P-PSDB; R33942.
XX Screening cpds. to determine ability to modulate effective concn.
XX of a morphogen - by assaying test tissue type cells for parameter
XX indicative of a prodn. level change of morphogen
XX
XX Disclosure; Page 116-118; 132pp; English.
XX
XX This sequence encodes the morphogen growth/differentiation factor 1
XX (GDF-1) isolated from human brain. This morphogen is inactive when
XX reduced but is active as an oxidised homodimer and when oxidised in
XX combination with other morphogens. These morphogens are capable of
XX stimulating proliferation of progenitor cell, stimulating the
XX differentiation of progenitor cells, stimulating the proliferation of
XX differentiated cells and supporting the growth and maintenance of
XX differentiated cells, including the redifferentiation of transformed
XX cells. These morphogens may also be capable of inducing rediffer-
XX entiation of committed cells under appropriate environmental
XX conditions.
XX
XX Sequence 1247 BP; 127 A; 497 C; 448 G; 175 T; 0 other;
SO
Query Match 19.0%; Score 30.8; DB 14; Length 1247;
Best Local Similarity 52.3%; Pred. No. 4.5;
Matches 68; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
OY 31 ccgagaccacgcgcctcccaagagatgaagcctgtggaacctgtgcgcgc 90
DB 711 ccgcgcagcctccgcctgcctgctgacgccccgcgcctgcgcgcgcgc 770
OY 91 gagccatcctcagcctgagaaactggaactgagcgtggaagcccatagctgag 150
DB 771 ctggcgcagagcctcgtcgtctgtgacccctgcgcgcgcctgtgtccacccctggcc 830
OY 151 gagcgcgtgc 160
DB 831 cggcgcgcgc 840
RESULT 14
ID Q58055 standard; cDNA; 1247 BP.
XX
XX Q58055;
XX
XX 25-AUG-1994 (first entry)

```

```

XX Human morphogenic protein GDF-1(fx) cDNA.
DE
XX Human morphogenic protein; GDF-1(fx); morphogen;
KW Infant food formulation; tissue morphogenesis; tissue development;
KW bone growth; morphogen-enriched nutritional product; ss.
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT CDS 84..1202
ET /tag= a
FT /function= morphogenic_protein
FT /note= "GDF-1(fx) cDNA"
XX
XX MO9403075-A.
XX 17-FEB-1994.
XX 29-JUL-1993; 93WO-US07190.
XX 31-JUL-1992; 92US-0923780.
XX 04-MAR-1993; 93US-0029335.
XX 31-MAR-1993; 93US-0040510.
XX 31-JUL-1992; 92US-0922813.
XX 16-SEP-1992; 92US-0946235.
XX (CREA-) CREATIVE BIOMOLECULES INC.
XX Jones WK, Kuberampath T, Oppermann H, Ozkaynak E;
XX Rueger DC, Tucker RF, Cohen CM, Pang RHL;
XX WPI; 1994-065304/08.
XX P-PSDB; R46750.
XX
XX Morphogen enriched dietary compositions and infant formula -
XX capable of enhancing tissue morphogenesis, development and
XX viability, e.g. in infants, aged individuals and metabolic
XX disorders, e.g. anorexia nervosa, etc
XX
XX Disclosure and Claims 25-26; Page 139-141; 160pp; English.
XX
XX Human GDF-1 (fx) morphogen and proteins having at least 70%
XX homology with it are preferred morphogens for inclusion in new
XX morphogen-enriched nutritional formulations. The formulations
XX are dietary compositions suitable for people at risk for tissue
XX damage due to protein energy malnutrition or to altered metabolism
XX function and infant formulations to enhance tissue development in
XX an infant or juvenile.
XX
XX Sequence 1247 BP; 127 A; 494 C; 451 G; 175 T; 0 other;
SO
Query Match 19.0%; Score 30.8; DB 15; Length 1247;
Best Local Similarity 52.3%; Pred. No. 4.5;
Matches 68; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
OY 31 ccggaaccacgcgcctcccaagagatgacgcctgtggaacctgtgcgcgc 90
DB 711 ccgcgcagcctccgcctgcctgctgacgccccgcgcgcctgcgcgcgcgc 770
OY 91 gagccatcctcagcctgagaaactggaactgagcgtggaagcccatagctgag 150
DB 771 ctggcgcagagcctcgtcgtctgtgacccctgcgcgcgcctgtgtccacccctggcc 830
OY 151 gagcgcgtgc 160
DB 831 cggcgcgcgc 840
RESULT 15
ID Q67315 standard; DNA; 1247 BP.

```

Job time: 8632 sec

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XX 067315;
AC 11-OCT-1994 (first entry)
DT
DE Human GDF-1(fx) morphogen.
XX
XX OP-1; OP-2; CBMP2; Vg1(fx); Vgr(fx); Dp1(fx);
KM GDF-1(fx); 60A(fx); BMP3(fx); BMP5(fx); BMP6(fx);
KM tooth socket; alveolus; osteogenic protein; morphogen;
KM morphogenic protein; periodontal tissue; regeneration;
KM tooth implant; integration; inhibition; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 84..1202
XX /*tag= a
XX /label= GDF-1
XX
XX MO9406399-A.
XX
XX 31-MAR-1994.
XX
XX 15-SEP-1993; 93MO-US08742.
XX
XX 15-SEP-1992; 92US-0945285.
XX 04-MAR-1993; 93US-0029335.
XX 31-MAR-1993; 93US-0040510.
XX
XX (CREA-) CREATIVE BIOMOLECULES INC.
XX
XX Cohen CM, Kuberanampath T, Oppermann H, Ozkaynak E;
XX Pang RHL, Rueger DC, Smart JE;
XX
XX WPI: 1994-118107/14.
XX P-PSDB: R57980.
XX
XX Morphogen-induced periodontal tissue regeneration - used in
XX integrating as implanted tooth in tooth socket or to inhibit
XX tissue loss associated with periodontal disease or injury
XX
XX Claim 28-29; Page 114-116; 132pp; English.
XX
XX Morphogens comprising an amino acid sequence sharing at least
XX 70% homology with OP-1, OP-2, CBMP2, Vg1(fx), Vgr(fx),
XX GDF-1(fx), 60A(fx) and at least 80% homology with BMP3(fx),
XX BMP5(fx) and BMP6(fx) are useful for integrating an implanted
XX tooth in a tooth socket and for inhibiting tissue loss associated
XX with periodontal disease or injury.
XX
XX Sequence 1247 BP; 127 A; 494 C; 451 G; 175 T; 0 other;
SQ

```

Query Match 19.0%; Score 30.8; DB 15; Length 1247;
 Best Local Similarity 52.3%; Pred. No. 4.5;
 Matches 68; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

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Oy 151 gaacgagctgc 160

Db 831 CGGCCGGCGC 840

US-08-406-672-32
; Sequence 32, Application US/08406672
; Patent No. 56744844

APPLI

APPLICANT: RUEGER, DAVID C.
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: OFFENMANN, HERMANN

APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: TREATMENT TO PRI

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1  TITLE OF INVENTION:  INCREASE BONE MASS IN METABOLIC BONE DISEASES
2
3  NUMBER OF SEQUENCES:  33
4
5  CORRESPONDENCE ADDRESS:

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ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES

; STREET: 45 SOUTH STRE
;
; CITY: HOPKINTON
; STATE: MA

COUNTRY: USA
ZIP: 01748

COMPUTER READABLE
MEDICINE

MEDIUM TIRE
COMPUTER:

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; OPERATING SYSTEM: PC
; SOFTWARE: PatentIn F

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406.672

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FILING DATE: 20-MAR-1995
CLASSIFICATION: 435

CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 752,857
FILING DATE: 30-AUG-1991

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 667.274

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FILING DATE: 11-MAR-1991
ATTORNEY/AGENT INFORMATION:

NAME: FENTON Esq., GILLIAN M.

REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-060CN

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7560

TELEFAX: (617) 248-7100 .
INFORMATION FOR SEC ID NO: 33,

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/ INFORMATION FOR SEQ ID NO: 32:
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/ SEQUENCE CHARACTERISTICS:
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/ LENGTH: 303
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; LENGTH: 1247 base pairs
; TYPE: nucleic acid

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STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: CDNA
FEATURE:

NAME/KEY: CDS

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; LOCATION: 84..1199
; OTHER INFORMATION: /product= "GDF-1"
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US-08-406-672-32

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Mismatches	0;	Indels	0;
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RESULT 4
US-08-643-563A-32

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; Sequence 32, Application US/08643563A
; Patent No. 5707810
; GENERAL INFORMATION:

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; APPLICANT: SMART, JOHN
; APPLICANT: OPPERMAN, HERMAN
; APPLICANT: OZKAYNAK, ENGİN

;
; APPLICANT: KUBERASAMPATH, T
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.

```

;      APPLICANT:  COHEN, CHARLES M.
;      TITLE OF INVENTION:  MORPHOGENIC PROTEIN SCREENING METHOD
;      NUMBER OF SEQUENCES:  33
;

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; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
 ; STREET: 45 SOUTH STREET
 ; CITY: NEWARK, NJ 07102

CITY: HOPKIN
 STATE: MA
 COUNTRY: USA
 01740

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;      ZIP: 01/48
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;      MEDIUM TYPE: Floppy
;      COMPUTER: IBM PC

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; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; CURRENT APPLICATION DATA:

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CONTRACT APPLICATION DATA
APPLICATION NUMBER: US/08/643,563A
FILING DATE: 06-MAY-1996
CLASSIFICATION: A35

ATTORNEY/AGENT INFORMATION:
NAME: TWOMEY ESQ., MICHAEL J.
REGISTRATION NUMBER. 38 349

/ RECORDING NUMBER: 20/24
 ; REFERENCE/DOCKET NUMBER: C
 ; TELECOMMUNICATION INFORMATION
 : TELEPHONE: (508) 435-9001

TELEPHONE: (508) 435-2001
TELEFAX: (508) 435-6951
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS.

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; LENGTH: 1247 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

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; CONFORMATION: 2
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; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
FEATURE:

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NAME/KEY: CDS
LOCATION: 84.1199
OTHER INFORMATION:

US-08-643-563A-32

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RESULT 5
US-08-643-763A-32

Sequence 32, Application US/08643/63A
Patent No. 5733878
GENERAL INFORMATION:
GENERAL INFORMATION:

; KUBERASAMPATH, THANGAVEL
 ; RUEGER, DAVID C.
 APPLICANT: OPPERMANN, HERMAN
 ;
 APPLICANT:

APPLICANT: COHEN, CHARLES M.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: MORPHOGENIC-INDUCED PERIODONTAL TISSUE
FIELD OF INVENTION: REGENERATION

TITLE OF INVENTION: REGENERATION.
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
INVENTOR: RICHARD J. ADAMS
ADDRESS: 1000 N. WILSON AVE., SUITE 100, CHICAGO, ILL. 60642

ADDRESS: PATE
STREET: 45 SOUTH
CITY: HOPKINTON
STATE: MA

STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTED READAB:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
MEDIUM TYPE: Floppy disk

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; OPERATING SYSTEM: PC DOS/MS DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: IIS/08/643-763A
;

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ATTORNEY/AGENT INFORMATION:
CLASSIFICATION: 514
FILING DATE: 06-MAY-1996

NAME: FENTON Esq., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-067CN

TELECOMMUNICATION INFORMATION
TELEPHONE: (617) 248-7560
TELEFAX: (617) 248-7100

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; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1247 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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: MOLECULE TYPE: CDNA
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: FEATURE:
: NAME/KEY: CDS
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; LOCATION: 84.1199
; OTHER INFORMATION: /product= "GDF-1"
US-08-643-763A-32

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Query Match 19.08; Score 30.8; DB 1; Length 1247

Best Local Similarity 52.3%; Pred. No. 0.82;
Matches 68; Conservative 0; Mismatches 62; Indels 0; Gaps 0.

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Db 831 CGGCCGGGC 840


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; Patent No. 5849686
; GENERAL INFORMATION:
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: OPPERMAN, HERMAN
; APPLICANT: PANG, ROY H. L.
; APPLICANT: COHEN, CHARLES M.
; TITLE OF INVENTION: MORPHOGEN-INDUCED LIVER REGENERATION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESS: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
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; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/445,468A
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: PENTON ESQ., GILLIAN M.
; REGISTRATION NUMBER: 36,508
; REFERENCE/DOCKET NUMBER: CRP-072FW2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7560
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1247 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 84..1199
; OTHER INFORMATION: /product= "GDF-1"
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; RESULT 9
; US-08-461-397A-32
; Sequence 32, Application US/08461397A
; Patent No. 5972884
; GENERAL INFORMATION:
; APPLICANT: COHEN, CHARLES M.
; APPLICANT: CHARETTE, MARC F.
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: OPPERMAN, HERMAN
```

```
; APPLICANT: PANG, ROY H. L.
; APPLICANT: OKAYNAK, ENGIN
; APPLICANT: SMART, JOHN E.
; TITLE OF INVENTION: MORPHOGEN TREATMENT FOR LIMITING
; TITLE OF INVENTION: PROLIFERATION OF EPITHELIAL CELLS.
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESS: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,397A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER ESQ., EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-074FW2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1247 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 84..1199
; OTHER INFORMATION: /product= "GDF-1"
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; US-08-461-397A-32
;
; Query Match          19.0%; Score 30.8; DB 2; Length 1247;
; Best Local Similarity 52.3%; Pred. No. 0.82;
; Matches 68; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
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; QY 91 gagctacatccagcgttggaagaaactggaactgtggaacgcgcacatagtcggag 150
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; DB 771 ctggccgagacctcctgcctgctgctgacccctgcaccccgccctggcc 830
;
; QY 151 gagcgagctgc 160
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; DB 831 ccgccccgcgc 840
;
; RESULT 10
; US-08-912-088-32
; Sequence 32, Application US/08912088
; Patent No. 5994131
; GENERAL INFORMATION:
; APPLICANT: SMART, JOHN
; APPLICANT: OPPERMAN, HERMAN
; APPLICANT: OKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H. L.
; APPLICANT: COHEN, CHARLES M.
; TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)
463.402 Million cell updates/sec

Title: US-09-587-574-8
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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23 39.8 24.6 43 13 AA913015
24 38.8 24.0 488 4 AA238939
25 38.8 24.0 975 144 BF133900
26 38.2 23.6 299 19 A1363868
27 36 22.2 542 230 CWS0313X
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35 33.4 20.6 721 144 BF120462
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37 33.2 20.5 484 150 BF586653
38 33.2 20.5 492 173 BG103866
39 33 20.4 533 31 AV642870
40 32.8 20.2 534 136 BE724140
41 32.6 20.1 276 170 BF896910
42 32.6 20.1 1114 173 BG109910
43 32.4 20.0 484 163 BE138253
44 32.2 19.9 370 29 AV392939
45 32.2 19.9 448 118 AW661648

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ALIGNMENTS

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BE394032 601312390
A1629343 fcl0h02.y
BF812711 RC3-C1019
BE379078 601237710
AA913015 o128e11.s
AA238939 my36b07.r
BF133900 601779134
A1363868 qy60a10.x
A1223062 Telradon
D24290 RICR1662A R
A0173197 A0173197
AM155149 me10002E
AW476930 ga39c05.y
BG169700 602324691
A2484715 IM0311620
BF442400 259095 MA
BF120462 601756624
BF034266 601456064
BF586653 FM1-29.H0
BG103866 RH722_37_
AV642870 AV642870
BE724140 198851 MA
BF896910 CM2-MT015
BG109910 602279583
BE138253 ug50d03.y
AV392939 AV392939
AW661648 833009H06

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RESULT 1
LOCUS AA937585 444 bp mRNA
DEFINITION of71h02.s1 NCI-CGAP Co8 Homo sapiens cDNA clone IMAGE:1435827 3'
similar to TR:O42400 O42400 AXIN. ;, mRNA sequence.
ACCESSION AA937585
VERSION AA937585.1 GI:3095696
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 444)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution Information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 537 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amerisham.
Location/Qualifiers
1. 444
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1435827"
/clone_lib="NCI-CGAP_Co8"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/notes="Organ: colon; Vector: p773D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
colon adenocarcinoma, and was then primed with a Not I -

```

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oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified p773
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo.
BASE COUNT 69 a 124 c 149 g 102 t
ORIGIN

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Query Match 81.2%; Score 131.6; DB 13; Length 444;
Best Local Similarity 88.3%; Pred. No. 1.5e-27;
Matches 143; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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Qy 1 gccaatggccaaagtgtctactcatttcgcgagaaccaccgcgtgcccaaggatg 60
Db 386 GCCAATGGCCAAAGTGTCTACTCATTTCGCCGAGAACCCACCGCTGCCAAGGAGATG 327
Qy 61 agcgctgtgaacctctgcctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 120
Db 326 ACCCGCTGGAACCCGCCACCTTTGCGACTGATCTCGAGGCTGGAAAAGCTGAG 267
Qy 121 ctggaagctggaagcgcgcacatagctggaagagcgcgcgcgcgcgcgcgcgcgcgc 162
Db 266 CTGGAAGTGGAGAGCGCGCCACGCTGGAGAGCGCCTGCAG 225

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RESULT 2
LOCUS A1272864 459 bp mRNA
DEFINITION q143h03.x1 NCI-CGAP Co8 Homo sapiens cDNA clone IMAGE:1875125 3'
similar to TR:O42400 O42400 AXIN. ;, mRNA sequence.
ACCESSION A1272864
VERSION A1272864.1 GI:3895132
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 459)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution Information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 867 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 387.
Location/Qualifiers
1. 459
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1875125"
/clone_lib="NCI-CGAP_Co8"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/notes="Organ: colon; Vector: p773D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
colon adenocarcinoma, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified p773
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo.

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FEATURES

source


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Db 409 CCAATGGCCAACTGCTCTACTCATTTCCGAGAACCCAGCCGCCCAAGAGATGA 350
Oy 62 cgcctgtggaacctgtcgtccttcgcgcgcgcagctcattccaggtcgtggaacctgaac 121
Db 349 CCCCCGTGGAAACCCGACCTTTGGCAGCTGAGCTGATCTCGAAGCTGAAAGCTGAAGC 290
Oy 122 tggagctggaagacgcgcagctagctcgtggaagagcggtcgtgag 162
Db 289 TGGAGTTGGAGAGCCGCCACAGCTGGAGAGCGCCTGCAG 249

RESULT 5
LOCUS A1139942 460 bp mRNA EST 30-MAR-1999
DEFINITION tg40d11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:2111253 3' similar to TR:042400 042400 AXIN. ;, mRNA
sequence.
ACCESSION A1419942
VERSION A1419942
KEYWORDS EST.
SOURCE A1419942.1 GI:4265873
ORGANISM Homo sapiens
human.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Unpublished (1997)
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 740 Std Error: 0.00
Seq primer: -40UP from Glbco
High quality sequence stop: 421.
Location/Qualifiers
source
1. 460
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2111253"
/clone_1lb="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: p773D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI-CGAP-GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "
BASE COUNT 67 a 124 c 162 g 107 t
ORIGIN
Query Match 80.2%; Score 130; DB 20; Length 460;
Best Local Similarity 87.7%; Pred. No. 4.2e-27;
Matches 142; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
Oy 1 gccaatggccaagtgtctactcaatttcgcgagaaccacgcgtgcgccaagagatg 60
Db 421 GCCAATGGCCAACTGCTCTACTCATTTCCGAGAACCCAGCCGCCCAAGAGATG 352
Oy 61 acgcctgtggaacctgtcgtccttcgcgcgcgcagctcattccaggtcgtggaacctgaac 120
Db 361 ACCCCGTGGAAACCCGACCTTTGGCAGCTGAGCTGATCTCGAAGCTGAAAGCTGAAG 302

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Oy 121 ctggaactggaagccgcacatagctcgtggaagcggtcgcag 162
Db 301 CTGGAAGTTGGAGAGCCGCCACAGCTGGAGAGCGCCTGCAG 260

RESULT 6
LOCUS A1220032 543 bp mRNA EST 30-NOV-1998
DEFINITION q978h02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:1841331 3' similar to TR:042400 042400 AXIN. ;, mRNA
sequence.
ACCESSION A1220032
VERSION A1220032
KEYWORDS EST.
SOURCE A1220032.1 GI:3802235
ORGANISM Homo sapiens
human.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Unpublished (1997)
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 752 Std Error: 0.00
Seq primer: -40UP from Glbco
High quality sequence stop: 224.
Location/Qualifiers
source
1. 543
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1841331"
/clone_1lb="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: p773D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI-CGAP-GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "
BASE COUNT 87 a 149 c 176 g 130 t 1 others
ORIGIN
Query Match 79.3%; Score 128.4; DB 17; Length 543;
Best Local Similarity 87.0%; Pred. No. 1.2e-26;
Matches 141; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
Oy 1 gccaatggccaagtgtctactcaatttcgcgagaaccacgcgtgcgccaagagatg 60
Db 408 GCCAATGGCCAACTGCTCTACTCATTTCCGAGAACCCAGCCGCCCAAGAGATG 349
Oy 61 acgcctgtggaacctgtcgtccttcgcgcgcgcagctcattccaggtcgtggaacctgaac 120
Db 348 ACCACCGTGGAAACCCGACCTTTGGCAGCTGAGCTGATCTCGAAGCTGAAAGCTGAAG 289
Oy 121 ctggaactggaagccgcacatagctcgtggaagcggtcgtgag 162
Db 288 CTGGAAGTTGGAGAGCCGCCACAGCTGGAGAGCGCCTGCAG 247

RESULT 7
A1818109/c

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	Locus	A1818109	591 bp	mRNA	EST	21-DEC-1999
	DEFINITION	wk27c05.xl NCI_CGAP_Brn25 Homo sapiens CDNA clone IMAGE:2413544	3'			
	ACCESSION	A1818109				
	VERSION	A1818109.1	GI:5437188			
	KEYWORDS					
	SOURCE	human.				
	ORGANISM	Homo sapiens				
	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;				
	AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
	TITLE	NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGA), Tumor Gene Index Unpublished (1998) Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert.Strausberg@nih.gov Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www.bio.linnl.gov/dbtpr/image/Image.html Insert Length: 700 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 465. Location/Qualifiers				
	JOURNAL					
	COMMENT					
	FEATURES					
	SOURCE					
	BASE COUNT	102 a	159 c	192 g	138 t	
	ORIGIN					
	Query Match	78.3%	Score 126.8;	DB 102;	Length 591;	
	Best Local Similarity	86.4%;	Pred. No. 3.6e-26;			
	Matches 140;	Conservative 0;	Mismatches 22;	Indels 0;	Gaps 0;	
OY	1 gccaatggcccaagtgcttcctaactatattttccgagaaccacgcgctgtgccaaaggagtg	60				
Dd	408 GCCAATGGCCCAAGTGCTTCCTCACCCTCATTTCCCAGAACAACCACGCCGTGCCTCCACAGAGATG	349				
OY	61 acgcctgtgaacctgcgcctcgcccgcgcagagcatcacctccagagcttgtgagaactgaaa	120				
Dd	348 ACCCCCGTGAACCCGCCACACTTTGCACTTAGCTGATTCTTGAGAGGCTGAAAACCTGAAG	289				
OY	121 ctggaagctygaagacgcgcgatagltctgtagagagcgygcctgac	162				
Dd	288 CTGGA GTTGA GAGAG CCGCAC AGGCTG A GAAG A GGCC CTCG AC G 247					
RESULT	8					
LOCUS	A1858567/c	418 bp	mRNA	EST	07-MAR-2000	
DEFINITION	w164d08.x1 NCI_CGAP_Brn25 Homo sapiens CDNA clone IMAGE:2429679	3'				

ACCESSION	A1858567	similar to TR:088566 O88566 CONDUCTIN., mRNA sequence.
VERSION	A1858567.1	GI:5512183
KEYWORDS		
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Euteria; Primates; Catarrhini; Homnidae; Homo.	
TITLE	1 (bases 1 to 418)	
	NCI/NINDS-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.	
	National Cancer Institute / National Institute of Neurological	
	Disorders and Stroke, Brain Tumor Genome Anatomy Project	
	(CCAP/RTGAP), Tumor Gene Index	
JOURNAL	Unpublished (1998)	
COMMENT	Contact: Robert Strausberg, Ph.D. Tel.: (301) 496-1550 Email: Robert.Strausberg@nih.gov Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D. Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www.bio.lnl.gov/dbt/p/image/image.html Insert Length: 541 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 402. Location/Qualifiers 1. 418 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:242679" /clone_lib="NCI CCAP Brn25" /tissue_type="anaplastic oligodendroglioma" /lab_host="DH10B" /note="Organ: brain; Vector: pRT730-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTCGAGCGGCCCATGAGGTCTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT73 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."	
FEATURES		
source		
BASE COUNT	62 a 115 c 149 g 89 t 3 others	
ORIGIN		
Query Match	72.5%; Score 117.4; DB 103; Length 418;	
Best Local Similarity	83.6%; Pred. No. 1.7e-23;	
Matches 133; Conservative	0; Mismatches 26; Indels 0; Gaps 0;	
Dy	4 aatggccaagtgctcctaactattttccgagaaccacgcgtgcccaagaagtgaacg 63	
Dd	418 AAGGGCGAAGTGTCTACTCATTATTCGCCGAACAACCACGCCTCCCAAGTAGATGACC 359	
Dy	64 cctgtggaacctgtgccttcgcgcgcagcctcatccaggctgtgagaactgaacty 123	
Dd	358 CCCGTGGAATCCGCCACACTTTTCGACGTAGCTGATCTCGAGGCTGGAAMAAGCTGAAGCTG 299	
Dy	124 gagctgaaagccgcgatagcttgtgagaagcgagctgcag 162	
Dd	298 GAGTTGAGAGCCGCCACAGCCAGGAGGAGCGCCTGCAG 260	
RESULT	9	
LOCUS	AA884421/c	
DEFINITION	AA884421 391 bp mRNA EST 27-MAR-1998	
	am16b12.s1 Soares NFL.T GGC SI Homo sapiens cDNA clone	
	IMAGE:1466975 3' similar to TR:042400 O42400 AXIN.; mRNA	
	sequence.	

ACCESSION AA884421
 VERSION AA884421.1 GI:2993951
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 391)
 AUTHORS NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Possible reversed clone: similarity on wrong strand
 Possible reversed clone: polyA not found
 Seq primer: -40m3 fwd. ET from Amersham
 High quality sequence stop: 234.
 Location/Qualifiers
 1..391
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="1466975"
 /clone_lib="Soares_NFL_T_GBC_S1"
 /lab_host="DH10B"
 /note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
 a modified polylinker; Site_1: Not I; Site_2: Eco RI;
 Equal amounts of plasmid DNA from three normalized
 libraries (fetal lung NBHL19W, testis NHT, and B-cell
 NCI-CGAP-GCB1) were mixed, and 5S circles were made in
 vitro. Following HAP purification, this DNA was used as
 tracer in a subtractive hybridization reaction. The driver
 was PCR-amplified cDNAs from pools of 5,000 clones made
 from the same 3 libraries. The pools consisted of
 1.M.A.G.E. clones 297480-302087, 682632-687229,
 726408-728711, and 729096-731399. Subtraction by Bento
 Soares and M. Fatima Bonaldo."
 BASE COUNT 58 a 148 g 85 t 1 others
 ORIGIN
 Query Match 66.0%; Score 107; DB 13; Length 391;
 Best Local Similarity 83.0%; Pred. No. 1.5e-20;
 Matches 122; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
 QY 16 tcttaccatcttcctcggaaccacccgctgcgaagaagatgacgtctggaact 75
 DB 391 tcttaccatcttcctcggaaccacccgctgcgaagaagatgacgtctggaact 332
 QY 76 gctcctcctcgccgcgagctcctcgaagctggaactgagctggaagc 135
 DB 331 cccacctttgcagctgagctgctgagctggaactgagctggaagc 272
 QY 136 cgcacatgctcgagagcgagctgcaag 162
 DB 271 cccacatctctgagagcgagctgcaag 245
 RESULT 10
 AW762829/c 508 bp mRNA EST 04-MAY-2000
 LOCUS ur66f04.y1 NCI-CCAP Mam3 mus musculus cDNA IMAGE:3155263 5'
 DEFINITION similar to TR:088566 088566 CONDUCTIN.; mRNA sequence.
 ACCESSION AW762829
 VERSION AW762829.1 GI:7694771
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 508)
 AUTHORS NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Other ESTs: ur66f04.x1
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CCAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov/image/html/lresources.shtml>
 MGI:1058019
 Possible reversed clone: similarity on wrong strand
 Seq primer: -40RP from Gibco
 High quality sequence stop: 429.
 Location/Qualifiers
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 /organism="Mus musculus"
 /strain="129 - C57/B6 - FVB/N"
 /db_xref="taxon:10090"
 /clone_image="3155263"
 /clone_lib="NCI-CCAP_Mam3"
 /tissue_type="tumor, gross tissue"
 /dev_stage="10 months"
 /lab_host="DH10B"
 /note="Organ: mammary; Vector: pCMV-Sport6; Site_1: SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Library constructed by Life Technologies. Investigators
 providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
 Reference for transgenic model: Xu et al., Nature Genetics
 22, 37-43 (1999)."
 BASE COUNT 118 a 154 c 108 g 128 t
 ORIGIN
 Query Match 62.3%; Score 101; DB 119; Length 508;
 Best Local Similarity 100.0%; Pred. No. 8.4e-19;
 Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 43 cgcctgcccaaggagatgacgcctggaactgctgcgcgcgagctcattcc 102
 DB 101 cgcctgcccaaggagatgacgcctggaactgctgcgcgcgagctcattcc 42
 QY 103 agcctggaagaactggaactggaactggaagccgcctatg 143
 DB 41 agcctggaagaactggaactggaactggaagccgcctatg 1
 RESULT 11
 A1336613/c 413 bp mRNA EST 13-FEB-1999
 LOCUS qo62c07.x1 NCI-CCAP Co8 Homo sapiens cDNA clone IMAGE:1913100 3'
 DEFINITION similar to TR:042400 042400 AXIN.; mRNA sequence.
 ACCESSION A1336613
 VERSION A1336613.1 GI:4073540
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 413)
 AUTHORS NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550

source

1. 546
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1473956"
/clone_lib="NCI-CGAP_C08"
/issue_type="adenocarcinoma"
/lab_host="DH10B"
/note="Organ: colon; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from colon adenocarcinoma, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 95 a 133 c 186 g 131 t 1 others

ORIGIN

Query Match 52.2%; Score 84.6; DB 13; Length 546;
Best Local Similarity 74.8%; Pred. No. 4.1e-14;
Matches 119; Conservative 0; Mismatches 39; Indels 1; Gaps 1;

OY 3 caatggccaagtctctacatcttccgagaacccacgcctgcgcaagagatgac 62
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DB 447 CAATTGCCAAGTATCTACATCA-TTCCGAGAACCCACCCCTTCCGAGAGATGAC 389
|||||
OY 63 gccctgtggaacctgctgctccgcgcgcagcatctccagctggaagaactgaact 122
|||||
DB 388 CCCCATGAAMCCCGCTACTTTCAGCTGAGCTGAGCTTGGAAGTGAAGCT 329
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OY 123 ggaagctggaagagcgcacatagctgtgagagcgagctgca 161
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DB 328 GGAGTTGGAGAGCCCAACACAGCTGAGAGATCTGCA 290
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RESULT 14
LOCUS A1660139 408 bp mRNA EST 18-DEC-1999
DEFINITION we61a09.x1 Soares.thymus.NHPTth Homo sapiens cDNA clone
IMAGE:2345560 3' similar to TR.088566 088566 CONDUCTIN.; mRNA
sequence.
ACCESSION A1660139
VERSION A1660139.1 GI:4763709
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 408)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 788 Std Error: 0.00
Seq primer: -40UP from Glibco
High quality sequence stop: 333.
Location/Qualifiers
1. 408
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/db_xref="taxon:9606"
/clone="IMAGE:2345560"
/clone_lib="Soares.thymus.NHPTth"
/dev_stage="Fetal"
/lab_host="DH10B (phage-resistant)"
/note="Organ: thymus, pooled; Vector: pT773D-Pac
(Pharmacia) with a modified polylinker; Site.1: Not I;
Site.2: Eco RI; 1st strand cDNA was primed with a Not I -

oligo(dT) primer [5',
TGTTCACCAATCGAGGAGGAGCGCCGACAGCTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT773 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 61 a 110 c 152 g 85 t

ORIGIN

Query Match 51.0%; Score 82.6; DB 23; Length 408;
Best Local Similarity 76.5%; Pred. No. 1.5e-13;
Matches 114; Conservative 0; Mismatches 34; Indels 1; Gaps 1;

OY 14 tgcctctacatcttccgagaacccacgcgcctgcgcaagagatgagctggaac 73
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DB 407 TTTCCTTCCACGCTCTGTAGAACCCACCGCTGCCCAAGAGATGAC-CCCTGGAAC 349
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OY 74 ctgctgctctgcgcgcgcagctcctcagcgctggaagaactgaactgagctggaac 133
|||||
DB 348 CCGGCACTTGCACAGCTGAGCTGATCTGAGCTGGAAGCTGAGCTTGAGAGA 289
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OY 134 gccgcacatgctggaagagcgctgcag 162
|||||
DB 288 GCCGCCACAGCTTGAGAGAGCGCCTGCAG 260
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RESULT 15
LOCUS R33823 361 bp mRNA EST 28-APR-1995
DEFINITION yH78f12.r1 Soares.placenta NB2HP Homo sapiens cDNA clone
IMAGE:135887 5', mRNA sequence.
ACCESSION R33823
VERSION R33823.1 GI:789681
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 361)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chippelli, B.,
Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins,
M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore,
B., Morris, M., Parsons, D., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevisan, E.,
Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
Insert Size: 445
High quality sequence stops: 235
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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High quality sequence stop: 235.
Location/Qualifiers
1. 361
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/db_xref="taxon:9606"
/clone="IMAGE:135887"
/clone_lib="Soares.placenta NB2HP"
/sex="Female"
/dev_stage="Placenta obtained at birth (full term)"

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 7, 2001, 00:35:43 ; Search time 4956.99 Seconds
(Without alignments)
615.859 Million cell updates/sec

Title: US-09-587-574-9

Perfect score: 207
Sequence: 1 cagatccggagagatgaaga.....gtcaagccacggtccgcg 207

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 7373929652 residues

Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba1: *
2: gb_ba2: *
3: gb_ba3: *
4: gb_in1: *
5: gb_in2: *
6: gb_in3: *
7: gb_om: *
8: gb_ov: *
9: gb_pat1: *
10: gb_pat2: *
11: gb_ph: *
12: gb_pl1: *
13: gb_pl2: *
14: gb_pl3: *
15: gb_pl4: *
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17: em_ba2: *
18: em_fun: *
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20: em_htgo_inv: *
21: em_htgo_rod: *
22: em_htg_hum1: *
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25: em_htg_hum4: *
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27: em_htg_hum6: *
28: em_htg_hum7: *
29: em_htg_hum8: *
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90: gb_pr6: *
91: gb_pr7: *
92: gb_pr8: *
93: gb_pr9: *
94: gb_ro1: *
95: gb_ro2: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	207	100.0	207	9 A98524	A98524 Sequence 9
2	207	100.0	2825	9 A98521	A98521 Sequence 6
3	207	100.0	2825	94 AF073788	AF073788 Mus muscu
4	207	100.0	3016	94 AF205889	AF205889 Mus muscu
5	195.4	94.4	191041	69 AC024114	AC024114 Mus muscu
6	192.6	93.0	3216	94 AF017757	AF017757 Rattus no
7	133.4	64.4	2104	89 AK025718	AK025718 Homo sapi
8	133.4	64.4	2538	88 AF205888	AF205888 Homo sapi
9	133.4	64.4	3072	88 AF078165	AF078165 Homo sapi
10	72.6	35.1	3485	8 AB032263	AB032263 Danto rer
11	44.8	21.6	3066	8 AB032262	AB032262 Danto rer

C 45	34	16.4	186797	67	AC021965	AF009012	Gallus ga
C 44	34	16.4	177826	66	AC016852	AF097313	Xenopus l
C 43	34	16.4	177826	66	AC016852	AF009011	Mus muscul
C 42	34	16.4	167725	82	AL53485	AF009011	Mus muscul
C 41	34	16.4	167725	82	AL53485	AC011505	Homo sapi
C 40	34	16.4	167725	82	AL53485	AC007786	Homo sapi
C 39	34	16.4	167725	82	AL53485	AC008569	Homo sapi
C 38	34.2	16.5	214561	71	AC026998	AF017756	Rattus no
C 37	34.2	16.5	214561	71	AC026998	AC011051	Homo sapi
C 36	34.2	16.5	187114	71	AC026998	AF057337	Aspergill
C 35	34.2	16.5	183000	69	AC025134	AL353052	Homo sapi
C 34	34.2	16.5	183000	69	AC025134	AF037057	Homo sapi
C 33	34.2	16.5	183000	69	AC025134	AF037057	Homo sapi
C 32	34.2	16.5	183000	69	AC025134	AF037057	Homo sapi
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C 8	34.2	16.5	183000	69	AC025134	AF037057	Homo sapi
C 7	34.2	16.5	183000	69	AC025134	AF037057	Homo sapi
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DEFINITION	Sequence 6 from Patent WO9111780.		PAT
ACCESSION	A98521		26-JAN-2000
VERSION	A98521.1	GI:6781607	
KEYWORDS			
SOURCE		unidentified.	
ORGANISM		unidentified	
REFERENCE		unclassified.	
AUTHORS		1 (bases 1 to 2825)	
TITLE		Birchmeier W. and Behrens J.	
JOURNAL		CONDUCTINE PROTEIN AND A RELATED AGENT FOR DIAGNOSING AND TREA	
FEATURES		TUMOR ILLNESSES	
source		Patent: WO 9111780-A 6 11-MAR-1999;	
		BIRCHMEIER WALTER (DE); BEHRENS JUERGEN (DE)	
		location/Qualifiers	
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Best Local Similarity	100.0%;	Pred. No. 3e-42;		
Matches 207; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

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DEFINITION	A98524	207 bp	DNA		PAT
ACCESSION	A98524	Sequence 9 from Patent WO9911780.			
VERSION	A98524.1	GI:6781610			
KEYWORDS					
SOURCE	unidentified.				
ORGANISM	unidentified				
	unclassified.				
REFERENCE	1 (bases 1 to 207)				
AUTHORS	BIRCHMEIER W. and BEHRNS J.				
TITLE	CONDUCTINE PROTEIN AND A RELATED AGENT FOR DIAGNOSING AND TREATING				
	TUMOR ILLNESSES				
JOURNAL	Patent: WO 99/11780-A 9 11-MAR-1999;				
FEATURES	BIRCHMEIER WALTER (DE); BEHRNS JUERGEN (DE)				
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Db	1	CAGATCCGGGAGGATGAGAAAGAGAGGGGCTGTGACAGGCCCTTAGCTCAGCGATGGA	60	
QY	61	gcaccgggtccagaaacccctggcctctctacccttcggaagctatgaagagaccacaa	120	

REFERENCE	AUTHORS	TITLE	JOURNAL
1	Behrens, J., Jerchow, B.-A., Mutzelle, M., Grimm, J., Asbrand, C., Wirtz, R., Kuhl, M., Medlich, D. and Birmelmeier, W.	Functional Interaction of an axlin homolog, conductin, with beta-catenin, APC, and GSK3beta	Science 280 (5365), 596-599 (1998)
		house mouse.	
		Mus musculus	
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclirognathi; Muridae; Murinae; N	
		(bases 1 to 2825)	

MEDLINE 9821239
REFERENCE 2 (bases 1 to 2825)
AUTHORS Behrens,J., Jerchow,B.-A. and Birchmeier,W.
TITLE Direct Submission
JOURNAL Submitted (22-JUN-1998) Cellular Biology, Max Delbrueck Center for
Molecular Medicine, Robert-Rössle 10, Berlin 13122, Germany
FEATURES
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BASE COUNT 703 a 815 c 813 g 494 t
ORIGIN

Query Match 100.0%; Score 207; DB 94; Length 2825;
Best Local Similarity 100.0%; Pred. No. 3e-42;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 gcaaccggtccagacaccccttgccctcctaccctccggcaagctatgaagaaccacaa 120
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DB 1463 GCACCGGTCCACACCCCTTGCCCTCCTACCTCCGGCAGCTATGAAGAGCCACCA 1522
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QY 121 accatttggacgacacactctcgaaggtctcgaagaccctggctgtcaatccctgtg 180
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DB 1523 ACCATTGTGACGACACCACTCTCCAGGTCCTCAAGACCCCGCGCTGTCAATCCCTG 1582
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QY 181 gtcgggtcgctacagaccacggtccgcg 207
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DB 1583 GTGGGTGCTACAGCCACGCTCCGC 1609
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RESULT 4
LOCUS AF205889 3016 bp mRNA ROD 03-JAN-2000
DEFINITION Mus musculus Ax1n2 (Ax1n2) mRNA, complete cds.
ACCESSION AF205889
VERSION AF205889.1 GI:6653585
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3016)
Zhang,T., Pagotto,F., Hsu,W., Zeng,L., Gilbert,D., Copeland,N.G.,
Jenkins,N.A., Waburton,D. and Costantini,F.
Properties of mouse Ax1n2 and human AXIN1: Chromosomal location,
expression pattern, interaction with Axin and effects on embryonic
axis formation

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3016)
AUTHORS Zhang,T. and Costantini,F.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-1999) Genetics & Development, Columbia
University, 701 M168th St. HSC 1416, New York, NY 10032, USA
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ERLQOIRDEDEKESQALSRDGAPOHPLALPSGSEEDPOTLDDHLSRLVLT
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TKHHNNYIHHNAVPKTEIEAETORVRCPCPGTDVYCYSKSHPKAPEPLGE
EQCSKSPHSNOSIRKSYPLESARAAPGERVSRHHLGASGHSVARAHPTODPAM
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BASE COUNT 766 a 858 c 837 g 555 t
ORIGIN

Query Match 100.0%; Score 207; DB 94; Length 3016;
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Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 gcaaccggtccagacaccccttgccctcctaccctccggcaagctatgaagaaccacaa 120
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DB 1303 GCACCGGTCCACACCCCTTGCCCTCCTACCTCCGGCAGCTATGAAGAGCCACCA 1362
|||||
QY 121 accatttggacgacacactctcgaaggtctcgaagaccctggctgtcaatccctgtg 180
|||||
DB 1363 ACCATTGTGACGACACCACTCTCCAGGTCCTCAAGACCCCGCGCTGTCAATCCCTG 1422
|||||
QY 181 gtcgggtcgctacagaccacggtccgcg 207
|||||
DB 1423 GTGGGTGCTACAGCCACGCTCCGC 1449
|||||

RESULT 5
LOCUS AC024114 191041 bp DNA HTG 06-NOV-2000
DEFINITION Mus musculus chromosome 11 clone RP23-278J12, WORKING DRAFT
SEQUENCE, 30 unordered pieces.
ACCESSION AC024114
VERSION AC024114.8 GI:11094615
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 191041)

AUTHORS
Metzker, M.L., Lewis, L.R., Hume, J., Edwards, C., Harris, C., Dederich, D., Thomas, S., Okwuonu, G., Carlack, C., Garner, T., Addyson, S., Pace, A., Williams, G., Bonnin, D., Brooks, A., Brown, J., Bunay, C., Bunac, C., Burkett, C., Chacko, J., Chen, G., Chen, Z., Cox, C., Davis, C., Delgado, O., Ding, Y., Dugan-Rocha, S., Fernandez, C., Ferraguto, D., Forcum-Tansey, J., Gill, R., Gorrell, J.H., Gunaratne, P., Haller, G., Hernandez, J., Hognes, M., Hosok, H., Hou, X., Huber, J., Jackson, L., Jia, Y., Kelly, J., Kelly, S., Kover, C., Liu, J., Liu, W., Louised, H., Lozado, R.T., Martin, R., Massey, E., McLeod, M.P., Mei, G., Moore, S., Morgan, M., Morris, S., Neal, D., Nelson, A., Nguyen, R., Nguyen, N., Ogih, M., Parish, B., Perez, L., Reller, D., Say, J., Shen, H., Vasquez, L., Watlington, S., Williamson, A., Wrensford, G., Zhou, X., Bouck, J., Hodgson, R., Murley, D.M., Rives, R., Scherer, S., Sodergren, E., Weinstein, G., Murley, K. and Glbbs, R.

TITLE
Direct Submission

REFERENCE
Unpublished

AUTHORS
2 (bases 1 to 191041)

JOURNAL
Worley, K.C.

Direct Submission
Submitted (24-FEB-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 4, 2000 this sequence version replaced gi:9929587.

Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
Project Information
Center project name: MACA
Center clone name: RP23-278J12

Summary Statistics
Sequencing vector: M13: 108821
Chemistry: Dye-primer Bodypy: 95% of reads
Assembly program: Phrap: Version 0.990329
Consensus quality: 158769 bases at least Q40
Consensus quality: 172780 bases at least Q30
Consensus quality: 179030 bases at least Q20
Estimated insert size: 180377; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-1p estimation
Quality coverage: 3.2x in Q20 bases; sum-of-contigs estimation

NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1
19344: contig of 19344 bp in length
19345 19444: gap of unknown length
19445 33763: contig of 14319 bp in length
33764 33863: gap of unknown length
33864 47738: contig of 13875 bp in length
47739 47838: gap of unknown length
47839 59611: contig of 11773 bp in length
59612 59711: gap of unknown length
59712 67897: contig of 8186 bp in length
67898 67998: gap of unknown length
67999 77929: contig of 9932 bp in length
77930 78029: gap of unknown length
78030 86605: contig of 8576 bp in length
86606 86705: gap of unknown length
86706 93904: contig of 7199 bp in length
93905 94004: gap of unknown length
94005 104236: contig of 10232 bp in length
104237 104336: gap of unknown length
104337 113241: contig of 8905 bp in length

113242 113341: gap of unknown length
113342 120171: contig of 6830 bp in length
120172 125989: contig of 5718 bp in length
125990 126089: gap of unknown length
126090 131870: contig of 5780 bp in length
131871 131970: gap of unknown length
131971 132994: contig of 7325 bp in length
132995 133295: gap of unknown length
133296 146006: contig of 6612 bp in length
146007 146106: gap of unknown length
146107 150788: contig of 4682 bp in length
150789 150888: gap of unknown length
150889 156925: contig of 6037 bp in length
156926 157025: gap of unknown length
157026 161170: contig of 4145 bp in length
161171 161270: gap of unknown length
161271 164311: contig of 3041 bp in length
164312 164411: gap of unknown length
164412 167354: contig of 2943 bp in length
167355 167454: gap of unknown length
167455 171291: contig of 3837 bp in length
171292 171391: gap of unknown length
171392 174233: contig of 2842 bp in length
174234 174333: gap of unknown length
174334 177744: contig of 3411 bp in length
177745 177844: gap of unknown length
177845 179402: contig of 1558 bp in length
179403 179502: gap of unknown length
179503 182420: contig of 2918 bp in length
182421 182520: gap of unknown length
182521 184923: contig of 2403 bp in length
184924 185023: gap of unknown length
185024 187054: contig of 2031 bp in length
187055 187154: gap of unknown length
187155 188272: contig of 1118 bp in length
188273 188372: gap of unknown length
188373 189634: contig of 1262 bp in length
189635 189735: gap of unknown length
189736 191041: contig of 1307 bp in length.

FEATURES
source
1. 191041
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="11"
/clone="RP23-278J12"

BASE COUNT 49790 a 43523 c 42989 g 51816 t 2923 others

ORIGIN

Query Match 94.4% Score 195.4; DB 69; Length 191041;
Best Local Similarity 99.5% Pred. No. 9.6e-40;
Matches 196; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 agatgaagaaagagagagctgagcagcctgagctcagcagatgagcacggttc
113242
DB 31065 AGGATGAAGAAAGAGAGGAGGCTAGCAGCGCCCTGAGCTCAGCGATGAGACACCGGTCC 31124
71 agcaccctgagcctcctacccctcgcagcagctatgaagagagaccacaacccatttgg 130
DB 31125 AGCACCCTGAGCCTCCTACCCCTCGGACGCTATGAAGAGAGACCCACAAACCATTTTGG 31184
QY 131 agcaccctcctcagagctcctcagagaccccgctgtcaatccctggtgtgtgtgc 190
DB 31185 AGCACCCTCCTCAGGAGGCTCTCAAGACCCCGCTGTCAATCCCTGTGTGTGTGTGCT 31244
QY 191 acagccacggtccgcg 207
DB 31245 ATAGCCACGCTCCCGC 31261

RESULT 6
AF017757

LOCUS AF017757 3216 bp. mRNA ROD 24-APR-1998
DEFINITION Rattus norvegicus GSK-3beta interacting protein Axin mRNA, complete cds.
ACCESSION AF017757
VERSION AF017757.1 GI:3080758
KEYWORDS
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 3216)
Yamamoto, H., Ikeda, S., Uochi, T., Ikeda, S., Koyama, S., Asashima, M. and Kikuchi, A.
Axin, a member of the Axin family, interacts with both glycogen synthase kinase 3beta and beta-catenin and inhibits axis formation of Xenopus embryos
Mol. Cell. Biol. 18 (5), 2867-2875 (1998)
98226558
2 (bases 1 to 3216)
Yamamoto, H., Ikeda, S., Murali, H., Kishida, S. and Kikuchi, A.
Direct Submission
Submitted (08-AUG-1997) Biochemistry, Hiroshima University, School of Medicine, 1-2-3 Kasumi, Minami-ku, Hiroshima, Hiroshima 734, Japan
FEATURES
source Location/Qualifiers
1..3216
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
85..2601
/note="GSK-3beta interacting protein; Axin like protein"
/codon_start=1
/product="Axin"
/protein_id="AAC40089.1"
/db_xref="GI:3080759"
/translation="MSSAVVTLPLPPSSFPREDAPRPVPEEGETPCPCSVKQVSTKPMVSSNARNEDGEGEPGRASPDLRTWTKSLSLISLGDGDAVLPFLPREKVDLPDFWPCNGFRWMLKPTKTRAKAYKRIENSVSKOKATRTYIRDCIKKQIGVWFQADQETIDAVENNYQVFLSDIYLEVRSNGGENTATMNGDLSLKYLCGYLPTLNEEEMTCADLCKLSPTVGLSSKTLRTASVSTETATMENSFRSKRSEPNVHVSGVYFAPATPANDSELSDALDDSSMTDSVDDGIPRYMGSKQLOREMHRSVKANGOVSLPHPRTRHRLPREKMPVPAFAELISLEKLELSRHSLEBRLQOIREDEEKESRQALSDGAQVONHLLPESGYEDPORTLIDHLSRYLKTPEGOSRPGVGRSPRSRSDHHHHHNOCHALLPTGKLPREAPCPILGSGSFETKQTKHNNHVIHNAVPAKTELEATQVRCLEPGTDYCYSKSKSRPEPLPGQFOGCSRGTLPRKNTKGTPEGLAPARGGSSAAGAOLPGEGRSDQWOMLSESRQSKRPHSTOSIRKSYPLESARAPGERVSRHLLGASGHPRAARAHFTDDPAMP LPPMTLOLEACRRLAEVSKPOKORCCVAAOORNRNRPATGOGAPTSFNSPLASEDHKEPKRLASVHALQASLELYVFCGCEIPIPRMILKASLTILGHKQDLSSKNTRY YRKASDFACGAVFEIWDITVLPMTGRIIGKVERID"
BASE COUNT 860 a 914 c 872 g 570 t
ORIGIN

Query Match 93.0%; Score 192.6; DB 94; Length 3216;
Best Local Similarity 95.7%; Pred. No. 1.2e-38;
Matches 198; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 cagatccggaggaatgaagaagaagggtctgtagcagccttgagctcaagggaatgga 60
|||||
DB 1273 CAGATCCGGAGAGATGAAGAAAGAGAGGCTCTGACGACGCTTGACCTACCGGATGGA 1332
|||||
QY 61 gcaacggatccagacacccctcgcctctacccctcgcgcagcagctatgaaggagacccacaa 120
|||||
DB 1333 GCACCGGATCCACACCCCGCTGCGCTTACCTCTGCGAGCTATGAAGAGACCCACAA 1392
|||||
QY 121 acaatttggagagacacacccctcgcaggtctcgaagaccccgagctgtaattccctcgt 180
|||||
DB 1393 ACCACTTGGACGACGATCTGTCAGAGGCTCTCAAGACCCCGGCTCCAGTCCCTGGT 1452
|||||
QY 181 gtgggtcgtacagccacagcgtccgcg 207
|||||
DB 1453 GTGGGCGGCTACAGCCGCTCCCGC 1479

RESULT 7
LOCUS AK025718
DEFINITION Homo sapiens cDNA: FLJ22065 fis, clone HEP10566, highly similar to AF078165 Homo sapiens conductin mRNA.
ACCESSION AK025718
VERSION AK025718.1 GI:10438327
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens hepatoma cell_line:HEPG2 cDNA to mRNA, clone_1lb:HEP clone:HEP10566.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (sites)
Kawabata, A., Hiki, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Ota, T., Suzuki, Y., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Nakamura, Y., Isogai, T. and Sugano, S.
MEDO human cDNA sequencing project
Unpublished (2000)
2 (bases 1 to 2104)
Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T., Shibahara, T., Tanaka, T. and Nakamura, Y.
Direct Submission
Submitted (29-AUG-2000) to the DDBJ/EMBL/Genbank databases. Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
(E-mail:cdna@lems.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
COMMENT MEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan. cDNA full insert sequencing: Research Association for Biotechnology: cDNA library construction, 5'- & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).
FEATURES
source Location/Qualifiers
1..2104
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="HepG2"
/cell_type="hepatoma"
/clone="HEP10566"
/clone_1lb="HEP"
/note="cloning vector pME18SFL3"
1..2104
/note="highly similar to AF078165 Homo sapiens conductin mRNA"
BASE COUNT 506 a 610 c 619 g 369 t
ORIGIN

Query Match 64.4%; Score 133.4; DB 89; Length 2104;
Best Local Similarity 77.8%; Pred. No. 9.3e-24;
Matches 161; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 1 cagatccggaggaatgaagaagaagggtctgtagcagccttgagctcaagggaatgga 60
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DB 500 CAGATCCGAAGAGATGAAGAGAGAGAGGCTCCGAGCTCACACTCAATTCGCGGAGAGG 559
|||||
QY 61 gcaacggatccagacacccctcgcctctacccctcgcgcagcagctatgaaggagacccacaa 120
|||||
DB 560 GCGCCACGACGACACCCCTCTCCTACTCCCTCCGAGCTCAGAGAGACCCCGAC 619
|||||
QY 121 acaatttggagagacacacccctcgcaggtctcgaagaccccgagctgtaattccctcgt 180
|||||
DB 620 ACGTACTGACGATACCTGTCAGAGGCTCTCAAGACCCCTGCTCCAGTCTCGGGC 679
|||||
QY 181 gtgggtcgtacagccacagcgtccgcg 207
|||||
DB 680 GTAGGCGGCTATAGCCCTGCTCCCGC 706

RESULT 8
AF205888 2538 bp mRNA PRI 03-JAN-2000
LOCUS Homo sapiens AXIN2 (AXIN2) mRNA, complete cds.
DEFINITION AF205888
ACCESSION AF205888.1 GI:6653583
VERSION
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS Zhang, T., Fagotto, F., Hsu, W., Zeng, L., Gilbert, D., Copeland, N.G.,
Jenkins, N.A., Warburton, D., and Costantini, F.
TITLE Properties of mouse Axin2 and human AXIN2: chromosomal location,
expression pattern, interaction with Axin and effects on embryonic
axis formation
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2538)
AUTHORS Zhang, T. and Costantini, F.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-1999) Genetics & Development, Columbia
University, 701 W168th St. HSC 1416, New York, NY 10032, USA
FEATURES
source
1. 2538
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="17"
/map="17q24"
/tissue_type="Brain; Lymphoblast"
/note="similar to ESTs 823683 and 446378"
1. 2538
/gene="AXIN2"
110..2443
/gene="AXIN2"
/codon_start=1
/product="AXIN2"
/protein_id="AA22799.1"
/db_xref="GI:6653584"
/translation="MSSAMLVTCLPDSSSFREDAPRPVPEEGEETPCPHHGGGPG
HOTVACLFQOAEKRWGEPEGRASPDSPITRWTKSLHSLGDQDGLFRFLERK
CVDLDFWFCNGFRQMLKDKTLRAKAIYKRIENNSIYVKOLKATKTYIRG
KQOQIDSLFDOATEIOSVMEANAYOMFLSDILEYVRSGEETAYMSNGSGSK
VYCGYLPITNEEWTGADFKCKLSPTVGLSSKTLRAVSRTETVDSGRKRS
DPVNPYHIGSGVFPATISANDSEISSALDSDSMSTDSVDGIPYRVGSKQLO
EMHRSVKANGRYSLPFRTHRLPKEMTPVEPATFAELISLEKLELSRHLLE
RLOQIREDEERSESLTNSREGAPTOHPLSLPGSYEDPOTLIDHLSRYLTPG
COSPVGRSPRSRSPDHHNHSHOYHSLPPGSKLPAAASPGACPLGGGKGYTK
TKYVNHNYIHNAVPTKTELEATQVHOCFPGSEYCYCKSKSHKAPETMP
EIOGQSTKKAAPLESARSPEGRSRHHNHSHOYHSLPPGSKLPAAASPGACPLGG
PNTLAHLEACGRLEAVSKPRQRCVVAOQDRHNSHTVGTGATPESNPSTLAPEDHK
EPKRLAGVHALDASELVVTFPGGEIYPRMLKQSLTLGHFKQLSKNGRYRDK
KASDFACGAVFEIWEDEVLPMEVGRILGVERID"

BASE COUNT 617 a 724 c 724 g 473 t
ORIGIN

Query Match 64.4%; Score 133.4; DB 88; Length 2538;
Best Local Similarity 77.8%; Pred. No. 8.9e-24;
Matches 161; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

OY 1 cagatccggaggaatgaagaaagaggggtctgagcagccctgagctcacggatga 60
|||||
DB 1295 CAGATCCGAGAGATGAGAGAGAGGGCTCCGAGCTCACACTCAATTCGGGGAGGG 1354
|||||
OY 61 gcaaccggtcagacacccccctgacctctaccctccgagcagctatgaagagcacaca 120
|||||
DB 1355 GCGCCACAGCAGACCCCTCTCCCTACCTGCGGAGCTAGAGAGAACCCGCGAG 1414
|||||
OY 121 accatttggagcagcaccctctcagggtctcctcaagacccccggctgtcaatccctgt 180
|||||

DB 1415 ACGTACTGACATCATCCTGTCCAGGGTCTCAACACCCCTGCTGCCAGTCTCCGGGC 1474
OY 181 gtgggtcgtctacagaccacgggtccgc 207
|||||
DB 1475 GTAGCCGCTATAGCCCTCGCTCCGC 1501
|||||

RESULT 9
AF078165 3072 bp mRNA PRI 21-MAR-1999
LOCUS Homo sapiens conductin mRNA, complete cds.
DEFINITION AF078165
ACCESSION AF078165
VERSION AF078165.1 GI:4454790
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS Ma, M., Qian, C., Yokomizo, A., Smith, D.I. and Liu, W.
TITLE Cloning of the human homolog of conductin (AXIN2), a gene mapping
to chromosome 17q23-q24
JOURNAL Genomics 55 (3), 341-344 (1999)
REFERENCE 9168905
AUTHORS Ma, M., Qian, C., Smith, D.I. and Liu, W.
TITLE Direct Submission
JOURNAL Submitted (15-JUL-1998) Lab Medicine and Pathology, Mayo Clinic,
200 First Street SW, Rochester, MN 55905, USA
FEATURES
source
1. 3072
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="17"
/map="17q23-q24"
90..2621
/note="AXIN2"
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/product="conductin"
/protein_id="AAD20976.1"
/db_xref="GI:4454791"
/translation="MSSAMLVTCLPDSSSFREDAPRPVPEEGEETPCPHHGGGPG
CVDLDFWFCNGFRQMLKDKTLRAKAIYKRIENNSIYVKOLKATKTYIRG
KQOQIDSLFDOATEIOSVMEANAYOMFLSDILEYVRSGEETAYMSNGSGSK
VYCGYLPITNEEWTGADFKCKLSPTVGLSSKTLRAVSRTETVDSGRKRS
DPVNPYHIGSGVFPATISANDSEISSALDSDSMSTDSVDGIPYRVGSKQLO
EMHRSVKANGRYSLPFRTHRLPKEMTPVEPATFAELISLEKLELSRHLLE
RLOQIREDEERSESLTNSREGAPTOHPLSLPGSYEDPOTLIDHLSRYLTPG
COSPVGRSPRSRSPDHHNHSHOYHSLPPGSKLPAAASPGACPLGGGKGYTK
TKYVNHNYIHNAVPTKTELEATQVHOCFPGSEYCYCKSKSHKAPETMP
EIOGQSTKKAAPLESARSPEGRSRHHNHSHOYHSLPPGSKLPAAASPGACPLGG
PNTLAHLEACGRLEAVSKPRQRCVVAOQDRHNSHTVGTGATPESNPSTLAPEDHK
EPKRLAGVHALDASELVVTFPGGEIYPRMLKQSLTLGHFKQLSKNGRYRDK
KASDFACGAVFEIWEDEVLPMEVGRILGVERID"

BASE COUNT 769 a 838 c 883 g 582 t
ORIGIN

Query Match 64.4%; Score 133.4; DB 88; Length 3072;
Best Local Similarity 77.8%; Pred. No. 8.6e-24;
Matches 161; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

OY 1 cagatccggaggaatgaagaaagaggggtctgagcagccctgagctcacggatga 60
|||||
DB 1278 CAGATCCGAGAGATGAGAGAGAGGGCTCCGAGCTCACACTCAATTCGGGGAGGG 1337
|||||
OY 61 gcaaccggtcagacacccccctgacctctaccctccgagcagctatgaagagcacaca 120
|||||
DB 1338 GCGCCACAGCAGACCCCTCTCCCTACCTGCGGAGCTAGAGAGAACCCGCGAG 1397
|||||
OY 121 accatttggagcagcaccctctcagggtctcctcaagacccccggctgtcaatccctgt 180
|||||

Db	1398	ACGATTACTGGACCATTA	CTCTGTCGACGGGTCTT	CAAGACCCCTGCGTCC	AGTCTCCGGGC	1457
Qy	181	gTgTgTcGctacagccac	gTgTccgG	207		
Db	1458	GTAAGCCCGCTATTA	AGCCCTGCGTCCGC	1484		

OY 181 g t g g t c g c t a c a g c c c a c g t c c c g c 207
 || | | | | | | | | | | | | |
Db 1458 G T A G C C G C T T A G C C C T G C T C C G C 1484

Db 1458 GTAGGCCGCTATAGCCCTCGCTCCGC 1484

RESULT 10

LOCUS	AB032263	3485 bp	VR	01-AUG-2000
DEFINITION	Danto rerlo mRNA for axln2, complete cds.			

ACCESSION	AB032263
VERSION	AB032263.1
	GT:7229079

KEYWORDS

SOURCE	Danio rerio cDNA to mRNA.
ORGANISM	Danio rerio

Eukaryota; Metazoa; Chord

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rasbora; Danio

REFERENCE
1 (sites)
CYPRINIDAE, CYPRINIDAE, DANIO.

AUTHORS
Shimizu, T., Yamanaoka, Y., Ryu, S.L., Hashimoto, H., Yabe, T.,
Hirata, T., Bao, Y. K., Uchi, M. and Hirano, T.

TITLE	Author(s)
Cooperative roles of Bozozok/Dharma and Nodal-rele	MIYATA, I., BAE, I., NISHI, M. and MIYANO, I.

the formation of the dorsal organizer in zebrafish

JOURNAL
MECH. DEV. 31 (1-2), 233-303 (2000)
MEDLINE
20171051

REFERENCE
2 (bases 1 to 3485)
H. J. Cantow and J. H. Drenth, *J. Biol. Chem.*, **234**, 1000 (1959).

TITLE	Direct Submission
ADJUNKS HIDAKO, I., HIDA, M. and SHIMIZU, I.	

JOURNAL
Submitted (09-SEP-1999) to the DDBJ/EMBL/GenBank databases. Toshio
Hasegawa, Department of Biology, Faculty of Science, Osaka University, Toyonaka, Osaka 565-0871, Japan

AF009011 3761 bp mRNA ROD 15-JUL-1997
LOCUS AF009011 Mus musculus Axin mRNA, partial cds.
ACCESSION AF009011 GI:2252815
VERSION AF009011.1
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Zeng, L., Fagotto, F., Zhang, T., Hsu, W., Vasilek, T.J., Perry, W.L.
1 (bases 1 to 3761)
3rd, Lee, J.J., Tilghman, S.W., Gumbiner, B.M. and Costantini, F.
The mouse fused locus encodes Axin, an inhibitor of the Wnt
signaling pathway that regulates embryonic axis formation
Cell 90 (1), 181-192 (1997)
97373830
JOURNAL
MEDLINE 2 (bases 1 to 3761)
Zeng, L., Zhang, T., Perry, W.L. III, Lee, J.J. and Costantini, F.
Direct Submission
AUTHORS Submitted (13-JUN-1997) Genetics and Development, Columbia
University, 701 W. 168th Street, New York, NY 10032, USA
JOURNAL Location/Qualifiers
FEATURES
source 1..3761
/organism="Mus musculus"
/db_xref="taxon:10090"
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/map="between Hba-ps4 and D17Leh54"
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1..2981
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HSLDDQGISLFRFLKQEGADLDLDFACSGFRKLEPCSNKRLKRLATYRK
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DEVPVPEFEKTIKVERVD" 771 c
BASE COUNT 890 a 1012 c 1088 g 771 t
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Best Local Similarity 62.5%; Pred. No. 5.6;
Matches 60; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

RESULT 15
AC011505/c
LOCUS AC011505 Homo sapiens chromosome 19 clone CTD-2081K17, WORKING DRAFT
DEFINITION
ACCESSION AC011505
VERSION AC011505.3 GI:7690143
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 19
JOURNAL Unpublished
2 (bases 1 to 171415)
DOE Joint Genome Institute.
AUTHORS
TITLE Direct Submission
JOURNAL Submitted (07-OCT-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On May 4, 2000 this sequence version replaced gi:5604364.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 658910, BC623934
Center clone name: CITB-H1_2081K17

Summary Statistics
Consensus quality: 162326 bases at least Q40
Consensus quality: 165118 bases at least Q30
Consensus quality: 166195 bases at least Q20
Estimated insert size: 169620; agarose-fp estimation
Estimated insert size: 169615; sum-of-contigs estimation
Quality coverage: 4.78 in Q20 bases; agarose-fp estimation
Quality coverage: 4.78 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 19 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 1832: contig of 1832 bp in length
1833 1932: gap of unknown length
1933 5043: contig of 3111 bp in length
5044 5143: gap of unknown length
5144 8167: contig of 3024 bp in length
8168 8267: gap of unknown length
8268 10591: contig of 2324 bp in length
10592 10691: gap of unknown length
10692 13471: contig of 2780 bp in length
13472 13571: gap of unknown length
13572 16253: contig of 2682 bp in length
16254 16353: gap of unknown length
16354 20637: contig of 4284 bp in length
20638 20737: gap of unknown length
20738 25626: contig of 4885 bp in length
25627 25726: gap of unknown length
25727 33181: contig of 7455 bp in length
33182 33282: gap of unknown length
33283 40894: contig of 7613 bp in length
40895 40995: gap of unknown length
40996 49304: contig of 8310 bp in length
49305 49404: gap of unknown length
49405 60431: contig of 11027 bp in length
60432 72480: gap of unknown length
72481 72480: contig of 11949 bp in length

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* 72481 72580: gap of unknown length
* 72581 88457: contig of 15877 bp in length
* 88458 88557: gap of unknown length
* 88558 101414: contig of 12857 bp in length
* 101415 101514: gap of unknown length
* 101515 115884: contig of 14370 bp in length
* 115885 115984: gap of unknown length
* 115985 133510: contig of 17526 bp in length
* 133511 133610: gap of unknown length
* 133611 151017: contig of 17407 bp in length
* 151018 151117: gap of unknown length
* 151118 171415: contig of 20298 bp in length.
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FEATURES
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1. 171415
Location/Qualifiers

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/db_xref="taxon:9606"
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Query Match 18.0%; Score 37.2; DB 62; Length 171415;
Best Local Similarity 51.9%; Pred. No. 4.8;
Matches 84; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

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    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 4476 GGAGAGGCGCACAGATGAGTGTATCCATACAGAGAGTGGAGAGAGTGGCGCACCACT 4417
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 69 ccagacccccctggccctctaccctcgcgcagctatgaagagagaccacaacattt 128
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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OY 129 ggaagacacactctccaggtctcctaagaagccccggcgtgtca 170
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 4356 GGATCTGCACATCACCAAGCCTCCAGGCCATACAGACCTCCA 4315
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Search completed: June 7, 2001, 00:36:12
Job time: 20986 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 7, 2001, 00:31:54 ; Search time 276.75 Seconds
(without alignments)
436.649 Million cell updates/sec

Title: US-09-587-574-9

Perfect score: 207

Sequence: 1 cagctccggggagatgaaga.....gtcacagccacggtccgcg 207

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

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- 21: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	207	100.0	2523	20	X23370 Human conductin CN
2	207	100.0	2825	20	X23369 Human conductin DN
3	38.4	18.6	3761	20	X09013 Murine axin gene.
4	35.2	17.0	402	21	C75493 Human ORFX ORF1048
5	33.2	16.0	3411	20	X09012 Human axin gene.
6	32.8	15.8	15202	20	X28371 Human imidazole
7	31.4	15.2	438	21	F11514 Aspergillus niger
8	31.2	15.1	2326	20	X86273 DNA encoding a hum
9	30.6	14.8	10384	21	X23256 HCV NS2-NS4 clone
10	30.4	14.7	849	13	O32483 HCV NS2-NS4 clone
11	30.4	14.7	849	13	O32482 HCV NS2-NS4 clone

C 12	30.4	14.7	1280	13	O32494
C 13	30.4	14.7	1280	13	O32495
C 14	30.4	14.7	1518	13	Z45454
C 15	30.4	14.7	3564	13	O32501
C 16	30.4	14.7	4447	21	C76436
C 17	30.4	14.7	5535	20	Z32057
C 18	30.4	14.7	5535	20	X21355
C 19	30.4	14.7	5535	22	C90314
C 20	30.4	14.7	7911	13	O32436
C 21	30.2	14.6	421	20	V87645
C 22	30.2	14.6	720	21	Z53528
C 23	30.2	14.6	720	21	Z53530
C 24	30.2	14.6	957	21	Z53533
C 25	30.2	14.6	960	21	Z53531
C 26	30.2	14.6	1212	20	Z20297
C 27	30.2	14.6	1520	21	Z90525
C 28	30.2	14.6	3362	21	C77294
C 29	30.2	14.6	3852	20	Z20298
C 30	30	14.5	849	13	O32472
C 31	30	14.5	1280	13	O32479
C 32	30	14.5	3564	13	O32442
C 33	29.8	14.4	1340	21	Z45317
C 34	29.8	14.4	1352	20	X85693
C 35	29.8	14.4	2045	14	O43374
C 36	29.8	14.4	10097	13	O24802
C 37	29.8	14.4	10279	13	O22487
C 38	29.8	14.4	10279	13	V81865
C 39	29.6	14.3	498	21	C99118
C 40	29.6	14.3	4024	20	X84595
C 41	29.6	14.3	4226	20	X84594
C 42	29.6	14.3	5828	20	X84592
C 43	29.6	14.3	6056	20	X84593
C 44	29.6	14.3	29879	14	O46806
C 45	29.4	14.2	705	20	Z15831

ALIGNMENTS

RESULT 1	
ID X23370	X23370 standard; cDNA; 2523 BP.
XX X23370;	
XX 17-JUN-1999 (first entry)	
DT	
XX Human conductin cDNA.	
DE	
XX Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour;	
KW therapy; cytoplasmic degradation; blockade; Wnt signalling pathway;	
KW Wingless signalling pathway; Adenomatous Polyposis Coll; APC;	
KW tumour suppressor; ss.	
XX	
OS Homo sapiens.	
XX	
PN W09911780-A2.	
XX	
PD 11-MAR-1999.	
XX	
PF 01-SEP-1998; 98MO-DE02621.	
XX	
PR 02-SEP-1997; 97DE-1038205.	
XX	
PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.	
XX	
PI Behrens J, Birnmeier W;	
XX	
DR WPI; 1999-214706/18.	
XX	
PT P-PSDB; W93570.	
PT Tumor-suppressing protein conductin - used for treatment and	
PT diagnosis of tumors	

HCV NS2-NS4 clone
HCV NS2-NS4 clone
Mouse voltage-gate
HCV NS2-NS4 clone
Human ORFX ORF191
Human METR2 relate
Human BAI1 gene.
AB005297 cDNA clon
HCV antigen clone
EST clone EC302.
Neisseria gonorrhoe
Neisseria meningit
Neisseria meningit
Neisseria gonorrhoe
Human G-protein co
Human GPCR protein
Human ORFX ORF2849
Human G-protein co
HCV NS2-NS4 clone
HCV NS2-NS4 clone
HCV NS2-NS4 clone
HCV NS2-NS4 clone
DNA encoding a GDP
Nucleic acid seque
Sequence of rat fi
Siymac239 nef-dele
Siymac239 proviral
Nucleic acid seque
Human pancreatic G
MTG16 protein cod
MTG16 protein cod
AML1-MTG16 fusion
eryA region of S.
Human gene express

XX PS Claim 18; Fig 3; 22pp; German.
XX
CC This invention describes a novel human conductin protein which has
CC anti-tumour activity. Detecting the presence or amount of conductin,
CC at protein or nucleic acid levels, is used to diagnose tumours, while
CC agents that (re)activate conductin are used for tumour therapy.
CC Conductin binds to beta-catenin and induces its cytoplasmic degradation,
CC resulting in blockade of the Wnt/Wingless signalling pathway in
CC vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC)
CC fragments and, in conjunction with APC, acts as a tumour suppressor.
XX
SQ Sequence 2523 BP; 620 A; 728 C; 723 G; 452 T; 0 other:

Query Match 100.0%; Score 207; DB 20; Length 2523;
Best Local Similarity 100.0%; Pred. No. 1,7e-48;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1189 cagatccggagagatgaagaaagaggggtctgagcagcgccctgagctcacggatga 1248
QY 61 gacccggtccagacacccctggccctctaccctccgagagctatgaagagaccacaa 120
DB 1249 gacccggtccagacacccctggccctctaccctccgagagctatgaagagaccacaa 1308
QY 121 accatttggagacacacctctccagggtccctcaagaccccgctgtcaatccctgt 180
DB 1309 accatttggagacacacctctccagggtccctcaagaccccgctgtcaatccctgt 1368
QY 181 gtgggtcgctacagcccaagcagtcgccg 207
DB 1369 gtgggtcgctacagcccaagcagtcgccg 1395

RESULT 2
X23369 ID X23369 standard; CDNA; 2825 BP.
XX AC X23369;
XX DT 17-JUN-1999 (first entry)
XX DE Human conductin DNA.
XX KW Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour;
KW therapy; cytoplasmic degradation; blockade; Wnt signalling pathway;
KW Wingless signalling pathway; Adenomatous Polyposis Coli; APC;
XX tumour suppressor; ss.
XX OS Homo sapiens.
XX FH Key
XX CDS 215..2737
FT /tag= a
FT /product= "Conductin"
FT 446..814
FT /tag= b
FT /note= "regulator of G-protein signalling region as
FT 1241..1402 described in Claim 19"
FT /tag= c
FT /bound_molety= GSK-3beta
FT /note= "as described in Claim 20"
FT 1403..1609
FT /tag= d
FT /bound_molety= beta-catenin
FT /note= "as described in Claim 21"
FT 2561..2713
FT /tag= e
FT /note= "Disvelled homology region as described in
FT Claim 22"

XX PN W09911780-A2.
XX PD 11-MAR-1999.
XX PF 01-SEP-1998; 98WO-DE02621.
XX PR 02-SEP-1997; 97DE-1038205.
XX PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX PI Behrens J, Birchemer W;
XX DR WPI: 1999-214706/18.
XX P-PSDB: W93569.
XX PT Tumor-suppressing protein conductin - used for treatment and
XX PT diagnosis of tumors
XX PS Claim 18; Fig 2; 22pp; German.
XX
CC This invention describes a novel human conductin protein which has
CC anti-tumour activity. Detecting the presence or amount of conductin,
CC at protein or nucleic acid levels, is used to diagnose tumours, while
CC agents that (re)activate conductin are used for tumour therapy.
CC Conductin binds to beta-catenin and induces its cytoplasmic degradation,
CC resulting in blockade of the Wnt/Wingless signalling pathway in
CC vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC)
CC fragments and, in conjunction with APC, acts as a tumour suppressor.
XX
SQ Sequence 2825 BP; 703 A; 815 C; 813 G; 494 T; 0 other:

Query Match 100.0%; Score 207; DB 20; Length 2825;
Best Local Similarity 100.0%; Pred. No. 1,8e-48;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagatccggagagatgaagaaagaggggtctgagcagcgccctgagctcacggatga 60
DB 1403 cagatccggagagatgaagaaagaggggtctgagcagcgccctgagctcacggatga 1462
QY 61 gacccggtccagacacccctggccctctaccctccgagagctatgaagagaccacaa 120
DB 1463 gacccggtccagacacccctggccctctaccctccgagagctatgaagagaccacaa 1522
QY 121 accatttggagacacacctctccagggtccctcaagaccccgctgtcaatccctgt 180
DB 1523 accatttggagacacacctctccagggtccctcaagaccccgctgtcaatccctgt 1582
QY 181 gtgggtcgctacagcccaagcagtcgccg 207
DB 1583 gtgggtcgctacagcccaagcagtcgccg 1609

RESULT 3
X09013 ID X09013 standard; DNA; 3761 BP.
XX AC X09013;
XX DT 14-JUN-1999 (first entry)
XX DE Murine axin gene.
XX KW Axin; cancer; breast cancer; colorectal cancer;
KW gastrointestinal cancer; esophageal cancer; carcinoma; melanoma;
KW diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;
XX beta-catenin; ss.
XX OS Mus musculus.
XX FH Key
XX CDS Location/Qualifiers
FT 1..2981


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FT      /*tag= a  
XX      /product= Axlin  
FN  
PN MO902179-AI.  
PD 21-JAN-1999.  
PE 09-JUL-1998;   98MO-USJ4414.  
PR 10-JUL-1997;   97US-0890865.  
PA (UYCO ) UNIV COLUMBIA NEW YORK.  
PI ConstantInt F, Zeng L;  
DR WPI: 1999-120510/10.  
P-PSDB: W96265.  
PT Newly isolated nucleic acid encoding "axis inhibition" protein  
PS (Axin) - useful for detecting, diagnosing and treating cancer  
CX Claim 7: Figure 9A-9B; 95pp; English.
```

Nucleic acids encoding mutant and wild type Axin and oligonucleotides derived from them are useful for detecting mutations in the Axin gene and for determining whether a subject is likely to develop cancer (including breast, colorectal, CC gastrointestinal, esophageal, carcinomas or melanomas). The wild type Axin and homologues of Axin are useful for treating subjects who are likely to develop cancer (thyroid carcinomas). The nucleic acids are also useful for diagnosing cancer and for detecting mutations in cancerous cells. Wild type Axin, its antisense molecule and identified compounds form pharmaceutical compositions in the treatment of cancer. The compositions are also useful for treating cancer by inhibiting tumorigenesis (by inducing degradation of beta-catenin), the nucleic acid encoding Axin acts through negative regulation of the Wnt pathway in the Nieuwkoop Center.

Sequence 3761 BP; 890 A; 1012 C; 1088 G; 771 T; 0 other;

Query Match

Best Local Similarity 18.6%; Score 38.4; DB 20; Length 3761;

Matches 60; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

[illegible]

KM expressed sequence tag; Fusarium venenatum; Aspergillus niger;
 KM Aspergillus oryzae; Trichoderma reesei; Identification; recombination;
 KM culture condition; environmental stress; spore morphogenesis;
 KM metabolic pathway engineering; catabolic pathway engineering; ss.
 XX
 OS Aspergillus niger.
 XX
 PN W0200056762-A2.
 XX
 PD 28-SEP-2000.
 XX
 PF 22-MAR-2000; 2000WO-US07781.
 XX
 XX 22-MAR-1999; 99US-0273623.
 PR
 PA (NOVO) NOVO NORDISK BIOTECH INC.
 PA (NOVO) NOVO NORDISK AS.
 XX
 XX Berka RM, Rey MM, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;
 XX
 DR WPI: 2000-594572/56.
 XX
 XX
 PT Monitoring differential expression of genes in filamentous fungal cells
 PT using fluorescence-labeled nucleic acids isolated from the cells and a
 PT substrate of expressed sequence tags -
 XX
 XX Claim 87: Page 1782; 3161pp; English.

CC The present invention describes a method for monitoring differential
CC expression of genes in a first filamentous fungal (FF) cell relative to
CC expression of the same genes in one or more second filamentous fungal
CC cells. The method uses fluorescence-labeled nucleic acids isolated from
CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs
CC are used in the methods for monitoring differential expression of genes
CC in a first filamentous fungal (FF) cell relative to expression of the
CC same genes in one or more second filamentous fungal cells. Monitoring
CC the global expression of genes from FF cells allows the production
CC potential of the microorganisms to be improved. New genes may be
CC discovered, possible functions of unknown open reading frames can be
CC identified and gene copy number variation and stability can be
CC monitored. The expression of genes can be used to study how FF cells
CC adapt to changes in culture conditions, environmental stress, spore
CC morphogenesis, recombination, metabolic or catabolic pathway engineering
CC using ESTs provides several advantages over genomic or random cDNA
CC clones including elimination of redundancy as one spot on an array
CC equals one gene or open reading frame, and organisation of the
CC microarrays based on function of the gene products to facilitate
CC analysis of the results. F074478 to F11247 represents ESTs from *Fusarium*
CC *venenatum*; F11448 to F11853 represents ESTs from *Aspergillus niger*;
CC F11854 to F14878 represents ESTs from *Aspergillus oryzae*; and F14879 to
CC F15337 represents ESTs from *Trichoderma reesei*, which are all
CC specifically claimed in the present invention.

```

Query Match      15.2%  Score 31.4:  DB 21:  Length 438:
Best Local Similarity 56.2%  Pred. No. 5.8:
Matches 59:  Conservative  0:  Mismatches 46:  Indels  0:  Gaps  0:

QY  100  AGCATGTAAGAGGACCCGCAACGATTTGTGACGAGCAGCCTCCAGGCTCAAGACC 159
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Db   160  AGGAAAGAAAAGGATTAAAGAAAGCTTTTGAAGCTAACCTTTCCAAACCGCTTCTTC 101

QY  160  CCGGCGTGTCAATCCCTCGTGTGTGTCGTACAGCCCAAGTCC 204
      ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db   100  TCCGCATTAATAGCCTCTTAATTTCCGGATCTGCACTCCAGACCC 56

RESULT      8
X86273
ID  X86273 standard; DNA; 2326 BP.
XX

```

AC	X86273.
XX	(first entry)
DT	22-SEP-1999
DE	DNA encoding a human p16 protein.
KW	p53 transcription tag; p53 status; cancer; cytotoxicity; carcinogenicity;
KM	neoplastic; PIG; ss.
OS	Homo sapiens.
PN	M09914356-A2.
PD	25-MAR-1999.
PF	17-SEP-1998; 98WO-USJ9300.
PR	30-MAR-1998; 98US-0079817.
PR	17-SEP-1997; 97US-0059153.
PA	(UOJO) UNIV JOHNS HOPKINS.
PI	Kinzel KW, Polyak K, Vogelstein B;
DR	WPI; 1999-443793/37.
PT	Use of p53 transcription tags to determine p53 status in, e.g.
PS	cancer diagnosis
PS	Disclosure: Page 64-65; 73pp; English.
CC	The specification describes the use of p53 transcription tags for
CC	developing products to determine p53 status, to diagnose cancer
CC	and to evaluate cytotoxicity or carcinogenicity of a test agent.
CC	A method for diagnosing cancer or determining p53 status in a sample
CC	suspected for being neoplastic comprises comparing the level of
CC	transcription of an RNA transcript in a first sample (s1) of a first
CC	tissue (t1) to the level of transcription of the transcript in a second
CC	sample (s2) of a second tissue (s2), where s1 is suspected of being
CC	neoplastic and s2 is a normal human tissue (of the same type) and the
CC	transcript is identified by a tag; and categorizing s1 as neoplastic
CC	or as having a mutant p53 when transcription is found to be the same
CC	or lower in the first, than in s2. The methods and products can be used
CC	to determine p53 status, to diagnose cancer and to evaluate cytotoxicity
CC	or carcinogenicity of a test agent. X86265-75 encode human p16 proteins.
SQ	Sequence 2326 BP: 544 A: 635 C: 637 G: 510 T: 0 other:
Query Match	15.1%; Score 31.2; DB 20; Length 2326;
Best Local Similarity	48.8%; Pred. No. 9.2;
Matches	84; Conservative 0; Mismatches 88; Indels 0; Gaps 0.
OY	23 agggagggtctgagcagccctgagtacgaatgcagaccggtgccagcccccttg 82
Db	1 aggcggagaagagcggtgcygcygtgcccgtgcggagaccggctccagacctgagc 60
Oy	83 cccctcaccccccgcaagcatataagaggagaccacaacacattttgatgcgaacctt 142
Db	61 gccgcggcagacaagaagcgcttcactccctcccgcagcgacaagccgcctcttc 120
Oy	143 ccagggtctccaagcccccgctgtaaatccctcggtgtgtggtcgctacag 194
Db	121 cgcggcctcgtcagtgcaagatgtctcctaccgtacgtagcgctccgg 172
RESULT	9
ID	236256/c
NC	Z36256 standard; DNA: 10384 BP.
AC	Z36256;
DT	22-FEB-2000 (first entry)

XX DNA sequence of the human longevity assurance gene 1 (LAG1).
DE
XX
XX Human: longevity assurance gene 1: LAG1; LAG1H; cell longevity;
KM cell tolerance; cellular stress; starvation; acidic pH;
KM cell reproductive capacity; ss.
XX
OS Homo sapiens.
XX
XX WO958671-A2.
PN
XX 18-NOV-1999.
PD
XX
XX 10-MAY-1999; 99WO-US10160.
PF
XX
XX 08-MAY-1998; 98US-0075014.
PR
XX (RESE) RESEARCH CORP TECHNOLOGIES INC.
PA
XX Jazwinski SM, Kirchner P, Jiang J;
PI
XX WPI: 2000-053098/04.
DR
XX
XX Novel human homologue for increasing longevity, tolerance and
PT reproductive capacity of a cell -
PS
XX Example 7: Page 92-99; 98pp; English.
XX
XX The present sequence represents the human longevity assurance gene 1
CC (LAG1), designated LAG1Hs. The LAG1Hs cDNA was isolated from total brain
CC mRNA. The LAG1 protein, or proteins with at least 25-30% homology to the
CC LAG1Hs protein, is administered to increase the longevity of a human
CC cell. Expression of these polypeptides is used to increase tolerance of
CC human cells to cellular stresses, such as starvation or acidic pH
CC (5-5.5). The LAG1 proteins are also used for increasing reproductive
CC capacity of human cells. LAG1 polynucleotides can be used as probes for
CC detecting LAG1 from different species, as the LAG1 gene is highly
CC conserved across the spectrum of eukaryotes.
XX
XX
SQ Sequence 10384 BP; 2135 A; 2839 C; 3598 G; 1812 T; 0 other;

Query Match 14.8%; Score 30.6; DB 21; Length 10384;
Best Local Similarity 51.9%; Pred. No. 18;
Matches 69; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 73 caccctcggccctcctaccctcggcagctatgaagagagaccacaacatttgac 132
DB 2032 CTCACCCAGCCGCGCCACACCCCGCATCTACCGGTTCCCGCCAGCAGCACTGTGTA 1973
QY 133 gaccacctcaggggtcctcaagacccccggctgtaatccctgggtgtggtgctac 192
DB 1972 AGGGGGCGCGCGCGCGCGAGAGACCTTATCTCTGGGGCTCCAACGCTCTGCTCTCC 1913
QY 193 agcccaaggtccc 205
DB 1912 AGCCCGAGGCCCC 1900

RESULT 10
Q32483/c
ID Q32483 standard; DNA; 849 BP.
XX
XX Q32483;
AC
XX 26-APR-1993 (first entry)
DT
XX
XX HCV NS2-NS4 clone MX25-2.
DE
XX
XX Clone: polypeptide; NS2-NS4; Hepatitis C; virus; HCV; serum; HC;
KM transcriptase; cDNA; primer; allele; ss.
XX
XX Hepatitis C virus.

XX
PN EP518313-A.
XX
XX 16-DEC-1992.
PD
XX
XX 11-JUN-1992; 92EP-0109812.
PF
XX
XX 11-JUN-1991; 91JP-0139268.
PR 12-JUL-1991; 91JP-0172794.
PR 07-OCT-1991; 91JP-0287008.
PR 16-DEC-1991; 91JP-0332329.
PR 20-APR-1992; 92JP-0099957.
XX
XX (MITU) MITSUBISHI KASEI CORP.
PA
XX
XX Hayashi N, Honda Y, Murakami T, Seki M, Takahashi K;
PI Teranishi Y;
XX
XX WPI: 1992-417213/51.
DR P-PSDB; R29852.
XX
XX
XX New hepatitis C virus gene and its encoded protein - used for
PT diagnosing and vaccinating against hepatitis C virus infections
PS
XX Disclosure; Page 147-49; 305pp; English.
XX
XX The sequences given in Q32483-501 are various clones which were used
CC in the isolation of the NS2-NS4 regions of the Hepatitis C virus
CC (HCV) gene of the invention (see also Q32442 and Q32472-82). These
CC sequences were isolated from the serum of a patient suffering from
CC hepatitis C (HC). The isolated RNA sequences were converted into
CC cDNA using transcriptase in the presence of one of the primer
CC sequences given in Q32578-79. The sequences were then amplified
CC using primer pairs. The cDNA sequences isolated represent different
CC alleles of the same region of the HCV gene. Sequence comparisons of
CC these clones showed that it is possible for a patient to carry more
CC than one HCV strain at one time. See also Q32436.
XX
XX
SQ Sequence 849 BP; 150 A; 250 C; 247 G; 202 T; 0 other;

Query Match 14.7%; Score 30.4; DB 13; Length 849;
Best Local Similarity 59.1%; Pred. No. 13;
Matches 52; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 16 gaagaagaaggaggtctgagcagccctgagctcaaggatggagacaggtccagcac 75
DB 123 GAAGAACAACAAGAAAGAGAGATGCCATGCCCTCCCGCATGATGCTGATGAGGAC 64
QY 76 cccctggccctcctaccctcggcagct 103
DB 63 CACGAGTTTCTCAAGCGCGGCTCACT 36

RESULT 11
Q32482/c
ID Q32482 standard; DNA; 849 BP.
XX
XX Q32482;
AC
XX 26-APR-1993 (first entry)
DT
XX
XX HCV NS2-NS4 clone MX25-1.
DE
XX
XX Clone: polypeptide; NS2-NS4; Hepatitis C; virus; HCV; serum; HC;
KM transcriptase; cDNA; primer; allele; ss.
XX
XX Hepatitis C virus.
PN EP518313-A.
XX
XX 16-DEC-1992.

PF 11-JUN-1992: 92EP-0109812.
XX
PR 11-JUN-1991: 91JP-0139268.
PR 12-JUL-1991: 91JP-0172794.
PR 07-OCT-1991: 91JP-0287008.
PR 16-DEC-1991: 91JP-0332329.
PR 20-APR-1992: 92JP-0099957.
XX
PA (MITU) MITSUBISHI KASEI CORP.
XX
PI Hayashi N, Honda Y, Murakami T, Seki M, Takahashi K;
PI Teranishi Y;
XX
DR WPI: 1992-417213/51.
DR P-PSDB: R29851.
XX
PT New hepatitis C virus gene and its encoded protein - used for
PT diagnosing and vaccinating against hepatitis C virus infections
XX
PS Disclosure: Page 146-47; 305pp; English.
XX
CC The sequences given in Q32472-82 and Q32442 are various clones which
CC encode the NS2-NS4 regions of the Hepatitis C Virus (HCV) gene of
CC the invention. These sequences were isolated from the serum of a
CC patient suffering from hepatitis C (HC). The isolated RNA sequences
CC were converted into cDNA using transcriptase in the presence of one
CC of the primer sequences given in Q32553-64. The sequences were
CC then amplified using primer pairs. The cDNA sequences isolated
CC represent different alleles of the same region of the HCV gene.
CC Sequence comparisons of these clones showed that it is possible for a
CC patient to carry more than one HCV strain at one time. See also
CC Q32436.
XX
SQ Sequence 849 BP; 146 A; 245 C; 249 G; 209 T; 0 other;

Query Match 14.7%; Score 30.4; DB 13; Length 849;
Best Local Similarity 59.1%; Pred. No. 13;
Matches 52; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 16 gaagaaagaggggtcgtgacagccctgagctcagggatgagcaccggtccagcac 75
DB 123 GAAGAACACAAAGAGAGAGATGCCATCGCTCCCGCATGATGCTCATTTGAGAGAC 64
QY 76 cccctggcctcctaccctccggcagct 103
DB 63 CACCAAGTCTCCAAAGCGGCTCAGCT 36

RESULT 12
Q32494/C
ID Q32494 standard; DNA: 1280 BP.
XX
AC Q32494;
XX

DT 26-APR-1993 (first entry)
XX

DE HCV NS2-NS4 clone MX25026A-1.
XX

XX Clone: polypeptide: NS2-NS4; Hepatitis C; Virus; HCV; serum; HC;
KM transcriptase; cDNA; primer; allele; ss.
XX
OS Hepatitis C virus.
XX

XX
FH Key Location/Qualifiers
FT CDS 1..1278
FT /*tag- a
XX

PN EP518313-A.
XX

PD 16-DEC-1992.
XX

PF 11-JUN-1992: 92EP-0109812.
XX

XX
PR 11-JUN-1991: 91JP-0139268.
PR 12-JUL-1991: 91JP-0172794.
PR 07-OCT-1991: 91JP-0287008.
PR 16-DEC-1991: 91JP-0332329.
PR 20-APR-1992: 92JP-0099957.
XX
PA (MITU) MITSUBISHI KASEI CORP.
XX
PI Hayashi N, Honda Y, Murakami T, Seki M, Takahashi K;
PI Teranishi Y;
XX
DR WPI: 1992-417213/51.
DR P-PSDB: R29863.
XX
PT New hepatitis C virus gene and its encoded protein - used for
PT diagnosing and vaccinating against hepatitis C virus infections
XX
PS Disclosure: Page 165-67; 305pp; English.
XX
CC The sequences given in Q32483-501 are various clones which were used
CC in the isolation of the NS2-NS4 regions of the Hepatitis C Virus
CC (HCV) gene of the invention (see also Q32442 and Q32472-82). These
CC sequences were isolated from the serum of a patient suffering from
CC hepatitis C (HC). The isolated RNA sequences were converted into
CC cDNA using transcriptase in the presence of one of the primer
CC sequences given in Q32578-79. The sequences were then amplified
CC using primer pairs. The cDNA sequences isolated represent different
CC alleles of the same region of the HCV gene. Sequence comparisons of
CC these clones showed that it is possible for a patient to carry more
CC than one HCV strain at one time. See also Q32436.
XX
SQ Sequence 1280 BP; 222 A; 385 C; 376 G; 297 T; 0 other;

Query Match 14.7%; Score 30.4; DB 13; Length 1280;
Best Local Similarity 59.1%; Pred. No. 14;
Matches 52; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 16 gaagaaagaggggtcgtgacagccctgagctcagggatgagcaccggtccagcac 75
DB 123 GAAGAACACAAAGAGAGAGATGCCATCGCTCCCGCATGATGCTCATTTGAGAGAC 64
QY 76 cccctggcctcctaccctccggcagct 103
DB 63 CACCAAGTCTCCAAAGCGGCTCAGCT 36

RESULT 13
Q32495/C
ID Q32495 standard; DNA: 1280 BP.
XX
AC Q32495;
XX

DT 26-APR-1993 (first entry)
XX

DE HCV NS2-NS4 clone MX25026B-1.
XX

XX Clone: polypeptide: NS2-NS4; Hepatitis C; Virus; HCV; serum; HC;
KM transcriptase; cDNA; primer; allele; ss.
XX
OS Hepatitis C virus.
XX

XX
FH Key Location/Qualifiers
FT CDS 1..1278
FT /*tag- a
XX

PN EP518313-A.
XX

PD 16-DEC-1992.
XX

PF 11-JUN-1992: 92EP-0109812.
XX

```

PR 11-JUN-1991; 91JP-0139268.
PR 12-JUL-1991; 91JP-0172794.
PR 07-OCT-1991; 91JP-0287008.
PR 16-DEC-1991; 91JP-0332329.
PR 20-APR-1992; 92JP-0099957.
XX
XX (MITU ) MITSUBISHI KASEI CORP.
XX
XX Hayashi N, Honda Y, Murakami T, Seki M, Takahashi K;
XX Teranishi Y;
XX
XX WPI: 1992-417213/51.
XX
XX P-PSDB; R29864.
XX
XX New hepatitis C virus gene and its encoded protein - used for
XX diagnosing and vaccinating against hepatitis C virus infections
XX
XX Disclosure; Page 167-69; 305pp; English.
XX
XX The sequences given in Q32483-501 are various clones which were used
XX in the isolation of the NS2-NS4 regions of the Hepatitis C virus
XX (HCV) gene of the invention (see also Q32442 and Q32472-82). These
XX sequences were isolated from the serum of a patient suffering from
XX hepatitis C (HC). The isolated RNA sequences were converted into
XX cDNA using transcriptase in the presence of one of the primer
XX sequences given in Q32578-79. The sequences were then amplified
XX using primer pairs. The cDNA sequences isolated represent different
XX alleles of the same region of the HCV gene. Sequence comparisons of
XX these clones showed that it is possible for a patient to carry more
XX than one HCV strain at one time. See also Q32436.
XX
XX Sequence 1280 BP; 222 A; 385 C; 376 G; 297 T; 0 other;
XX
XX
XX Query Match 14.7%; Score 30.4; DB 13; Length 1280;
XX Best Local Similarity 59.1%; Pred. No. 14;
XX Matches 52; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
XX
XX 16 gaagaaagagggtctcagcagccctcagctcagcgatgagcagcagcagc 75
XX 123 GAAAGAACACAAAGAAAGAGAGATGCCATGCCCTCCGCCATGATGCTGATAGAGAC 64
XX
XX 76 cccctgagccctcctaccctcgcgcagct 103
XX 63 CACCAAGTTCCTCCAGCGCGCATCAAGCT 36
XX
XX
XX RESULT 14
XX ID 249454
XX 249454 standard; DNA; 1518 BP.
XX
XX AC 249454;
XX
XX 04-APR-2000 (first entry)
XX
XX Mouse Voltage-gated Potassium channel monomer, Kv6.2 gene.
XX
XX Voltage gated potassium channel; Kv6.2; mouse; excitability; ion flux;
XX resting potential; alpha subunit; modulator; hearing/vision problem;
XX migraine; central nervous system; CNS; seizure; neuroprotective agent;
XX psychotic disorder; reporter; treatment; detection; antibody; probe;
XX primer; ds.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
XX mat_peptide 1..1518
XX /*tag= a
XX /label= Mouse_Kv6.2_polypeptide
XX /note= "Voltage gated potassium channel subunit"
XX 1381..1389
XX /*tag= b
XX /note= "This region encodes the amino acid sequence

```

```

FT ELK, which is represented in the specification
FT as the typographical error Kv6.2 (an insertion
FT of the protein name)"
XX
XX WO200001811-A1.
XX
XX 13-JAN-2000.
XX
XX 30-JUN-1999; 99WO-US14945.
XX
XX 01-JUL-1998; 98US-0091466.
XX
XX (ICAG-) ICAGEN INC.
XX
XX Jegla TJ;
XX
XX WPI: 2000-126937/11.
XX
XX P-PSDB; Y44564.
XX
XX New voltage-gated potassium channel alpha subunit, useful for
XX identifying modulators of voltage-gated channel activity useful for
XX treating central nervous system disorders e.g. migraines and as
XX neuroprotective agents -
XX
XX Claim 5; Page 65-66; 80pp; English.
XX
XX The present sequence is the gene encoding the mouse Kv6.2 monomer, which
XX is an alpha subunit of heteromeric voltage-gated potassium channel. It
XX is isolated from brain tissue and maintains the resting potential and
XX controls the excitability of a cell. Kv6.2 polypeptide can be used to
XX identify compounds, that modulate the ion flux through heteromeric
XX voltage-gated potassium channels. Such modulators are used as
XX neuroprotective agents and for treating CNS disorders, such as migraines,
XX hearing and vision problems, psychotic disorders and seizures. It can
XX also be used as reporter molecules in assays and to produce antibodies.
XX Kv6.2 DNA sequence can be used to produce specific primers or probes
XX for detection purposes.
XX
XX Sequence 1518 BP; 271 A; 467 C; 470 G; 310 T; 0 other;
XX
XX
XX Query Match 14.7%; Score 30.4; DB 21; Length 1518;
XX Best Local Similarity 51.5%; Pred. No. 14;
XX Matches 70; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
XX
XX 2 agatccggagatgaagaaagggtctcagcagccctcagctcagcgatgag 61
XX 176 agatccctagtgatgtgtgtggtgcagcaggtacctcgtcctcagcagcagcgatgacct 235
XX
XX 62 caacggtccagcagcccccctcctaccctcgcgcagcgtatgaagagaccacaaa 121
XX 236 tcccgctgagccgcctcagcagcagctccgcgtgtgcccagcagcatgtgagatcagcagc 295
XX
XX 122 ccatttggagacaca 137
XX
XX 296 tctgcgatgactaca 311
XX
XX
XX RESULT 15
XX Q32501/c
XX ID Q32501 standard; DNA; 3564 BP.
XX
XX AC Q32501;
XX
XX 26-APR-1993 (first entry)
XX
XX HCV NS2-NS4 clone N25N15-1.
XX
XX Clone; polypeptide; NS2-NS4; Hepatitis C; Virus; HCV; serum; HC;
XX transcriptase; cDNA; primer; allele; ss.
XX
XX Hepatitis C virus.
XX

```

PN EP518313-A.
 XX
 PD 16-DEC-1992.
 XX
 XX
 PF 11-JUN-1992; 92EP-0109812.
 XX
 XX 11-JUN-1991; 91JP-0139268.
 PR 12-JUL-1991; 91JP-0172794.
 PR 07-OCT-1991; 91JP-0287008.
 PR 16-DEC-1991; 91JP-033329.
 PR 20-APR-1992; 92JP-0099957.
 XX
 XX (MITU) MITSUBISHI KASEI CORP.
 PI Hayashi N, Honda Y, Murakami T, Seki M, Takahashi K;
 PI Teranishi Y;
 XX
 XX WPI: 1992-417213/51.
 DR P-PSDB; R29870.
 XX
 PT New hepatitis C virus gene and its encoded protein - used for
 PT diagnosing and vaccinating against hepatitis C virus infections
 XX
 PS Disclosure; Page 186-92; 305pp; English.
 XX
 CC The sequences given in Q32483-501 are various clones which were used
 CC in the isolation of the NS2-NS4 regions of the Hepatitis C Virus
 CC (HCV) gene of the invention (see also Q32442 and Q32472-82). These
 CC sequences were isolated from the serum of a patient suffering from
 CC hepatitis C (HC). The isolated RNA sequences were converted into
 CC cDNA using transcriptase in the presence of one of the primer
 CC sequences given in Q32578-79. The sequences were then amplified
 CC using primer pairs. The cDNA sequences isolated represent different
 CC alleles of the same region of the HCV gene. Sequence comparisons of
 CC these clones showed that it is possible for a patient to carry more
 CC than one HCV strain at one time. See also Q32436.
 XX
 SQ Sequence 3564 BP; 668 A; 1064 C; 1046 G; 786 T; 0 other;

Query Match 14.7%; Score 30.4; DB 13; Length 3564;
 Best Local Similarity 59.1%; Pred. No. 17;
 Matches 52; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
 QY 16 gaagaaagagggtctgagcagccctgagctcagggatgagacccggtccagcac 75
 DB 123 GAAGAACAACAGAGAGAGAGATGCCATGCCCTCCGCTATGATGCTCATTTGAGGAC 64
 QY 76 gccctggccctcctaccctccggcagct 103
 DB 63 CACCAGGTTCTCCAGGCGGCTCAGCT 36

Search completed: June 7, 2001, 00:31:59
 Job time: 8637 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 7, 2001, 00:26:34 ; Search time 136.23 Seconds
(without alignments)
265.307 Million cell updates/sec

Title: US-09-587-574-9

Sequence: 1 cagatccggagagatgaaga.....gtctacagccacggtccgc 207

Scoring table: IDENTITY_NUC
Gap 10.0 , Gapext 1.0

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : Issued Patents, NA: *
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2: /cgn2_6/ptodata/2/1na/5B.COMB.seq: *
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4: /cgn2_6/ptodata/2/1na/6B.COMB.seq: *
5: /cgn2_6/ptodata/2/1na/6C.COMB.seq: *
6: /cgn2_6/ptodata/2/1na/6D.COMB.seq: *

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32.8	15.8	15202	3	US-08-922-635-21
2	29.8	14.4	1352	2	US-08-937-972-4
3	29.6	14.3	20235	1	US-07-642-734C-3
4	29.6	14.3	20235	3	US-08-439-009A-3
5	29.2	14.1	3900	2	US-08-356-060A-42
6	29.2	14.1	3900	4	US-08-460-900C-42
7	29.2	14.1	4434	2	US-08-540-406-5
8	29.2	14.1	4434	3	US-08-656-055-5
9	29.2	14.1	4434	4	US-08-954-668-5
10	29.2	14.1	4434	5	PCT-US95-13233-5
11	28.8	13.9	732	1	US-07-953-230A-2
12	28.8	13.9	80161	4	US-09-036-987A-1
13	28.6	13.7	2824	2	US-09-010-928B-3
14	28.4	13.7	474	2	US-08-403-852D-14
15	28.4	13.7	474	3	US-08-510-646B-14
16	28.4	13.7	474	4	US-09-231-818-14
17	28.2	13.6	99	1	US-07-918-953-3
18	28.2	13.6	99	1	US-08-081-661-3
19	28.2	13.6	275	1	US-07-918-953-12
20	28.2	13.6	275	1	US-07-918-953-12
21	28.2	13.6	275	1	US-08-081-661-12
22	28.2	13.6	275	1	US-08-081-661-14
23	28.2	13.6	276	1	US-07-918-953-16
24	28.2	13.6	276	1	US-08-081-661-16
25	28.2	13.6	298	1	US-07-826-928A-28
26	28.2	13.6	330	5	PCT-US95-08596-1
27	28.2	13.6	359	3	US-08-589-028-3

28	28.2	13.6	359	4	US-08-784-582-3	Sequence 3, Appl1
29	28.2	13.6	359	4	US-08-785-271-3	Sequence 3, Appl1
30	28.2	13.6	510	1	US-07-918-953-7	Sequence 7, Appl1
31	28.2	13.6	510	1	US-08-081-661-7	Sequence 7, Appl1
32	28.2	13.6	515	3	US-08-589-028-1	Sequence 1, Appl1
33	28.2	13.6	515	3	US-08-784-582-1	Sequence 1, Appl1
34	28.2	13.6	515	4	US-08-785-271-1	Sequence 1, Appl1
35	28.2	13.6	2156	2	US-08-899-514-1	Sequence 1, Appl1
36	28.2	13.6	4895	4	US-09-053-866-1	Sequence 1, Appl1
37	28	13.5	1302	1	US-08-913-050A-2	Sequence 2, Appl1
38	28	13.5	6312	4	US-09-011-745-7	Sequence 7, Appl1
39	28	13.5	8535	3	US-08-716-351A-1	Sequence 1, Appl1
40	27.8	13.4	2451	2	US-08-820-170A-29	Sequence 29, Appl1
41	27.8	13.4	2451	3	US-09-055-699-29	Sequence 29, Appl1
42	27.8	13.4	2451	4	US-09-273-565-29	Sequence 29, Appl1
43	27.8	13.4	2487	2	US-08-820-170A-32	Sequence 32, Appl1
44	27.8	13.4	2487	3	US-09-055-699-32	Sequence 32, Appl1
45	27.8	13.4	2487	4	US-09-273-565-32	Sequence 32, Appl1

ALIGNMENTS

```
RESULT 1
US-08-922-635-21/C
Sequence 21, Application US/08922635A
Patent No. 6033871
GENERAL INFORMATION:
APPLICANT: PILETZ, John E.
APPLICANT: IVANOV, Tina R.
TITLE OF INVENTION: DNA MOLECULES ENCODING IMIDALINE RECEPTIVE POLYPEPTIDES
FILE REFERENCE: Corrected Sequence Listing
Patent No. 6033871
CURRENT APPLICATION NUMBER: US/08/922,635A
CURRENT FILING DATE: 1997-09-03
EARLIER APPLICATION NUMBER: 08/650,766
EARLIER FILING DATE: 1996-05-20
EARLIER APPLICATION NUMBER: 60/012,600
EARLIER FILING DATE: 1996-03-01
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
LENGTH: 15202
TYPE: DNA
ORGANISM: Homo sapiens
US-08-922-635-21

Query Match 15.8%; Score 32.8; DB 3; Length 15202;
Best Local Similarity 54.0%; Pred. No. 1.5;
Matches 67; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

OY 1 cagatccggagagatgaagaagggtctgagagagccctgaagctaacggatgga 60
DB 9992 CAACCCGGGGGTGCTGATGAGAGAGGCCCGGGGGCGAGGGCGAGGGG 9933
OY 61 gccacggttcagacacccctgcctctacccctcgcgcagctatgaagagacccacaa 120
DB 9932 GCCCAGGTCTCGCAGCACTCCAGCCACACTAGCCGAGATGCTGATGACACACAT 9873
OY 121 acca 124
DB 9872 GCCA 9869

RESULT 2
US-08-937-972-4
Sequence 4, Application US/08937972
Patent No. 5932443
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
```

RESULT 3
 US-07-642-734C-3
 ; Sequence 3, Application US/07642734C
 ; Patent No. 5824513
 ; GENERAL INFORMATION:
 ; APPLICANT: Katz, L
 ; APPLICANT: Donadio, S
 ; APPLICANT: McAlpine, J B
 ; TITLE OF INVENTION: Recombinant DNA Method for Producing
 ; TITLE OF INVENTION: Erythromycin Analogs
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Edward H. Gorman

```

STREET: Abbott Laboratories D377/AP6D-2 One Abbott
STREET: Park Rd
CITY: Abbott Park
STATE: IL
COUNTRY: US
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/642,734C
FILING DATE: 17-JAN-91
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dancikers, Andreas M
REGISTRATION NUMBER: 32652
REFERENCE/DOCKET NUMBER: 4952. US. 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-9396
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20235 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Saccharopolyspora erythraea
STRAIN: NRRL 238
FEATURE:
NAME/KEY: CDS
LOCATION: 19..10722
OTHER INFORMATION: /codon_start= 19
OTHER INFORMATION: /function= "gene eryA"
OTHER INFORMATION: /product= "eryA ORF2 encoding modules 3 & 4 for
OTHER INFORMATION: 6-deoxyerythronolide B"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 19..4470
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: module 3"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 97..1482
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacyl ACP synthase of module 3"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1693..2670
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain module 3"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 3406..3921
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoreductase domain of module 3"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 4171..4428
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyl carrier domain of module 3"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 4471..10722
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: module 4"
FEATURE:
NAME/KEY: misc_feature

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LOCATION: 4471..5847
OTHER INFORMATION: /function- "approximate span of
OTHER INFORMATION: beta-ketoacylACPSynthase domain of module "
FEATURE:
NAME/KEY: misc_feature
LOCATION: 6054..7026
OTHER INFORMATION: /function- "approximate span of
OTHER INFORMATION: acyltransferase domain of module 4"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 7165..9216
OTHER INFORMATION: /function- "approximate span of
OTHER INFORMATION: dehydratase and enoylreductase domains m"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 9433..9984
OTHER INFORMATION: /function- "approximate span
OTHER INFORMATION: beta-ketoreductase of module 4"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 10225..10483
OTHER INFORMATION: /function- "approximate span of
OTHER INFORMATION: acyl carrier domain of module 4"
FEATURE:
NAME/KEY: CDS
LOCATION: 10723..20235
OTHER INFORMATION: /codon_start- 10723
OTHER INFORMATION: /function- "gene -eryA"
OTHER INFORMATION: /product- "orf3 encoding modules 5 & 6
OTHER INFORMATION: 6-deoxyerythronolide B formatio"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 10723..15165
OTHER INFORMATION: /function- "approximate span of
OTHER INFORMATION: module 5"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 10831..12174
OTHER INFORMATION: /function- "approximate span of
OTHER INFORMATION: beta-ketoacylACPSynthase domain of modul"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 12379..13350
OTHER INFORMATION: /function- "approximatr span of
OTHER INFORMATION: acyltransferase domain of module 5"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 14062..14610
OTHER INFORMATION: /function- "approximate span of
OTHER INFORMATION: beta-ketoreductase of module 5"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 14857..15114
OTHER INFORMATION: /function- "approximate span of
OTHER INFORMATION: acyl carrier domain of module 5"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 15166..20235
OTHER INFORMATION: /function- "approximate span of
OTHER INFORMATION: module 6"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 15172..16569
OTHER INFORMATION: /function- "approximate span of
OTHER INFORMATION: beta-ketoacylACPSynthase domain of modul"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 16768..17721
OTHER INFORMATION: /function- "approximate span of
OTHER INFORMATION: acyltransferase domain of module 6"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 18379..18921

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OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoreductase domain of module 6"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 19149..19398
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyl carrier domain of module 6"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 19492..20235
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: thioesterase domain of module 6"
US-07-642-734C-3

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Query Match          14.3% Score 29.6; DB 1, Length 20235;
Best Local Similarity 57.6%; Pred. No. 13;
Matches 53; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Db      3262 GACGACGGGGCGCTCGTGTGTCGTGGAGACTCGCGGGGGGGCCGCTCCAGGAC 3321
Oy      115 ccacaaccatttggagcaccactctccag 146
       | | | | | | | | | | | | | | | |
Db      3322 CACTCAGCGGTCGCCGAGCGCGCGCTCCAGG 3353

RESULT 4
US-08-439-009A-3
; Sequence 3, Application US/08439009A
; Patent No. 6004787
; GENERAL INFORMATION:
; APPLICANT: Donadio, S
; APPLICANT: Katz, L
; APPLICANT: McAlpine, J B
; TITLE OF INVENTION: Method of Directing Biosynthesis of
; TITLE OF INVENTION: Specific Polyketides
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven F. Weinstock
STREET: Abbott Laboratories D377/APD-2 One Abbott
STREET: Park Rd
CITY: Abbott Park
STATE: IL
COUNTRY: US
ZIP: 60064-3500

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,009A
FILING DATE: 11-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 4952.US.D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
INFORMATION FOR SEQ ID NO.: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20235 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Saccharopolyspora erythraea

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OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: module 5"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 10831..12174
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacylACPSynthase domain of modul
FEATURE:
NAME/KEY: misc_feature
LOCATION: 12379..13350
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain of module 5"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 14062..14610
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoreductase of module 5"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 14857..15114
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyl carrier domain of module 5"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 15166..20235
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: module 6"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 15172..16569
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacylACPSynthase domain of modul
FEATURE:
NAME/KEY: misc_feature
LOCATION: 16768..17721
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain of module 6"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 18379..18921
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoreductase domain of module 6"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 19149..19398
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyl carrier domain of module 6"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 19492..20235
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: thioesterase domain of module 6"
US-08-439-009A-3

Query Match      14.3%; Score 29.6; DB 3; Length 20235;
Best Local Similarity 57.6%; Pred. No. 13;
Matches 53; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

OY   55 gatggagcaccggtccacgcaccccccttgccctctacccctcgcgcaagtatgaaggagac 114
      ||| |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |
Db   3262 GAGCAGCGGCGGGCTGCCTGTCTGTGTGCAATGCTTGCGCGGCGGCGCGTCCGAGGAC 3321

OY   115 ccacaacccatttggagcagcacacctccacg 146
      ||| |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |
Db   3322 CACTTCGGGCTCCGGAGCGGCCCTCCACGG 3353

RESULT      5
US-08-356-060A-42/c
Sequence 42; Application US/08356060A
Patent No. 5844079
GENERAL INFORMATION:
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DB 321 CTGATGAGCGCCATTGGGCGTCCACCCAGCTGTCGTATGTAAGATCCGAGATAA 262
QY 124 atttgagcagcaccctccagggcctcaagacc 161
DB 261 TTTCTCATGACCAATCGCGCTGTGTCTCCGGAACGC 224

RESULT 10

PCT-US95-13233-5/C
Sequence 5, Application PC/TUS9513233
GENERAL INFORMATION:
APPLICANT: THE BOARD OF TRUSTEES OF THE LELAND STANFORD JUNIOR UNIVERSITY
TITLE OF INVENTION: Patched Genes and their use
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13233
FILING DATE: 06-OCT-1990
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Berttram I
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A60190-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4434 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
PCT-US95-13233-5

Query Match 14.1%; Score 29.2; DB 5; Length 4434;
Best Local Similarity 56.1%; Pred. No. 12;
Matches 55; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 64 ccggtccagcaccctccgctccctaccctccgagcgtatgaagagagaccacaacc 123
DB 321 CTGATGAGCGCCATTGGGCGTCCACCCAGCTGTCGTATGTAAGATCCGAGATAA 262
QY 124 atttgagcagcaccctccagggcctcaagacc 161
DB 261 TTTCTCATGACCAATCGCGCTGTGTCTCCGGAACGC 224

RESULT 11

US-07-953-230A-2
Sequence 2, Application US/07953230A
Patent No. 5476779
GENERAL INFORMATION:
APPLICANT: CHEN, Thomas T
APPLICANT: SHAMLOTT, Michael J
TITLE OF INVENTION: INSULIN-LIKE GROWTH FACTORS ISOLATED
TITLE OF INVENTION: FROM RAINBOW TROUT
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.

CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/953,230A
FILING DATE: 30-SEP-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feary, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 028755-010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 732 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-953-230A-2

Query Match 13.9%; Score 28.8; DB 1; Length 722;
Best Local Similarity 52.5%; Pred. No. 10;
Matches 63; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 1 cagatccggagagatgaagaaaggaggtctgagcagggccttgagctcagggatga 60
DB 594 CAGGGCCCGGAAGTTCGGAGCGCGGTGAAGATCAAGCCCAAGACGAGCGATGT 653
QY 61 gcaacggtccagcaccctccgctccctaccctccgagcgtatgaagagagaccaca 120
DB 654 CCACGGCCCTGTGATCATCCTGCCACAGCAAGCTTCCGCCAGCTGCCCCACGACAA 713

RESULT 12

US-09-036-987A-1/C
Sequence 1, Application US/09036987A
Patent No. 6143526
GENERAL INFORMATION:
APPLICANT: Baltz, Richard H.
APPLICANT: Broughton, Mary C.
APPLICANT: Crawford, Kathryn P.
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Merlo, Donald J.
APPLICANT: Treadway, Patti J.
APPLICANT: Turner, Jan R.
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
TITLE OF INVENTION: Production
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dow Agrosciences LLC Patent Department
STREET: 9330 Zionsville Road
CITY: Indianapolis
STATE: Indiana
COUNTRY: USA
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/036,987A

FILING DATE: 09-MAR-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stuart, Donald R.
REGISTRATION NUMBER: 28,479
REFERENCE/DOCKET NUMBER: 50,608
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317)337-4816
TELEFAX: (317)337-4847
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 80161 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-036-987A-1

Query Match 13.9%; Score 28.8; DB 4; Length 80161;
Best Local Similarity 52.5%; Pred. No. 29;
Matches 63; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 43 ctgaactcagggatgagacacggtccagacccctgacctccctaccctccggcagc 102
DB 78772 CTCACCGGACACGACGCGGACCGGTGACACCGCTCTCCACTCCAGCGGGGCGGAC 78713
QY 103 tatgaagagaccacacacatttggagacacacctctccaggtctcctaaagacccc 162
DB 78712 GCCGCTACACCGGACACACCGCTGAGCGCGGCTGCTGTGTGACGAGGCGGTCC 78653

RESULT 13
US-09-010-928B-3/c

Sequence 3, Application US/09010928B
Patent No. 5994099

GENERAL INFORMATION:

APPLICANT: Lewis, Randolph V

APPLICANT: Hayashi, Cheryl Y

TITLE OF INVENTION: EXTREMELY ELASTIC SPIDER SILK PROTEIN AND DNA

TITLE OF INVENTION: CODING THEREFOR

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH

STREET: 8110 GATEHOUSE RD, SUITE 500E

CITY: FALLS CHURCH

STATE: VIRGINIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 22042

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/010,928B

FILING DATE: 22-JAN-1998

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Murphy Jr., Gerald M

REGISTRATION NUMBER: 28977

REFERENCE/DOCKET NUMBER: 1447-109P

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 2824 base pairs

TYPE: nucleic acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: -

LOCATION: 1..2824

OTHER INFORMATION: /note="Flagelliform DNA sequence
OTHER INFORMATION: taken from 3' region. Stop codon begins at position 2722.
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2724
US-09-010-928B-3

Query Match 13.8%; Score 28.6; DB 2; Length 2824;
Best Local Similarity 55.6%; Pred. No. 16;
Matches 55; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 64 ccggtccagacacccctcctccctaccctccgagctatgaagagaccacaaacc 123
DB 883 CTGCTCAGACACTCCAGGCTCTACACTCTGTGTCGAGCCACAGCCTACACCTC 824
QY 124 atttggacacacacctctccaggtctcctaaagacccc 162
DB 823 CTGCTCAGACACACCGGGTCCGGAACCTCCAGCACAC 785

RESULT 14
US-08-403-852D-14

Sequence 14, Application US/08403852D
Patent No. 5891695

GENERAL INFORMATION:

APPLICANT: Blanc, Veronique

APPLICANT: Blanche, Francis

APPLICANT: Crouzet, Joel

APPLICANT: Jacques, Nathalie

APPLICANT: Lacroix, Patricia

APPLICANT: Thibaut, Denis

APPLICANT: Zagorec, Monique

APPLICANT: Debussche, Laurent

APPLICANT: De Crey-Lagard, Valerie

TITLE OF INVENTION: Polypeptides Involved In The

TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences

TITLE OF INVENTION: Coding For These Polypeptides And Their Use

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: Flunegan, Henderson, Farabow, Garrett & Dunner

STREET: 1300 I Street, N.W., Suite 700

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/403,852D

FILING DATE: 10-MAY-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/FR 93/00923

FILING DATE: 25-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 92/11441

FILING DATE: 25-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.

REGISTRATION NUMBER: 25,146

REFERENCE/DOCKET NUMBER: 03806.0054-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 408-4400

TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 474 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear


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MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: S.pristinaespiralis
FEATURE:
NAME/KEY: CDS
LOCATION: 1..474
OTHER INFORMATION: /product= "Partie du gene Smdb"
US-08-403-852D-14

Query Match      13.7% Score 28.4; DB 2; Length 474;
Best Local Similarity 51.6%; Pred.No.12;
Matches 65; Conservative 0; Mismatches 61; Indels 0; Gaps 0

Qy 40 gccccgagctcgcggatgagacaccgcgccagcaccccccttgccctctactcccgagc 99
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 184 GCCCTGCTACCCGGCAGCGGCCCGGCACCAGCATCCCGTGGCAGCCCCGTGCGCGG 243

Qy 100 agctatgaaggagaccacaacacatttgyagcagaccacctctcaagytctcaagacc 159
    || | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 244 CGCACCGACGACGCCCTCGACGACCTGTGGGCTTCCTGTCAACACCCGTCCTCGCG 303

Qy 160 cccggc 165
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Db 304 ACCGAC 309

RESULT 15
US-08-510-646B-14
Sequence 14, Application US/08510646B
Patent No. 6077699
GENERAL INFORMATION:
APPLICANT: Blanc, Veronique
APPLICANT: Crouzet, Francis
APPLICANT: Jacques, Nathalie
APPLICANT: Lacroix, Patricia
APPLICANT: Thibaut, Denis
APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent
TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flanagan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/510,646B
FILING DATE: 03-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/403,852
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:

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1  NAME: Meyers, Kenneth J.
2  REGISTRATION NUMBER: 25.146
3  REFERENCE/DOCKET NUMBER: 03806.0054-01000
4  TELECOMMUNICATION INFORMATION:
5  TELEPHONE: (202) 408-4000
6  TELEFAX: (202) 408-4400
7  INFORMATION FOR SEQ ID NO: 14:
8  SEQUENCE CHARACTERISTICS:
9  LENGTH: 474 base pairs
10  TYPE: nucleic acid
11  STRANDEDNESS: double
12  TOPOLOGY: linear
13  MOLECULE TYPE: cDNA
14  HYPOTHEICAL: NO
15  ANTI-SENSE: NO
16  ORIGINAL SOURCE:
17  ORGANISM: S.pristinaespiralis
18  FEATURE:
19  NAME/KEY: CDS
20  LOCATION: 1..474
21  OTHER INFORMATION: /product= "Partie du gene Smbd"
22
23  US-08-510-646B-14
24
25  Query Match 13.7%; Score 28.4; DB 3; Length 474;
26  Best Local Similarity 51.6%; Pred. No.12;
27  Matches 65; Conservative 0; Mismatches 61; Indels 0; Gaps 0.
28
29  QY 40 gccctcagctcagcgatgagacacgggtlccagacccctctgacctctacccctcgggc 99
30  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
31  Db 184 gccctgcgtcaccggcgacagggccggcgacacgacgacgtccggtgggagacccctcgccggcg 243
32
33  QY 100 agctatgagagagaccacaacacatttcttgacgacacacattctcagtggtccttaagacc 159
34  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
35  Db 244 gcgacacgacgacgacgacctgcgacgacctggtggaccttcttgcacaaacacctgcttgcgcg 303
36  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
37  QY 160 cccggc 165
38  |||||
39  Db 304 accgac 309

```

Search completed: June 7, 2001, 00:26:48
Job time: 19751 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 6, 2001, 23:00:46 ; Search time 3054.04 Seconds
(without alignments)
592.125 Million cell updates/sec

Title: US-09-587-574-9

Perfect score: 207

Sequence: 1 cagatccggggagatgaaga.....gtacacgccacagtcgcgc 207

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 4368049070 residues

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
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 186: gb_est117:*
 187: gb_est118:*
 188: gb_est119:*
 189: gb_est120:*

Result	No.	Score	Query	Match	Length	DB	ID	Description
C	1	133.4	64.4	345	24	AI742962	AI742962 wg76d09.x	AI742962 wg76d09.x
C	2	133.4	64.4	408	23	AI660139	AI660139 we61a09.x	AI660139 we61a09.x
C	3	133.4	64.4	543	17	AI220032	AI220032 qg78b02.x	AI220032 qg78b02.x
C	4	133.4	64.4	591	102	AI818109	AI818109 wk27c05.x	AI818109 wk27c05.x
C	5	131.8	63.7	460	20	AI149942	AI149942 t940d11.x	AI149942 t940d11.x
C	6	130.4	63.0	418	103	AI858567	AI858567 w164d08.x	AI858567 w164d08.x
C	7	122	58.9	383	112	AI336613	AI336613 qo62c07.x	AI336613 qo62c07.x
C	8	121.4	58.6	413	19	AI336613	AI336613 qo62c07.x	AI336613 qo62c07.x
C	9	121.4	58.6	459	18	AI272864	AI272864 q143b03.x	AI272864 q143b03.x
C	10	121.4	58.6	487	18	AI307112	AI307112 q189f01.x	AI307112 q189f01.x
C	11	117.6	56.8	299	19	AI363868	AI363868 qy60a10.x	AI363868 qy60a10.x
C	12	111.6	53.9	346	13	AA915999	AA915999 oh86g11.s	AA915999 oh86g11.s
C	13	111	53.6	282	115	AA474251	AA474251 xs23a05.x	AA474251 xs23a05.x
C	14	106.8	51.6	409	8	AA489644	AA489644 aa43d02.s	AA489644 aa43d02.s
C	15	101.2	48.9	444	13	AA937585	AA937585 of71h02.s	AA937585 of71h02.s
C	16	90.4	43.7	181	111	AA172276	AA172276 xj36f12.x	AA172276 xj36f12.x
C	17	82.6	39.9	391	13	AA884421	AA884421 am16b12.s	AA884421 am16b12.s
C	18	81.6	39.4	360	155	R33824	R33824 yh78f12.s1	R33824 yh78f12.s1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

/db_xref="taxon:9606"
/clone="IMAGE:1879513"
/clone_1lb="Soares.NbHMPu.S1"
/tissue_type="pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pT73D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHMPu, pregnant uterus
NBHMPu, and fetal heart NBHMPu) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."

BASE COUNT 71 a 133 c 177 g 106 t
ORIGIN

Query Match 58.6%; Score 121.4; DB 18; Length 487;
Best Local Similarity 77.3%; Pred. No. 7.7e-23;
Matches 160; Conservative 0; Mismatches 46; Indels 1; Gaps 1;

QY 1 cagatccggagagatgaagaaagaggggtctgagcagccctgagctcagcgatgga 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 286 CAGATCCGAGAGATGAAAGAGAGAGGGCTCCGACCTCACTCAATTCGCGGAGGGG 227
QY 61 gacccggtcagcagccctgagctcctaccctccgagcagctatgaagagacacaa 120
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 226 GCGCCACGACGACCTCT-TCCTACTGCTCCGCGAGCTACGAGAGACCCGCGAG 168
QY 121 accatttggagcagcagcctctccagaggtctcgaagcccggtcgtataccctgt 180
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 167 AGGATCTGAGAGATCACTGTCTCAAGGCTCTCAAGACCCCTGGCTGCCAGTCTCCGGC 108
QY 181 gtcggtcgtacagccagcagctccgc 207
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 107 GTAAGCGCTATAGCCCTCGCTCCGC 81

RESULT 11
AI363868 299 bp mRNA EST 16-FEB-1999
LOCUS qy60a10.x1 NCI-CGAP Brn25 Homo sapiens cDNA clone IMAGE:2016378 3'
DEFINITION similar to TR:042400 042400 AXIN.; mRNA sequence.
ACCESSION AI363868
VERSION AI363868.1 GI:4123557
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 299)
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BRGAP), Tumor Gene Index
UNPUBLISHED (1998)
CONTACT: Robert Strausberg, Ph.D.
COMMENT Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbp/image/image.html
Insert Length: 504 Std Error: 0.00

JOURNAL
COMMENT

Seq primer: -40UP from Gibco
High quality sequence stop: 292.
FEATURES
Source location/Qualifiers
1..299
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2016378"
/clone_1lb="NCI-CGAP Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
/note="Organ: Brain; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTACCATCTGAGATGAGAGCGGCGCATGATGTTTCTTTTCTTTTCTTTTCTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."

BASE COUNT 40 a 83 c 111 g 65 t
ORIGIN

Query Match 56.8%; Score 117.6; DB 19; Length 299;
Best Local Similarity 76.0%; Pred. No. 7.8e-22;
Matches 158; Conservative 0; Mismatches 49; Indels 1; Gaps 1;

QY 1 cagatccggagagatgaagaaagaggggtctgagcagccctgagctcagcgatgga 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 247 CAGATCCGAGAGATGAAAGAGAGAGGGCTCCGACCTCACTCAATTCGCGGAGGGG 188
QY 61 gacccggtcagc-accctctgagctcctaccctccgagcagctatgaagagaccaca 119
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 187 GCGCCACGACACACCCCTCTCTCTGCTCCGCGACTACGAGAGACCCGCA 128
QY 120 aaccatttggagcagcagcctctccagaggtctcgaagcccggtcgtataccctgt 179
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 127 GACGATCTGAGAGATCACTGTCTCAAGGCTCTCAAGACCCCTGGCTGCCAGTCTCCGGG 68
QY 180 tctggtcgtacagccagcagctccgc 207
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 67 CGTAGCGCTATAGCCCTCGCTCCGC 40

RESULT 12
AA915999 546 bp mRNA EST 29-APR-1998
LOCUS oh86g11.s1 NCI-CGAP C08 Homo sapiens cDNA clone IMAGE:1473936 3'
DEFINITION similar to TR:042400 042400 AXIN.; mRNA sequence.
ACCESSION AA915999
VERSION AA915999.1 GI:3055391
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 546)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
UNPUBLISHED (1997)
CONTACT: Robert Strausberg, Ph.D.
COMMENT Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbp/image/image.html
Insert Length: 524 Std Error: 0.00

JOURNAL
COMMENT

/clone_1lb="Soares_NbHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pT73D-Pac
(Pharmacia) with a modified polylinker; Site: 1: Not I;
Site 2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NbHPU, and fetal heart NbH19M) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479." 1 others

BASE COUNT 59 a 108 c 152 g 89 t
ORIGIN

Query Match 51.6%; Score 106.8; DB 8; Length 409;
Best Local Similarity 75.8%; Pred. No. 6.7e-19;
Matches 157; Conservative 0; Mismatches 48; Indels 2; Gaps 2;

QY 1 cagatccggagagatgaagaaagaggggtctgagcagccctgagctcagggatgga 60
|||||
Db 248 CAGATCCGAGAGATGAGAGAGAGAGGGCTCCGAGCTCACACTCAATTCGCGGAGAGG- 188
|||||
QY 61 gacacgggtccagacccccctgacctctaccctcggcgagctatgagagagagccacaa 120
|||||
Db 189 GCGCCGACGAGACGCCCTCTCCCTTAAT-CTCCGCGACGATACGAGAGACCCGCGAG 131
|||||
QY 121 accatttgaagcagcaacctctcagaggtctcctaagagccccggctgtcaatccctgt 180
|||||
Db 130 ACGATTAAGTGGAGATGATGCTGCTCCAGAGGCTCTCAAGACCCCTGCGTCCGAGG 71
|||||
QY 181 gtggtctgctacagccagcggtccggc 207
|||||
Db 70 GTAGCCCGCTATAGCCNCCTGCTCCGC 44

RESULT 15
AA937585 444 bp mRNA EST 24-AUG-1998
LOCUS cf71h02.s1 NCI-CGAP_C08 Homo sapiens cDNA clone IMAGE:1435827 3'
DEFINITION Similar to TR:042400 042400 AXIN.; mRNA sequence.
ACCESSION AA937585
VERSION AA937585.1 GI:3095696
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 444)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
found through the I.M.A.G.E. Consortium/distribution information can be
www-bio.ln1.gov/bbrp/image/image.html
Insert Length: 537 Std Error: 0.00
Seq primer: 40m13 fwd. ET from Amersham.
Location/Qualifiers
1. .444
/organism="Homo sapiens"

FEATURES
SOURCE

/db_xref="taxon:9606"
/clone_1lb="NCI-CGAP_C08"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
colon adenocarcinoma, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT73
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo."

BASE COUNT 69 a 124 c 149 g 102 t
ORIGIN

Query Match 48.9%; Score 101.2; DB 13; Length 444;
Best Local Similarity 75.5%; Pred. No. 2.2e-17;
Matches 139; Conservative 0; Mismatches 43; Indels 2; Gaps 1;

QY 1 cagatccggagagatgaagaaagaggggtctgagcagccctgagctcagggatgga 60
|||||
Db 224 CAGATCCGAGAGATGAGAGAGAGAGGGCTCCGAGCTCACACTCAATTCGCGGAGAGG 165
|||||
QY 61 gacacgggtccagacccccctgacctctaccctcggcgagctatgagagagagccacaa 120
|||||
Db 164 GCGCCGACGAGACGCCCTCTCCCTTAAT-CTCCGCGACGATACGAGAGACCCGCGAG 107
|||||
QY 121 accatttgaagcagcaacctctcagaggtctcctaagagccccggctgtcaatccctgt 180
|||||
Db 106 ACGATTAAGTGGAGATGATGCTGCTCCAGAGGCTCTCAAGACCCCTGCGTCCGAGG 47
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QY 181 gtggt 184
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Db 46 TAGG 43

Search completed: June 6, 2001, 23:00:49
Job time: 15533 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 7, 2001, 00:36:12 ; Search time 4956.99 Seconds
(without alignments)
455.200 Million cell updates/sec

Title: US-09-587-574-10
153
Sequence: 1 ttgacctggccacttcaa.....tgtacgaagcagatcctg 153

Scoring table: IDENTITY_NUC
Gapop 10.0 / Gapext 1.0

Searched: 1283235 seqs, 7373929652 residues
Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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13: gb_pl2:*
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17: em_ba2:*
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71: gb_hcgl12:*
72: gb_hcgl13:*
73: gb_hcgl14:*
74: gb_hcgl15:*
75: gb_hcgl16:*
76: gb_hcgl17:*
77: gb_hcgl18:*
78: gb_hcgl19:*
79: gb_hcgl20:*
80: gb_hcgl21:*
81: gb_hcgl22:*
82: gb_hcgl23:*
83: gb_hcgl24:*
84: gb_hcgl25:*
85: gb_pr1:*
86: gb_pr2:*
87: gb_pr3:*
88: gb_pr4:*
89: gb_pr5:*
90: gb_pr6:*
91: gb_pr7:*
92: gb_pr8:*
93: gb_pr9:*
94: gb_rnd1:*
95: gb_rnd2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	153	100.0	153	9 A98525	A98525 Sequence 10
2	153	100.0	2825	9 A98521	A98521 Sequence 6
3	153	100.0	2825	9 AF073788	AF073788 Mus muscu
4	153	100.0	3016	9 AF205889	AF205889 Mus muscu
5	143.4	93.7	3216	9 AF017757	AF017757 Rattus no
6	121	79.1	1863	85 AB052751	AB052751 Homo sapi
7	121	79.1	2104	89 AK025718	AK025718 Homo sapi
8	121	79.1	2538	88 AF205888	AF205888 Homo sapi
9	121	79.1	3072	88 AF078165	AF078165 Homo sapi
10	91.8	60.0	3156	8 AF009012	AF009012 Gallus ga
11	88.6	57.9	3411	88 AF009674	AF009674 Homo sapi

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12 88.6 57.9 3485 8 AB032263
13 85.6 55.9 2529 8 AF097313
14 83.8 54.8 3460 9 AF017756
15 82.2 53.7 3781 94 AF009011
16 79.7 51.6 3066 8 AB032262
17 68.8 45.0 2121 8 AF140243
18 55.8 36.5 31557 91 HS314G4
19 55.8 36.5 13069 70 AC026836
20 55.8 36.5 187272 74 AC069076
21 52 34.0 191041 69 AC024114
22 38.2 25.0 278229 76 AC074322
23 38 24.8 2232 5 AF086811
24 38 24.8 3990 5 AF091813
25 36.2 23.7 2177 93 HS046461
26 36.2 23.7 2889 88 AF006011
27 36.2 23.7 2955 94 AF143545
28 36.2 23.7 2955 94 AF143546
29 36 23.5 3286 94 MM010115
30 33.4 21.8 5596 1 AF026544
31 32.6 21.3 36308 2 D88802
32 32.6 21.3 213190 2 BSUB0004
33 32.4 21.2 79663 12 AC006593
34 32.4 21.2 122557 91 HS22948
35 32.4 21.2 157875 91 HS272116
36 32.2 21.0 145294 61 AC009856
37 32.2 21.0 178518 80 AL357632
38 32 20.9 12217 1 AE004520
39 32 20.9 219785 74 AC069035
40 31.8 20.8 347660 2 AP002994
41 31.6 20.7 130379 92 HSDJ31316
42 31.6 20.7 176277 70 AC025941
43 31.2 20.4 128639 63 AC013527
44 31 20.3 9200 1 AF130422
45 30.8 20.1 135468 64 AC016503
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ALIGNMENTS

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RESULT 1
LOCUS A98525 153 bp DNA
DEFINITION Sequence 10 from Patent WO9911780.
ACCESSION A98525
VERSION A98525.1 GI:6781611
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 153)
AUTHORS Birchmeier,W. and Behrens,J.
TITLE CONDUCTINE PROTEIN AND A RELATED AGENT FOR DIAGNOSING AND TREATING
JOURNAL TUMOR ILLNESSES
PATENT: WO 9911780-A 10 11-MAR-1999;
BIRCHMEIER WALTER (DE); BEHRENS JUERGEN (DE)
FEATURES
source
location/Qualifiers
BASE COUNT 43 a 32 c 46 g 32 t
ORIGIN
Query Match 100.0%; Score 153; DB 9; Length 153;
Best Local Similarity 100.0%; Pred. No. 7,1e-38;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ttgacctggggccacttcaagagcagctcagcaaaagggaattacaggtattattc 60
DB 1 TTGACCTGGGGCCACTTCAAGAGCAGCTCAGCAAAAGGGAATTACAGGTATTATTTC 60
QY 61 aagaagcgagtgaggaatttcctcgagcagcttttgaggaatctggagcagcag 120
DB 61 aagaagcgagtgaggaatttcctcgagcagcttttgaggaatctggagcagcag 120
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DB 61 AAGAAGCGAGTGAGCAATTTCCTCCGAGCAGTCTTTTGAGAGATCTGGAGCAGCAG 120
QY 121 acagtgctcccatgtacgaagcagagatcctg 153
DB 121 ACAGTGCTCCCATGTACGAGAGCAGAGATCCTG 153
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RESULT 2
LOCUS A98521 2825 bp DNA
DEFINITION Sequence 6 from Patent WO9911780.
ACCESSION A98521
VERSION A98521.1 GI:6781607
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 2825)
AUTHORS Birchmeier,W. and Behrens,J.
TITLE CONDUCTINE PROTEIN AND A RELATED AGENT FOR DIAGNOSING AND TREATING
JOURNAL TUMOR ILLNESSES
PATENT: WO 9911780-A 6 11-MAR-1999;
BIRCHMEIER WALTER (DE); BEHRENS JUERGEN (DE)
FEATURES
source
location/Qualifiers
BASE COUNT 703 a 815 c 813 g 494 t
ORIGIN
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Query Match 100.0%; Score 153; DB 9; Length 2825;
Best Local Similarity 100.0%; Pred. No. 1,1e-37;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 2561 TTGACCTGGGGCCACTTCAAGAGCAGCCTCAGCAAAAGGGAATTACAGGTATTATTTC 2620
QY 61 aagaagcgagtgaggaatttcctcgagcagcttttgaggaatctggagcagcag 120
DB 2621 AAGAAGCGAGTGAGCAATTTCCTCCGAGCAGTCTTTTGAGAGATCTGGAGCAGCAG 2680
QY 121 acagtgctcccatgtacgaagcagagatcctg 153
DB 2681 ACAGTGCTCCCATGTACGAGAGCAGATCCTG 2713
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RESULT 3
LOCUS AF073788 2825 bp mRNA
DEFINITION Mus musculus conductin mRNA, complete cds.
ACCESSION AF073788
VERSION AF073788.1 GI:3309246
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 2825)
AUTHORS Behrens,J., Jerchow,B.-A., Wurttele,M., Grimm,J., Asbrand,C.,
Wirtz,R., Kuhl,M., Wedlich,D. and Birchmeier,W.
TITLE Functional interaction of an axin homolog, conductin, with
JOURNAL Science 280 (5363), 596-599 (1998)
MEDLINE 98221239
REFERENCE 2 (bases 1 to 2825)
AUTHORS Behrens,J., Jerchow,B.-A. and Birchmeier,W.
TITLE Direct Submission
JOURNAL Submitted (22-JUN-1998) Cellular Biology, Max Delbrueck Center for
Molecular Medicine, Robert-Rössle 10, Berlin 13122, Germany
FEATURES
source
location/Qualifiers
1..2825
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CDs

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STKPMVSSNARNEDGLEPEGRASPDPLRTWKSLHSLGDODGALPFTFLERE
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IKKOOLGSMFOAOETIOAVEMNAVOFLSDIYLEVRSRGENTATMNSGGSL
KVLGCTLPILNEEEMTCADLCKLSPTVYSSKTLRATASVRSSTETANENPESKR
SDPVNHYVSGVTFAPATSDNSLSDALTDSSMTDSSVDGVPPYRMGSKOLO
RBMHRSVANKGVSLPFPRTNRLPKEMTPVEPAFAELISRLKLELSRHSLE
ERLQOIRDEDEEKEGSEOLASRDGAPOVQHPALLPESGYEEDPOTILDHLSRVLT
GCOSSPGVGRSPRSRDPDHHQHNNHOCCHTLPTGSKLPVPAACPLLGKSELTQOT
TKHVNHHYIHHNAVPTKTEIEAATORVRCLPQGTDDYCYSKCKSHKAPPLDGE
OCCSGRGTLPRKNAKTEPRGLASRDGMSAAGPOLPEEGDRSDVNMOMIES
ERQSKSPHSAQSIKSTIPLESARAPGERVSRHHLGASGHSRVARAHPTQDPAM
PULTPNTLAOLEACRLAEVSKPOKRCVAAOQRNNSAAGQASPARANPDLA
PEDHKEPKLASVHALQASLAVTYVTFECGEELPYRMLKAQSLTLGHFEKQLSKKNY
RYVFKASDEFAAGAVFEIIMDETVLPWYEGRIILKVERID"

BASE COUNT 703 a 815 c 813 g 494 t

ORIGIN

Query Match 100.0%; Score 153; DB 94; Length 2825;
Best Local Similarity 100.0%; Pred. No. 1.1e-37;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 aagaagcgagtgacgaatttcctgcgagagcagtttttgaagagatcttgagcagcag 120
|||||
Db 2621 aagaagcgagtgacgaatttcctgcgagagcagtttttgaagagatcttgagcagcag 2680
|||||

Qy 121 acagtgctcccatgtacgaagcagagatcctg 153
|||||
Db 2681 acagtgctcccatgtacgaagcagagatcctg 2713
|||||

RESULT 4
AF205889 3016 bp mRNA ROD 03-JAN-2000
LOCUS Mus musculus Axln2 (Axln2) mRNA, complete cds.
DEFINITION AF205889
ACCESSION AF205889.1 GI:6653585
VERSION
KEYWORDS house mouse.
SOURCE
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3016)
Zhang, T., Fagotto, F., Hsu, W., Zeng, L., Gilbert, D., Copeland, N.G.,
Jenkins, N.A., Warburton, D. and Costantini, F.
Properties of mouse Axln2 and human AXIN2: chromosomal location,
expression pattern, interaction with Axin and effects on embryonic
axis formation
Unpublished
2 (bases 1 to 3016)
Zhang, T. and Costantini, F.
Direct Submission
Submitted (16-NOV-1999) Genetics & Development, Columbia
University, 701 M168th St. HSC 1416, New York, NY 10032, USA
Location/Qualifiers
1..3016
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="11"
/map="between Wnt3 and Pkca"

FEATURES
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55..2577
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IKKOOLGSMFOAOETIOAVEMNAVOFLSDIYLEVRSRGENTATMNSGGSL
KVLGCTLPILNEEEMTCADLCKLSPTVYSSKTLRATASVRSSTETANENPESKR
SDPVNHYVSGVTFAPATSDNSLSDALTDSSMTDSSVDGVPPYRMGSKOLO
RBMHRSVANKGVSLPFPRTNRLPKEMTPVEPAFAELISRLKLELSRHSLE
ERLQOIRDEDEEKEGSEOLASRDGAPOVQHPALLPESGYEEDPOTILDHLSRVLT
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ERQSKSPHSAQSIKSTIPLESARAPGERVSRHHLGASGHSRVARAHPTQDPAM
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PEDHKEPKLASVHALQASLAVTYVTFECGEELPYRMLKAQSLTLGHFEKQLSKKNY
RYVFKASDEFAAGAVFEIIMDETVLPWYEGRIILKVERID"

BASE COUNT 766 a 858 c 837 g 555 t

ORIGIN

Query Match 100.0%; Score 153; DB 94; Length 3016;
Best Local Similarity 100.0%; Pred. No. 1.1e-37;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2401 ttgacctgggccaacttcagaagagcagctcagcaaaaaggaaattacaggtatttc 2460
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Qy 61 aagaagcgagtgacgaatttcctgcgagagcagtttttgaagagatcttgagcagcag 120
|||||
Db 2461 aagaagcgagtgacgaatttcctgcgagagcagtttttgaagagatcttgagcagcag 2520
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Qy 121 acagtgctcccatgtacgaagcagagatcctg 153
|||||
Db 2521 acagtgctcccatgtacgaagcagagatcctg 2553
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RESULT 5
AF017757 3216 bp mRNA ROD 24-APR-1998
LOCUS Rattus norvegicus GSK-3beta interacting protein Axli mRNA, complete
DEFINITION AF017757
ACCESSION AF017757.1 GI:3080758
VERSION
KEYWORDS Norway rat.
SOURCE
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 3216)
Yamamoto, H., Kishida, S., Uochi, T., Ikeda, S., Koyama, S., Asashima, M.,
Axli, a member of the Axin family, interacts with both glycogen
synthase kinase 3beta and beta-catenin and inhibits axis formation
of Xenopus embryos
Mol. Cell. Biol. 18 (5), 2867-2875 (1998)
98226558
2 (bases 1 to 3216)
Yamamoto, H., Ikeda, S., Murai, H., Kishida, S. and Kikuchi, A.
Direct Submission
Submitted (08-AUG-1997) Biochemistry, Hiroshima University, School
of Medicine, 1-2-3 Kasumi, Minami-Ku, Hiroshima, Hiroshima 734,
Japan
Location/Qualifiers
1..3216

FEATURES
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CDS

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85..2601
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IKKQDTGVDFDQOTELQAVMEENAVYFLTSDIYLYVRSGGNTAYMNGIGSL
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SEPNPVHVGSGYVAPATPANDSELSDSLDSMTDSVDGIIPYRMGSKQLQ
REMRHVSANGQVSLPHPTTHRLPKEMTPVEPAFAELISRLKLELSRHSLE
ERLQOIRDEDEKESESLSSRDGAPVOHPIALLPSGSEEDPOTIIDHLSTYIKTP
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QSKSPHTOSIRKSYPLESARAPGERVSHHLLGASGPRSAARAHFQDAMP
LTPPTLAOLEEACRLAEVSKPOKRCVSAQOORHNPATGAGPTFSNPISLSE
DHKEPKRLASVHALOASLIYTFEFCGEETIYRRLMKOSLTLGHFKQLSKKNYR
YFKASDFACGAVPEEIMDETVLPMEGRILGVERID"

BASE COUNT 860 a 914 c 872 g 570 t

ORIGIN

Query Match 93.7% Score 143.4: DB 94; Length 3216;
Best Local Similarity 96.1% Pred. No. 1.2e-34;
Matches 147; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Db 2425 TTGACCTGGCCACTTCAAGAGCAGCTCAGCAAAAGGAATTACGGTATTACTTC 2484
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Db 2485 AAGAAGCGCAGTGAGCAAAATTCCTGTGAGCAGCTTTGAGAGATCTGGGATGATGAG 2544
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Qy 121 acagtgctcccatgtacgaagcagatctctg 153
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Db 2545 ACAGTGCTCCCATGTACGAGCAGCATCTG 2577
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RESULT 6
AB052751 1863 bp mRNA PRI 21-DEC-2000
LOCUS Homo sapiens Axin2 mRNA for conductin, partial cds and 3'UTR.
DEFINITION AB052751
ACCESSION AB052751.1 GI:11967903
KEYWORDS
SOURCE Homo sapiens
ORGANISM Homo sapiens
Homology: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (sites)
AUTHORS Takahashi, M. and Furukawa, Y.
JOURNAL Identification of 3' UTR of Axin2
REFERENCE Published Only in Database (2000) In press
AUTHORS 2 (bases 1 to 1863)
Nakamura, Y., Furukawa, Y. and Takahashi, M.
JOURNAL Direct Submission
COMMENT Submitted (16-DEC-2000) to the DDBJ/EMBL/GenBank databases. Yotchi
Furukawa, Institute of Medical Science, Human Genome Center; 4-6-1-
Shirokane-dai, Minato-Ku, Tokyo 108-1639, Japan
(E-mail: furukawa@ims.u-tokyo.ac.jp, Tel: 81-35449-5373,
Fax: 81-35449-5406)
FEATURES
Source 1..1863 Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
1..1863
/gene="Axin2"

CDS

<1..446
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/product="conductin"
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447..1863
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BASE COUNT 484 a 375 c 452 g 552 t

ORIGIN

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Best Local Similarity 86.9% Pred. No. 1.3e-27;
Matches 133; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

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Db 270 TTGACCTGGCCACTTCAAGAGCAGCTCAGCAAAAGGAATTATAGTATTACTTC 329
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Qy 61 aagaagcgagtgagcaattctgctcgagagcagttttgagagatctggagacagag 120
|||||
Db 330 AAAAAAGCAGCAGATGAGTGTGCTGTGAGCAGCTTTGAGAGATCTGGGAGATGAG 389
|||||

Qy 121 acagtgctcccatgtacgaagcagatctctg 153
|||||
Db 390 ACAGTGCTCCCATGTACGAGCAGCATCTG 422
|||||

RESULT 7
AK025718 2104 bp mRNA PRI 29-SEP-2000
LOCUS Homo sapiens cDNA: FLN22065 fls, clone HEP10566, highly similar to
DEFINITION AF078165 Homo sapiens conductin mRNA.
ACCESSION AK025718
VERSION AK025718.1 GI:10438327
KEYWORDS oligo capping; fls (full insert sequence).
SOURCE Homo sapiens hepatoma cell_line: HepG2 cDNA to mRNA, clone lib: HEP
clone: HEP10566.
ORGANISM Homo sapiens
Homology: Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (sites)
AUTHORS Kawabata, A., Hiki, T., Kobatake, N., Inagaki, H., Ikema, Y.,
Okamoto, S., Okitani, R., Ota, T., Suzuki, Y., Odayashi, M., Nishi, T.,
Shibahara, T., Tanaka, T., Nakamura, Y., Isogai, T. and Sugano, S.
JOURNAL NEBO human cDNA sequencing project
REFERENCE Unpublished (2000)
AUTHORS 2 (bases 1 to 2104)
Sugano, S., Suzuki, Y., Ota, T., Odayashi, M., Nishi, T., Isogai, T.,
Shibahara, T., Tanaka, T. and Nakamura, Y.
JOURNAL Direct Submission
COMMENT Submitted (29-AUG-2000) to the DDBJ/EMBL/GenBank databases. Sumio
Sugano, Institute of Medical Science, University of Tokyo,
Laboratory of Genome Structure Analysis, Human Genome Center;
Shirokane-dai, 4-6-1, Minato-Ku, Tokyo 108-8639, Japan
(E-mail: cdnals@ims.u-tokyo.ac.jp, Tel: 81-3-5449-5286,
Fax: 81-3-5449-5416)
FEATURES
Source 1..2104 Location/Qualifiers
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misc_feature
1. 2104
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mRNA"
BASE COUNT      506 a      610 c      619 g      369 t
ORIGIN

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Best Local Similarity 86.9%; Pred. No. 1.3e-27; Length 2104;
Matches 133; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

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QY 121 acagtgctcccatgtacgaagcagagctctc 153
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DB 1787 acggtctcccatgtatgagagcggcagattctg 1819
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RESULT 8
AF205888 2538 bp mRNA PRI 03-JAN-2000
LOCUS Homo sapiens AXIN2 (AXIN2) mRNA, complete cds.
DEFINITION AF205888
ACCESSION AF205888.1 GI:6653583
VERSION
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 2538)
Zhang,T., Fagotto,F., Hsu,W., Zeng,L., Gilbert,D., Copeland,N.G.,
Jenkins,N.A., Warburton,D. and Costantini,F.
Properties of mouse Axin2 and human AXIN2: chromosomal location,
expression pattern, interaction with Axin and effects on embryonic
axis formation
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2538)
Zhang,T. and Costantini,F.
AUTHORS Direct Submission
TITLE Submitted (16-NOV-1999) Genetics & Development, Columbia
JOURNAL University, 701 W168th St. HHSC 1416, New York, NY 10032, USA
FEATURES
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110. 2443
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/db_xref="GI:6653584"
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KQOIDSIMFDOAGTIEIGVMEBNAYOMFLTSDIYLEYRSGGENTAVYNSNGIGSLK
VVCGLPTLNEEEMTCADFCKLSPTVGLSKTLRATVASYRSTETVDSGYRSPKRS
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ORIGIN

Query Match
Best Local Similarity 86.9%; Pred. No. 1.4e-27; Length 2538;
Matches 133; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

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DB 2267 ttgaccctggcaccctttaaagacagctcagcaaaaaggaaattatagctattcttc 2326
|||||

QY 61 aagaagcgagtgacgaatttgcctcgagagcagcttttgaagagatcggagcagcag 120
|||||
DB 2327 aaaaaagcaagcagatgagttgcttgcagcggctgttgagagagatctggagagatgag 2386
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QY 121 acagtgctcccatgtacgaagcagagctctc 153
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DB 2387 acggtctcccatgtatgagagcggcagattctg 2419
|||||

RESULT 9
AF078165 3072 bp mRNA PRI 21-MAR-1999
LOCUS Homo sapiens conductin mRNA, complete cds.
DEFINITION AF078165
ACCESSION AF078165
VERSION AF078165.1 GI:4454790
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 3072)
Mali,M., Qian,C., Yokomizo,A., Smith,D.I. and Liu,W.
Cloning of the human homolog of conductin (AXIN2), a gene mapping
to chromosome 17q23-q24
JOURNAL Genomics 55 (3), 341-344 (1999)
MEDLINE 99168905
REFERENCE 2 (bases 1 to 3072)
Mali,M., Qian,C., Smith,D.I. and Liu,W.
AUTHORS Direct Submission
TITLE Submitted (15-JUL-1998) Lab Medicine and Pathology, Mayo Clinic,
JOURNAL 200 First Street SW, Rochester, MN 55905, USA
FEATURES
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1. 3072
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1. 2621
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CDS

mutation due to an IAP insertion in the Axin gene"

<1. .2981

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/function="may inhibit embryonic axis formation"
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HSLLDDQDGISLFRFLKQEGCADDLDFWACSGFRKLEPCDSNEEKRLKLARAIYRK

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EQQSLSSDADTLSTLSDSSVDGIPPRIRKQKRRREMQESIQVNGRVPPLPHIPRTYRMPKPKK

ΕΙΡΕΡΟΚΕΑΕΕΛΙΗΡΛΕΑΥΟΤΤΡΕΑΕΕΚΛΕΕΡΛΚΡΥΜΕΕΕΓΕΔΓΕΜΡΣΓΜΑΗΚΛ

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GAVHPWWSAQLRNSVQPSHLEIQDDPTMPNPAPNPILTQLEARRRLEEKKRANKLPSS

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DEPVLPRFEKKLIGKVEKD-
1012 g 1088 g 771 t

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Best Local Similarity 71.5%; Pred. No. 2.5e-15;
Matches 108; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Matches	108;	Conservative	0;	Mismatches	43;	Indels	0;	Gaps	0;
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62 agaaagcagacgacgaatctgcctcgagagcaagcttcttgaggagatctcgagacgagaga 121

2025

[illegible]

122 cagtcgcctcccaatgacgaagcgacgattcc 152

Search completed: June 7, 2001, 00:36:17
Job time: 20991 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 7, 2001, 00:31:59 ; Search time 276.75 Seconds
(without alignments)
322.741 Million cell updates/sec

Title: US-09-587-574-10
Perfect score: 153
Sequence: 1 ttgaacctggccacttcaa.....ttgacgaagcagatctctg 153

Scoring table: IDENTITY-NUC
Gapop 10.0, Gapext 1.0

Searched: 678276 seqs, 291890651 residues
Total number of hits satisfying chosen parameters: 1336552

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	153	100.0	2523	20	X23370 Human conductin CD
2	153	100.0	2825	20	X23369 Human conductin DN
3	121	79.1	401	21	A77754 cDNA encoding huma
4	121	79.1	1205	21	A77843 cDNA encoding huma
5	88.6	57.9	3411	20	X09012 Human axin gene.
6	82.2	53.7	3761	20	X09013 Murine axin gene.
7	33	21.6	925	12	Q12839 Variable region of
8	30.2	19.7	657	14	Q36133 M4H7 Mab heavy ch
9	29.6	19.3	363	21	C41830 Arabidopsis thalia
10	29.6	19.3	575	21	C33133 Arabidopsis thalia
11	29.6	19.3	623	21	C51167 Arabidopsis thalia

12	29.6	19.3	627	21	C38945 Arabidopsis thalia
13	29.6	19.3	811	21	C51169 Arabidopsis thalia
14	29.6	19.3	825	21	C35517 Arabidopsis thalia
15	29.2	19.1	340	16	T19983 Human gene signatu
16	29.2	19.1	1397	21	A52642 Eosinophil activat
17	29.2	19.1	1484	21	C47412 Arabidopsis thalia
18	29.2	19.1	1487	21	C36225 Arabidopsis thalia
19	28.8	18.8	1815	21	C79811 Human secreted pro
20	28.8	18.8	5503	21	C74570 Human ORX ORF125
21	28.4	18.6	1021	21	C37835 Arabidopsis thalia
22	28.2	18.4	457	21	A67611 Eucalyptus grandis
23	28	18.3	1130	21	C40313 Arabidopsis thalia
24	28	18.3	1130	21	C48750 Arabidopsis thalia
25	27.6	18.0	1404	18	T93777 cDNA encoding Arab
26	27.6	18.0	1890	20	Z52940 Human prostate tum
27	27.4	17.9	1041	21	A49788 Arabidopsis wax sy
28	27.4	17.9	1041	21	A38860 Arabidopsis wax sy
29	27.4	17.9	10942	20	V171742 Human V3 loop HIV
30	27.2	17.8	559	21	C65784 Human lung cancer-
31	27.2	17.8	1289	21	P12525 Aspergillus oryzae
32	27	17.6	6741	21	A10595 Gene encoding a su
33	26.8	17.5	300	20	Z14749 Human gene express
34	26.8	17.5	765	20	Z16081 Human gene express
35	26.8	17.5	8102	20	X13181 Enterococcus faeca
36	26.6	17.4	744	20	Z15741 Human gene express
37	26.6	17.4	1935	20	Z30413 Arabidopsis thalia
38	26.6	17.4	2148	21	C44660 Arabidopsis thalia
39	26.4	17.3	770	20	Z15585 Human gene express
40	26.4	17.3	1166	20	Z19440 M. tuberculosis an
41	26.4	17.3	1166	20	Z19228 Arabidopsis thalia
42	26.4	17.3	1242	21	C35947 Arabidopsis thalia
43	26.4	17.3	1377	21	C91259 Coa ligase fccf nu
44	26.4	17.3	8648	20	X20550 Polynucleotide seq
45	26.4	17.3	24494	21	Z91253 Bacterium 2412.1 f

ALIGNMENTS

RESULT 1	
ID X23370	standard; CDNA: 2523 BP.
XX X23370:	
XX	17-JUN-1999 (first entry)
XX	
DE	Human conductin cDNA.
XX	
KW	Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour;
KW	therapy; cytoplasmic degradation; blockade; Wnt signalling pathway;
KW	Wingless signalling pathway; Adenomatous Polyposis Coll.; APC;
KW	tumour suppressor; ss.
XX	
OS	Homo sapiens.
XX	
PN	W09911780-A2.
XX	
PD	11-MAR-1999.
XX	
PF	01-SEP-1998: 98WO-DE02621.
XX	
PR	02-SEP-1997: 97DE-1038205.
XX	
PA	(DELB-) DELBRUECK CENT MOLECULAR MEDIZIN MAX.
XX	
PI	Behrens J, Birchmeier W;
XX	
DR	WPI; 1999-214706/18.
XX	
PT	P-PSDB; W93570..
XX	
PT	Tumor-suppressing protein conductin - used for treatment and
	diagnosis of tumors

XX Claim 18; Fig 3; 22pp; German.
PS
XX
CC This invention describes a novel human conductin protein which has
CC anti-tumour activity. Detecting the presence or amount of conductin,
CC at protein or nucleic acid levels, is used to diagnose tumours, while
CC agents that (re)activate conductin are used for tumour therapy.
CC Conductin binds to beta-catenin and induces its cytoplasmic degradation,
CC resulting in blockade of the Wnt/Wingless signalling pathway in
CC vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC)
CC fragments and, in conjunction with APC, acts as a tumour suppressor.
XX
SQ Sequence 2523 BP; 620 A; 728 C; 723 G; 452 T; 0 other;

Query Match 100.0%; Score 153; DB 20; Length 2523;
Best Local Similarity 100.0%; Pred. No. 5.1e-41;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2407 aagaagcgagtgacgaatttgcctcgcgagcagcttttgaaggagactcggagcagcag 2466
QY 121 acagtgtcccccatacgaaggcagcagctcgt 153
|||
Db 2467 acagtgtcccccatacgaaggcagcagcagctcgt 2499

RESULT 2
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ID X23369 standard; cDNA; 2825 BP.
XX
AC X23369;
XX
DT 17-JUN-1999 (first entry)
XX
DE Human conductin DNA.
XX
KW Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour;
KW therapy; cytoplasmic degradation; blockade; Wnt signalling pathway;
KW Wingless signalling pathway; Adenomatous Polyposis Coli; APC;
KW tumour suppressor; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 215..2737
FT /tag= a
FT /product= "Conductin"
FT 446..814
FT /tag= b
FT /note= "regulator of G-protein signalling region as
FT 1241..1402 described in Claim 19"
FT /tag= c
FT /bound_moiety= GSK-3beta
FT 1403..1609 /note= "as described in Claim 20"
FT /tag= d
FT /bound_moiety= beta-catenin
FT /note= "as described in Claim 21"
FT 2561..2713 /tag= e
FT /note= "Dishevelled homology region as described in
FT Claim 22"
XX
XX WO9911780-A2.
XX
XX 11-MAR-1999.
XX
PD

XX
PF 01-SEP-1998; 98WO-DE02621.
XX
XX
PR 02-SEP-1997; 97DE-1038205.
XX
XX
PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI Behrens J, Birchmeier W;
XX
DR WPI: 1999-214706/18.
DR P-PSDB; W93569.
XX
PT Tumor-suppressing protein conductin - used for treatment and
PT diagnosis of tumors
XX
PS Claim 18; Fig 2; 22pp; German.
XX
CC This invention describes a novel human conductin protein which has
CC anti-tumour activity. Detecting the presence or amount of conductin,
CC at protein or nucleic acid levels, is used to diagnose tumours, while
CC agents that (re)activate conductin are used for tumour therapy.
CC Conductin binds to beta-catenin and induces its cytoplasmic degradation,
CC resulting in blockade of the Wnt/Wingless signalling pathway in
CC vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC)
CC fragments and, in conjunction with APC, acts as a tumour suppressor.
XX
SQ Sequence 2825 BP; 703 A; 815 C; 813 G; 494 T; 0 other;

Query Match 100.0%; Score 153; DB 20; Length 2825;
Best Local Similarity 100.0%; Pred. No. 5.3e-41;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2561 ttgacctgggccaactcaaggagcagctcagcaaaaagggaattacaggtattttc 2620
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QY 121 acagtgtcccccatacgaaggcagcagctcgt 153
|||
Db 2681 acagtgtcccccatacgaaggcagcagcagctcgt 2713

RESULT 3
A77754
ID A77754 standard; cDNA; 401 BP.
XX
AC A77754;
XX
DT 14-NOV-2000 (first entry)
XX
DE cDNA encoding human colon tumour polypeptide, SEQ ID NO:33.
XX
KW Human colon tumour polypeptide; tumour antigen; cancer; vaccine;
KW immunotherapy; diagnosis; progression; ss.
XX
OS Homo sapiens.
XX
XX WO200037643-A2.
XX
XX
XX
PD 29-JUN-2000.
XX
PF 23-DEC-1999; 99WO-US30909.
XX
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XX 23-DEC-1998; 98US-0221298.
XX
XX 02-JUL-1999; 99US-0347496.
XX
XX 22-SEP-1999; 99US-0401064.
XX
XX 19-NOV-1999; 99US-0444242.
XX
XX 02-DEC-1999; 99US-0454150.
XX

xx	DT		14-JUN-1999	(first entry)
xx	DE		Human axin gene.	
xx	KW	Axin; cancer; breast cancer; colorectal cancer;		
xx	RW	gastrointestinal cancer; esophageal cancer; melanoma;		
xx	KM	diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;		
xx	OS	beta-catenin; ss.		
xx	Key	Location/Qualifiers		
xx	CDS	2..2704		
xx	FT	/tag= a		
xx	FT	/product= Axin		
xx	PN	MO9902179-A1.		
xx	PD	21-JAN-1999.		
xx	PF	09-JUL-1998; 98WO-US14414.		
xx	PR	10-JUL-1997; 97US-0890865.		
xx	PA	(UYCO) UNIV COLUMBIA NEW YORK.		
xx	PI	Constantini F, Zeng L;		
xx	DR	WPI; 1999-120510/10.		
xx	P-PSDB:	W96264.		
xx	PT	Newly isolated nucleic acid encoding "axis inhibition" protein		
xx	PT	(Axin) - useful for detecting, diagnosing and treating cancer		
xx	PS	Disclosure; Figure 10A-10B; 95pp; English.		
xx	CC	Nucleic acids encoding mutant and wild type Axin and		
xx	CC	oligonucleotides derived from them are useful for detecting		
xx	CC	mutations in the Axin gene and for determining whether a subject is		
xx	CC	likely to develop cancer (including breast, colorectal,		
xx	CC	gastrointestinal, esophageal, carcinomas or melanomas). The wild		
xx	CC	type Axin and homologues of Axin are useful for treating subjects		
xx	CC	who are likely to develop cancer (thyroid carcinomas). The nucleic		
xx	CC	acids are also useful for diagnosing cancer and for detecting		
xx	CC	mutations in cancerous cells. Wild type Axin, its antisense		
xx	CC	molecule and identified compounds form pharmaceutical compositions		
xx	CC	in the treatment of cancer. The compositions are also useful for		
xx	CC	treating cancer by inhibiting tumorigenesis (by inducing degradation		
xx	CC	of beta-catenin). The nucleic acid encoding Axin acts through		
xx	CC	negative regulation of the Wnt pathway in the Nieuwkoop Center.		
xx	Sequence	3411BP; 752 A; 1010 C; 1066 G; 582 T; 1 other;		

[illegible]

ID	XO9013
XX	standard; DNA; 3761 BP.
AC	XO9013;
DT	14-JUN-1999 (first entry)
DE	Murine axin gene.
KW	Axin; cancer; breast cancer; colorectal cancer;
KW	gastrointestinal cancer; esophageal cancer; melanoma;
KW	diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;
KW	beta-catenin; ss.
OS	Mus musculus.
FH	Key Location/Qualifiers
FT	CDS 1..2981
FT	/tag= a
FT	/product= Axin
PN	WO9902179-A1.
XX	21-JAN-1999.
PD	09-JUL-1998; 98WC-US14414.
PF	10-JUL-1997; 97US-0890865.
PR	(UYCO) UNIV COLUMBIA NEW YORK.
PA	Constantini F, Zeng L;
P1	WPI: 1999-120510/10.
DR	P-PSDB; W96265.
PT	Newly isolated nucleic acid encoding "axis inhibition" protein
XX	(Axin) - useful for detecting, diagnosing and treating cancer
PS	Claim 7; Figure 9A-9B; 95pp; English.
CC	Nucleic acids encoding mutant and wild type Axin and
CC	oligonucleotides derived from them are useful for detecting
CC	mutations in the Axin gene and for determining whether a subject is
CC	likely to develop cancer (including breast, colorectal,
CC	gastrointestinal, esophageal, carcinomas or melanomas). The wild
CC	type Axin and homologues of Axin are useful for treating subjects
CC	who are likely to develop cancer (thyroid carcinomas). The nucleic
CC	acids are also useful for diagnosing cancer and for detecting
CC	mutations in cancerous cells. Wild type Axin, its antisense
CC	molecule and identified compounds form pharmaceutical compositions
CC	in the treatment of cancer. The compositions are also useful for
CC	treating cancer by inhibiting tumorigenesis (by inducing degradation
CC	of beta-catenin). The nucleic acid encoding Axin acts through
CC	negative regulation of the Wnt pathway in the Nieuwkoop Center.
XX	Sequence 3761 BP; 890 A; 1012 C; 1088 G; 771 T; 0 other;

Query Match	53.7%	Score 82.2	DB 20	Length 3761
Best Local Similarity	71.5%	Pred. No. 1.5e-17		
Matches 108	Conservative 0	Mismatches 43	Indels 0	Gaps 0
QY	2	tgacctgtggccacttcaagagacagctcagcaaaaagggaattacagtattatttca	61	
Db	2806	tcacctgtggccagtctcaagagagctgtcaacaaaggagagctacagctactacttca	2865	
QY	62	agaaagcaggtacgaatttctgcgtcggaagcagtttttggggagatctgggaagagaa	121	
Db	2866	agaaagctgagtgatgagcttgcagctgctgtgtgtgattcttggaggaatcagggagagc	2925	
QY	122	cagtgctcccatgtacgaagcaggaatcct	152	

DB 2926 ccgcttcgctcttcttgagaagaatcat 2956

RESULT 7

ID 012839 standard; DNA: 925 BP.

AC 012839;

DT 17-OCT-1991 (first entry)

DE Variable region of u type heavy chain specific for LPS of
Pseudomonas aeruginosa.

XX Monoclonal antibody; ss.

XX Homo sapiens.

Key Location/Qualifiers
FH 366..729
FT /tag= a
FT /label= VH
FT /note= "Claim 3"

PN JP03151876-A.

PD 28-JUN-1991.

PF 08-NOV-1989; 89JP-0291981.

PR 08-NOV-1989; 89JP-0291981.

PA (SUMO) SUMITOMO CHEM IND KK.
(SUMI -) SUMITOMO SEIYAKU KK.

XX WPI: 1991-234064/32.

DR P-PSDB; R13182.

XX Human antibody gene and corresp. recombinant plasmid or virus -
PT useful in mass -prodn. of human anti Pseudomonas aeruginosa LPS
PT outside core antibody.

XX Disclosure: Fig 2; 16pp; Japanese.

XX The region encoding the VH region is used to construct a recombinant
CC antibody with a lambda light chain. The antibody recognises an
CC antigenic determinant on the outside core in LPS of P. aeruginosa.
CC See also Q12840.

XX

XX

SQ Sequence 925 BP; 186 A; 231 C; 270 G; 237 T; 1 other;

Query Match 21.6%; Score 33; DB 12; Length 925;
Best Local Similarity 53.5%; Pred. No. 0.17;

Matches 69; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 21 gggagcgcgcgaagaaaggaattacaggtatttcaagaagcgagtgacgaatt 80
DB 608 gcaactgaaacagcctgaattctgagacacgcctcttactctgtgagagagaata 667

QY 81 tgcctcggagcagcgttttggagagatctggagcagcagcagtgctcccatgtacga 140
DB 668 tgcctcggcctggggtcttctgatactcgggccaaggaacaatgctacgcgtcttc 727

QY 141 aggcaggaat 149
DB 728 aggtaaagat 736

RESULT 8

Q36133 standard; DNA: 657 BP.

AC Q36133;

DT 25-MAY-1993 (first entry)

DE MH4H7 MAb heavy chain coding sequence.

XX Human; heavy chain; recombinant; monoclonal; antibody; MAb; MH4H7;
KW Namalwa; microbial infection; ss.

XX Synthetic.

Key Location/Qualifiers
FH 134..657
FT /tag= a
FT /tag= b
FT /tag= c
FT /tag= d

FT /number= Exon 1
FT /number= Exon 2

FT /number= Intron 1
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RESULT 9

C41830 standard; DNA: 363 BP.

Query Match 19.7%; Score 30.2; DB 14; Length 657;
Best Local Similarity 52.8%; Pred. No. 1.3;

Matches 65; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 21 gggagcgcgcgaagaaaggaattacaggtatttcaagaagcgagtgacgaatt 80
DB 534 gcaactgaaacagcctgaattctgagacacgcctcttactctgtgagagagaata 593

QY 81 tgcctcggagcagcgttttggagagatctggagcagcagcagtgctcccatgtacga 140
DB 594 tgcctcggcctggggtcttctgatactcgggccaaggaacaatgctacgcgtcttc 653

QY 141 agg 143
DB 654 agg 656

AC C41830;
XX 17-OCT-2000 (first entry)
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 33289.
DE
XX
XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX Arabidopsis thaliana.
OS
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
PF
XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0123788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
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Best Local Similarity 54.6%; Pred. No. 1.6;
Matches 59; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Oy 22 gagcagctcagcaagaaggaaattacaggtatattcaagaaggcgagcaaat 81
Db 148 gagagaacactacgaagactctcttcaagaagcttcttcaagtgactgtgactaact 207
Oy 82 gctctgagagcagtttcttgagagactctggaagcagcagacagtgtc 129
Db 208 gtaccgcgcctgtgtctatgatctggaaggaagaagtgtgtc 255

RESULT 10
C33133
ID C33133 standard; DNA; 575 BP.
XX
AC C33133;
XX
DT 17-OCT-2000 (first entry)

XX Arabidopsis thaliana DNA fragment SEQ ID NO: 1908.
DE Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX Arabidopsis thaliana.
OS EP1033405-A2.
PN
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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PR 18-JUN-1999; 99US-0139763.

KW Hybridisation assay; genetic mapping; gene expression control;
KM protein identification; signal transduction pathway;
XX metabolic pathway; promoter; termination sequence; ss.
OS Arabidopsis thaliana.
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
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PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
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PR 11-MAY-1999; 99US-0134256.
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PR 20-MAY-1999; 99US-0135124.
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PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136821.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
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QY 82 gctctggagagcagcttttggagagcagtcggaagcagcagtcgctc 129
DB 468 gtatccggccctgtgtgtctatgactctggagaaagaatgtgtgc 515

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XX 17-OCT-2000 (first entry)
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KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX Arabidopsis thaliana.
OS
PN EP1033405-A2.
XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.
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Oy 82 gctcgcgagcagtttcttgaggagatctggagcagcagacagtgctc 129
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AC T19983;
XX 17-JUL-1996 (first entry)
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DE
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XX Gene signature; messenger RNA; mRNA; relative abundance; frequency;
KW human cloning; mapping; non-biased library; diagnosis; detection;
KW cell typing; abnormal cell function; ss.
XX
XX Homo sapiens.
OS
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XX W09514772-A1.
PN
XX 01-JUN-1995.
XX
XX
XX 11-NOV-1994; 94WO-JP01916.
XX
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 7, 2001, 00:26:48 ; Search time 136.23 Seconds

(Without alignments)
196.096 Million cell updates/sec

Title: US-09-587-574-10

Sequence: 1 ttgacctggccactca.....ttctgaagcagctctg 153

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	27.6	18.0	1167	1	US-08-261-110A-3	Sequence 3, Appl
2	27.6	18.0	1404	1	US-08-261-110A-1	Sequence 1, Appl
3	27.2	17.8	559	4	US-09-040-984-45	Sequence 45, Appl
4	26.6	17.4	4565	3	US-08-776-265-2	Sequence 2, Appl
5	26	17.0	1902	2	US-09-258-257-1	Sequence 1, Appl
6	26	17.0	1902	2	US-09-258-371-1	Sequence 1, Appl
7	26	17.0	1902	4	US-08-569-721A-1	Sequence 1, Appl
8	26	17.0	1902	4	US-08-751-230-1	Sequence 1, Appl
9	26	17.0	1902	4	US-09-499-082-1	Sequence 1, Appl
10	26	17.0	2061	4	US-09-258-371-9	Sequence 9, Appl
11	26	17.0	2061	4	US-08-751-230-9	Sequence 9, Appl
12	26	17.0	2061	4	US-08-846-762-1	Sequence 9, Appl
13	26	17.0	24417	2	US-08-469-412A-3	Sequence 3, Appl
14	25.4	16.6	2432	2	US-09-021-715-3	Sequence 3, Appl
15	25.4	16.6	2667	2	US-08-469-412A-1	Sequence 1, Appl
16	25.4	16.6	2667	4	US-09-021-715-1	Sequence 1, Appl
17	25.4	16.6	10825	3	US-08-652-265-3	Sequence 3, Appl
18	25.4	16.6	10825	3	US-08-652-265-5	Sequence 5, Appl
19	25.4	16.6	10825	3	US-08-652-265-7	Sequence 7, Appl
20	25.4	16.6	10825	4	US-08-834-497A-1	Sequence 1, Appl
21	25.4	16.6	10825	4	US-08-834-497A-3	Sequence 3, Appl
22	25.4	16.6	10825	4	US-08-834-497A-5	Sequence 5, Appl
23	25.4	16.6	10825	4	US-08-834-497A-7	Sequence 7, Appl
24	25.4	16.6	10825	4	US-08-834-497A-9	Sequence 9, Appl
25	25.4	16.6	51952	4	US-08-947-823-1	Sequence 1, Appl
26	25.4	16.6	246240	2	US-08-724-394A-20	Sequence 20, Appl

28	25.4	16.6	246240	2	US-08-724-394A-21	Sequence 21, Appl
29	25.4	16.6	246240	4	US-08-724-394A-22	Sequence 22, Appl
30	25	16.3	1289	4	US-08-358-627F-22	Sequence 22, Appl
31	25	16.3	1620	6	5449756-10	Patent No. 5449756
32	25	16.3	2306	6	5198359-3	Patent No. 5198359
33	25	16.3	2306	6	5449756-3	Patent No. 5449756
34	25	16.3	5057	3	US-08-651-999A-6	Sequence 6, Appl
35	25	16.3	11461	3	US-08-669-161A-29	Sequence 29, Appl
36	24.8	16.2	2574	2	US-08-677-734A-8	Sequence 8, Appl
37	24.6	16.1	3523	4	US-08-860-635A-20	Sequence 20, Appl
38	24.6	16.1	34303	2	US-08-735-609-4	Sequence 4, Appl
39	24.6	16.1	34303	2	US-08-735-609-4	Sequence 4, Appl
40	24.6	16.1	34303	3	US-09-315-372-4	Sequence 4, Appl
41	24.6	16.1	34303	3	US-09-244-752-4	Sequence 4, Appl
42	24.6	16.1	34303	3	US-09-245-497-4	Sequence 4, Appl
43	24.6	16.1	35935	2	US-08-735-609-1	Sequence 1, Appl
44	24.6	16.1	35935	2	US-08-735-609-1	Sequence 1, Appl
45	24.6	16.1	35935	3	US-08-379-452-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-08-261-110A-3

Sequence 3, Application US/08261110A
Patent No. 5674992

GENERAL INFORMATION:

APPLICANT: JACENDORF, ANDRE

APPLICANT: CERUTTI, HERBERTO

TITLE OF INVENTION: CDNA ENCODING A RECA HOMOLOG IN

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESSES:

ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP

STREET: CLINTON SQUARE, P.O. BOX 1051

CITY: ROCHESTER

STATE: NEW YORK

COUNTRY: USA

ZIP: 14603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

FILING DATE: 16-JUN-1994

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/938,332

FILING DATE: 28-AUG-1992

ATTORNEY/AGENT INFORMATION:

NAME: TIMIAN, SUSAN J.

REGISTRATION NUMBER: 34,103

REFERENCE/DOCKET NUMBER: 19603/10231(D-1292A)

TELEPHONE: (716) 263-1636

TELEFAX: (716) 263-1600

INFORMATION FOR SEQ. ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1167 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-08-261-110A-3

Query Match 18.0%; Score 27.6; DB 1; Length 1167;
Best Local Similarity 58.5%; Pred. No. 2.4;
Matches 48; Conservative 0; Mismatches 34; Indels 0; Gaps 0;


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Query Match          17.4%: Score 26.6; DB 3; Length 4565;
Best Local Similarity 63.1%: Pred. No. 9.1;
Matches 41: Conservative 0; Mismatches 24; Indels 0; Gaps 0.

Oy 13 cacttcagaagcgacgctcagcaaaaagggaattcaggtcattcctcaagaagcgagt 72
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4273 CACCTCGATGATGATGCTACACCTAAAAAGAAATTAAGAAAAATTATTTCATTAAGGTGCA 4214

Oy 73 gagcga 77
      ||||
Db 4213 CACGA 4209

RESULT 5
: Sequence 1, Application US/09258257
: Patient No. 5965398
: GENERAL INFORMATION:
: APPLICANT: GARKAVTSEV, Igor
: APPLICANT: RIABOMOL, Karl
: TITLE OF INVENTION: DNA SEQUENCE ENCODING A TUMOR
: TITLE OF INVENTION: SUPPRESSOR GENE
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Burns, Doane, Swecker & Mathis
: STREET: P.O. Box 1404
: CITY: Alexandria
: STATE: Virginia
: COUNTRY: United States
: ZIP: 22313-1404
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/258,257
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/569,721
: FILING DATE: 08-DEC-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Mool, Leslie A.

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Query Match Similarity      17.0%; Score 26; DB 2; Length 1902;
Best Local Similarity      57.3%; Pred. NO. 10;
Matches 47; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY      6  cctgggcacttcaaggagcagctcagcaaaaagggaattcaggtatttccaagaa 65
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      1132 CATGCCAATTAAAAAAATGTTCTATAAGTAATAATATTCTGTATTAATAAAAA 1073

QY      66  ggcgagtgacgaatttcgctgc 87
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      1072 AGCTAATGAATAATATTTCCTTC 1051

RESULT      6
US-09-258-371-1/C
; Sequence 1, Application US/09258371
; Patent No. 5986078
; GENERAL INFORMATION:
; APPLICANT: Garkavtsev, Igor
; APPLICANT: Ribowol, Karl
; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
; TITLE OF INVENTION: SUPPRESSOR GENE INCI
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/258.371
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/751,230
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mool, Leslie A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 028722-144
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1902 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

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? APPLICANT: Helbing, Caren C.
? APPLICANT: Riabowol, Karl
? APPLICANT: Johnston, Randall N.
? APPLICANT: Garkavtsev, Igor
? TITLE OF INVENTION: METHODS OF MODULATING APOPTOSIS
? NUMBER OF SEQUENCES: 23
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Burns, Doane, Swecker & Mathis
? STREET: 699 Prince Street
? CITY: Alexandria
? STATE: VA
? COUNTRY: USA
? ZIP: 22313-1404
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/499,082
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/08/828,158
? FILING DATE: 27-MAR-1997
? APPLICATION NUMBER: US 08/751230
? FILING DATE: 15-NOV-1996
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/569721
? FILING DATE: 08-DEC-1995
? ATTORNEY/AGENT INFORMATION:
? NAME: Mool, Leslie A.
? REGISTRATION NUMBER: 37,047
? REFERENCE/DOCKET NUMBER: 028722-148
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 650-854-7400
? TELEFAX: 650-854-8275
? INFORMATION FOR SEQ. ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1902 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 109..741
?
? US-09-499-082-1
?
Query Match 17.0%; Score 26; DB 4; Length 1902;
Best Local Similarity 57.3%; Pred. No. 10;
Matches 47; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
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OY 6 cctgggaccattcaaggagcgtcagcaaaagggaattacaggtatattccaagaa 65
DB 1132 CATGGCCAAATTAATAAAATTTTCATTAAGTATATATTACTTGTTAATAATAA 1073
?
OY 66 ggcgagtgacgaattgctgc 87
DB 1072 ACCTAATGAATATTTTCCTTC 1051
?
RESULT 10
? US-09-258-371-9/C
? Sequence 9, Application US/09258371
? Patent No. 5986078
? GENERAL INFORMATION:
? APPLICANT: Garkavtsev, Igor
? APPLICANT: Riabowol, Karl
? TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
? NUMBER OF SEQUENCES: 23
? SUPPRESSOR GENE INGI
```

```

? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Burns, Doane, Swecker & Mathis
? STREET: 699 Prince Street
? CITY: Alexandria
? STATE: VA
? COUNTRY: USA
? ZIP: 22313-1404
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/258,371
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/751,230
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Mool, Leslie A.
? REGISTRATION NUMBER: 37,047
? REFERENCE/DOCKET NUMBER: 028722-144
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415-854-7400
? TELEFAX: 415-854-8275
? INFORMATION FOR SEQ. ID NO: 9:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 2061 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 16..900
?
? US-09-258-371-9
?
Query Match 17.0%; Score 26; DB 2; Length 2061;
Best Local Similarity 57.3%; Pred. No. 11;
Matches 47; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
?
OY 6 cctgggaccattcaaggagcgtcagcaaaagggaattacaggtatattccaagaa 65
DB 1291 CATGGCCAAATTAATAAAATTTTCATTAAGTATATATTACTTGTTAATAATAA 1232
?
OY 66 ggcgagtgacgaattgctgc 87
DB 1231 ACCTAATGAATATTTTCCTTC 1210
?
RESULT 11
? US-08-751-230-9/C
? Sequence 9, Application US/08751230
? Patent No. 6117633
? GENERAL INFORMATION:
? APPLICANT: Garkavtsev, Igor
? APPLICANT: Riabowol, Karl
? TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
? NUMBER OF SEQUENCES: 23
? SUPPRESSOR GENE INGI
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Burns, Doane, Swecker & Mathis
? STREET: 699 Prince Street
? CITY: Alexandria
? STATE: VA
? COUNTRY: USA
? ZIP: 22313-1404
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,230
FILING DATE: 15-NOV-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: MOOI, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-144
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2061 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 16..900
US-08-751-230-9

Query Match 17.0%; Score 26; DB 4; Length 2061;
Best Local Similarity 57.3%; Pred. No. 11;
Matches 47; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

OY 6 cctgggccactcaaggagcagctcagcaaaagggaattcaggtattttcaagaa 65
DB 1291 CATGGCCATTAAAAAATTTGTCATTAAGTAATTAATTTACTGTATTAATAAAAA 1232
OY 66 ggcgagtgacgaattgcctgc 87
DB 1231 ACCTAATGAATATTTTCCTTC 1210

RESULT 12
US-09-499-082-9/C
Sequence 9, Application US/09499082
Patent No. 6143522
GENERAL INFORMATION:
APPLICANT: Heibing, Caren C.
APPLICANT: Rabbowol, Karl
APPLICANT: Johnston, Randall N.
APPLICANT: Garkavtsev, Igor
TITLE OF INVENTION: METHODS OF MODULATING APOPTOSIS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/499,082
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/828,158
FILING DATE: 27-MAR-1997
APPLICATION NUMBER: US 08/751230
FILING DATE: 15-NOV-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: MOOI, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-148
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-854-7400
TELEFAX: 650-854-8275
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2061 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 16..900
US-09-499-082-9

Query Match 17.0%; Score 26; DB 4; Length 2061;
Best Local Similarity 57.3%; Pred. No. 11;
Matches 47; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

OY 6 cctgggccactcaaggagcagctcagcaaaagggaattcaggtattttcaagaa 65
DB 1291 CATGGCCATTAAAAAATTTGTCATTAAGTAATTAATTTACTGTATTAATAAAAA 1232
OY 66 ggcgagtgacgaattgcctgc 87
DB 1231 ACCTAATGAATATTTTCCTTC 1210

RESULT 13
US-08-846-762-1/C
Sequence 1, Application US/08846762A
Patent No. 5994072
GENERAL INFORMATION:
APPLICANT: Lam, Joseph S.
APPLICANT: Burrows, Lori
APPLICANT: Charter, Deborah
APPLICANT: de Kievit, Teresa
TITLE OF INVENTION: OF O-Antigen in Pseudomonas Aeruginosa
FILE REFERENCE: 6580-089
CURRENT APPLICATION NUMBER: US/08/846,762A
CURRENT FILING DATE: 1997-04-30
NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 24417
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-08-846-762-1

Query Match 17.0%; Score 26; DB 2; Length 24417;
Best Local Similarity 50.8%; Pred. No. 28;
Matches 62; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

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DB 20093 TGGCCATGGCCAGACGACGCGCATGACGACGATGCTCAACCCAGTAGTTGAAC 20034
OY 61 aagaagcgagtgacgaatttcctcgagcaggttttgagagatctggagcagcag 120
DB 20033 ACCAGGGAACGGCGACACCGCCGGGGAGCGGTACCAATAGACGACAGCAGG 19974
OY 121 ac 122
11

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 6, 2001, 23:00:49 ; Search time 3054.04 Seconds
(without alignments)
437.657 Million cell updates/sec

Title: US-09-587-574-10
Perfect score: 153
Sequence: 1 ttgaacccgggcacactcaa.....tgtaagaagcagatcctcg 153

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 4368049070 residues

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

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116: gb_est116:*

44: em_esthum10:*
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114: em_esthum80:*
115: em_esthum81:*
116: em_esthum82:*

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117: gb_est48:*
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189: gb_est120:*

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190: em_gss_pln1:*
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192: em_gss_pro:*
193: em_gss_rod1:*
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231: gb_gss31:*
232: gb_gss32:*
233: gb_gss33:*
234: gb_gss34:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	121	79.1	548	7	AA446378	AA446378 zw58b07.r
2	116.8	76.3	495	139	BE755017	BE755017 208720 MA
3	116.8	76.3	546	138	BE668565	BE668565 158407 MA
4	88.6	57.9	1070	165	BE315156	BE315156 601140956
5	88.2	57.6	427	149	BE521997	BE521997 UI-R-YO-a
6	87.6	57.3	319	156	R75687	R75687 y121d06.r1
7	85	55.6	601	165	BE314898	BE314898 601140035
8	83.8	54.8	460	140	BE808273	BE808273 213437 MA
9	83.8	54.8	487	111	AM140896	AM140896 EST290630
10	83.8	54.8	503	143	BF076794	BF076794 226536 MA
11	83.8	54.8	562	143	BF076028	BF076028 225414 MA
12	82.2	53.7	435	3	AA170717	AA170717 ms70a09.r
13	82.2	53.7	476	165	BE333754	BE333754 us27f06.y
14	82.2	53.7	516	1	AA028403	AA028403 m121f04.r
15	82.2	53.7	526	4	AA258709	AA258709 va36f09.r
16	82.2	53.7	553	3	AA153185	AA153185 ms62d10.r
17	80	52.3	471	143	BF039925	BF039925 BP250015A
18	79.8	52.2	443	170	BF889872	BF889872 289473 MA

	Query Match	Best Local Similarity	Matches	Score	DB	Length
	76.3%	85.5%	130	116.8	139	495
			Conservative	Pred. No. 1.2e-26		
			Mismatches	22	Indels	0
			Gaps	0		
QY	2	tgacccttggccactctcaagagacagcagctcaagaanaaggaattacaggtatttca	61			
Db	249	TGACCTTGGGCCACTTTTAAGGAGCAGCTCAGAAAAAGGAACTACCGGTTTACTTCA	308			
QY	62	agaagagcgaatgagcaaatctgccttcgcgagacagtttttgagagagatctggagacagaga	121			
Db	309	AAAAGGCGACGACACAGCTTCGGCTCCGGAGCGCTGTTTGAGAGAGCTCTGGAGCAGCAGAG	368			
QY	122	caatgctcccatcattagagaagcagaatccctg	153			
Db	369	TGGTCTTCCCATGATGACAGAGGCGCCCATCTCTG	400			

RESULT	3						
LOCUS	BE668565						
DEFINITION	BE668565	546 bp	mRNA				
ACCESSION	158407	MARC	ABOV	Bos taurus	CDNA 5',	mRNA sequence.	08-SEP-2000
VERSION	BE668565						
KEYWORDS	BE668565.1	GI:10029156					
SOURCE	EST.						
ORGANISM	COW.						
	Bos taurus						

REFERENCE	1 (Bases 1 to 546)
AUTHORS	Smith, T. P., Casas, E., Stone, R. T., Heaton, M. P., Grosse, W. M., Bennett, G. A., Fahrenkrug, S. C., Fekling, B. A., Rohrer, G. A., Laegreid, W. W., and Keefe, J. W.
TITLE	Design and use of four pooled tissue normalized cDNA libraries for EST discovery in cattle
JOURNAL	Unpublished (2000)
COMMENT	Contact: Smith rpl

Email: smiththemall.marco.usda.gov
 Single pass sequencing. Bases called and alt. trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -mismatch 18
 and -minmatch 12 options.
 PCR Primers
 FORWARD: AGGAACAGCATACGACAT
 BACKWARD: GTTTCACAGTCACGACG
 Plate: 60 row: 0 column: 14
 Seq primer: ATTGAGGACACTATG.
 Location/Qualifiers
 1..546

BASE COUNT	108 a	157 c	200 g	81 t
ORIGIN				

Query Match	76.3%	Score 116.8	DB 138	Length 546
Best Local Similarity	85.5%	Pred. 11.2e-26		
Matches 130	Conservative 0	Mismatches 22	Indels 0	Gaps 0
QY	2	tgaccctggggcactttcaagagcagccctccagcaaaaagggaattacaggtattttca	61	
		TTGACCTTGGGGCACCCTTTAGGAGCAGCGCTCAGCAAAAAAGGAAATACCGGATATCTTCA	100	

[illegible]

RESULT	4
BE315156	
LOCUS	
DEFINITION	BE315156 1070 bp mRNA
ACCESSION	60114095F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140965 5' ,
VERSION	mRNA sequence.
KEYWORDS	BE315156 BE315156 GI:9145550
SOURCE	EST .
ORGANISM	human.
	Homo sapiens

REFERENCE	1 (bases 1 to 1070)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

Email: Robert.Strausberg@nih.gov
 Tissue Procurement: DCDP/DMP
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (ULNL)
 Clone distribution: MGC Clone distribution information can be
 found through the I.M.A.G.E. Consortium/ULNL at: Image.lnl.gov
 Plate: L1CM109 row: 0 column: 14
 High quality sequence stop: 673.
 Location/Qualifiers
 1..1070

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3140965"
/clone_1b="NH_MCC_9"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGCACGAC(G).. Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

```

Query Match	57.9%	Score 88.6	DB 165	Length 1070
Best Local Similarity	74.2%	Pred. No. 1.3e-17		
Matches 112; Conservative	0	Mismatches 39	Indels 0	Gaps 0

QY	2	tgacctggcgccacttcagagagcagctcagcaaaaaagggaattacagytattattca	61
DB	367	TCACCTGGGCGCATTCAGAGAGTGCTGCTGACCAAAAAAGGCGACGTACAGTACTACTTCA	426
QY	62	agaagcgagtgacgaatttgcctcgagagcagtttttggagatctggagcagcagaga	121
DB	427	AGAAAGTGAGCGAGCAGAGTTTACCTGTGTGGGGTGGCTTTGAGGAGGTTCCAGAGACGAGG	486
QY	122	cagtgctcccatgtacgaagcagagctctc	152
DB	487	CCGTCTTCCCGTCTTTGAGAGGAAGATCAT	517

Db 96 AGAAGTACGACGAGAGCTTGCAGTGTGGGCTGTGAGAGAGGTTCCAGAGAGACGAG 155
OY 122 cagtgctcccaagtgacgaagcagagctct 152
Db 156 CCGTCTGCTCCGCTTTNAGAGAGATCAT 186

RESULT 7
LOCUS BE314898 601 bp mRNA EST 26-OCT-2000
DEFINITION 601140055F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049328 5',
mRNA sequence.
ACCESSION BE314898
VERSION BE314898.1 GI:9144981
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 601)
NIH-MGC <http://mhc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: DCTD/DRP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at: image.llnl.gov
Plate: L1CM93 row: e column: 09
High quality sequence stop: 600.

FEATURES
source Location/Qualifiers
1..601
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="3049328"
/clone_lib="NIH_MGC_9"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 127 a 189 c 194 g 91 t
ORIGIN

Query Match 55.6%; Score 85; DB 165; Length 601;
Best Local Similarity 75.2%; Pred. No. 1.5e-16;
Matches 106; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

OY 2 tgaccctgggcacactcaagagcagctcagcaaaaggaattacaggtattattca 61
Db 367 TCACCTGGGCGCAGTTCAAGAGAGCTGCTGACCAAAAAGCAGCTACGATCACTTCA 426
OY 62 agaagcgagtgaggaatttcctcgtcgagcagttttgagagatctggagcagcaga 121
Db 427 AGAAGTACGACGAGAGTGTGACTGTGGGTGAGGTTTGAAGAGGTTGAGAGAGCAGG 486
OY 122 cagtgctcccaagtgacgaagcagagctct 142
Db 487 CCGTCTGCTCCGCTTTTGAGG 507
RESULT 8

BE808273
LOCUS BE808273 460 bp mRNA EST 20-SEP-2000
DEFINITION 213437 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE808273
VERSION BE808273.1 GI:10239385
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 460)
Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid
,W.M. and Keele,J.W.
Design and use of four pooled tissue normalized cDNA libraries for
EST discovery in cattle
Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -mnscore 18
and -mismatch 12 options.
PCR primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCAGCAG
Plate: 68 row: O column: 3
Seq primer: ATTAGGTGACACTATAG.

FEATURES
source Location/Qualifiers
1..460
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from testis, thymus,
semintendonous muscle, longissimus muscle, pancreas,
adrenal, and endometrium."
BASE COUNT 86 a 133 c 166 g 74 t 1 others
ORIGIN

Query Match 54.8%; Score 83.8; DB 140; Length 460;
Best Local Similarity 72.2%; Pred. No. 3.5e-16;
Matches 109; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

OY 2 tgaccctgggcacactcaagagcagctcagcaaaaggaattacaggtattattca 61
Db 147 TCACCTGGGCGCAGTTCAAGAGAGCTGCTGACCAAAAAGCAGCTACGATCACTTCA 206
OY 62 agaagcgagtgaggaatttcctcgtcgagcagttttgagagatctggagcagcaga 121
Db 207 AGAAGTACGACGAGAGTGTGACTGTGGGTGAGGTTTGAAGAGGTTGAGAGAGCAGG 266
OY 122 cagtgctcccaagtgacgaagcagagctct 152
Db 267 CCGTCTGCTCCGCTTTTGAGG 297
RESULT 9
LOCUS AW140896 487 bp mRNA EST 30-OCT-1999
DEFINITION EST290830 Normalized rat embryo, Bonto Soares Rattus sp. cDNA clone
sequence.
ACCESSION AW140896
VERSION AW140896.1 GI:6160589
KEYWORDS EST.

[illegible]

Tel: 402 762 4366
Fax: 402 762 4390
Email: smltlhemail.marc.usda.gov

Single pass sequencing. Bases called and alt.trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -mismatch 12 options.

PCR primers

FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACGTCCAGCAGC
Plate: 87 row: N column: 19
Seq primer: ATTTAGGTGACACTATGAC.

FEATURES

SOURCE

Location/Qualifiers

1..503

/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_id="MARC_2BOV"
/tissue_type="pooled"
/lab_host="DH10B"

/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from testis, thymus,
semiteendonous muscle, longissimus muscle, pancreas,
adrenal, and endometrium."

BASE COUNT

98 a 146 c 185 g 74 t

ORIGIN

Query Match 54.8%; Score 83.8; DB 143; Length 503;
Best Local Similarity 72.2%; Pred.No. 3,5e-16;
Matches 109; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Oy 2 tgacctggccactcttaagagacggtccagcaaaagggaattaccggtatattcca 61
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 267 TCACCCCTGGGCAGATTCAAGAGCGTGACCCAAAGAGGCAACTACAGGTTCACTTCA 326

Oy 62 agaagcgagtcgacaattgcctcgcgagcagtttttgagaagatctcggaacgagaga 121
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 327 AGAAGTAGACGACGACAGTTCGAGTCCGCCGCTGTCGTTTCGAAGAGGTGCGTCGACGACAGG 386

Oy 122 caqtgctcccactgtacgaagcgaggaatcct 152
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 387 CTGTCTGCCCGCTTTCGAGAGAAGATCAT 417

RESULT 11

BFO76028 EST 18-OCT-2000

LOCUS BFO76028 562 bp mRNA

DEFINITION 225414 MARC_2BOV Bos taurus CDNA 5', mRNA sequence.

ACCESSION BFO76028

VERSION BFO76028.1 GI:10869476

KEYWORDS EST.

SOURCE cow.

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 562)
Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grose,W.M.,
Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid
,W.W. and Keele,J.W.

TITLE Design and use of four pooled tissue normalized cDNA libraries for
EST discovery in cattle

JOURNAL Unpublished (2000)

COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel.: 402 762 4366
Fax: 402 762 4390
Email: smltlhemail.marc.usda.gov

Single pass sequencing. Bases called and alt.trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.

PCR primers

FORWARD: AGGAACAGCTATGACCAT

Query Match	Best Local Similarity	Matches 108; Conservative	53.7%; 71.5%;	Score 82.2; Pred. No. 1.1e-15;	DB 165;	Length 476;
0y	2	tgacctggagcacttcgaagagcagctcagcaaaagaaggaataatcaggtatattca	61			
Db	31	TCACCTCGGCCACTTTCACGACGCTGCTACACCAAGAACGGCAGCTACGATACCTTCA	90			
0y	62	agaagagcagatgacacgaattcgcttcgagagcagtttttgaagagatctcggagacgagca	121			
Db	91	AGAAAGTCAGCATGATGAGCTTGTACTGTGTGTGTGTATTTGAGGAACATACGGAGGATGAGG	150			
0y	122	cagtcctcccatgtgtaagaaagcaggtacct	152			
Db	151	CCGCTTGCCTGCTCTTTGAGAAAGATCAT	181			

RESULT	14
AA028403	
LOCUS	AA028403 516 bp mRNA EST 16-AUG-1996
DEFINITION	m211104.c1 Soares mouse embryo NDMEJ3.5 14.5 Mus musculus CDNA
ACCESSION	clone IMAGE:464191 5', mRNA sequence.
VERSION	AA028403
KEYWORDS	AA028403.1 GI:1494524
SOURCE	EST.
ORGANISM	mouse mouse.
	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathl; Muridae; Murinae; Mus. 1 (bases 1 to 516)
AUTHORS	Marras, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Thelning, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
TITLE	The WashU-HHMI Mouse EST Project
JOURNAL	Unpublished (1996)
COMMENT	Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:278007 Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 493.
FEATURES	Location/Qualifiers
source	1..516
	/organism="Mus musculus"
	/strain="C57BL/6J"
	/db_xref="taxon:10090"
	/clone="IMAGE:464191"
	/clone_1tp="Soares mouse embryo NDMEJ3.5 14.5"
	/sex="unknown"

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/issue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/notes: pr773D-Pac (Pharmacia) with a modified
polylinker; site_1: Not I; site_2: Eco RI; 1st strand cDNA
was primed with a Not I - Oligo(dt) primer [5',
TGTGTACCAATCTGTAGAGGAGGCGCCGGAATTTTTTTTTTTTTTTT
T 3'], on equal amounts of mRNA from 2.13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2.1]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pr773 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M.Fatima Bonaldo.

```

Query Match 53.7%; Score 82.2; DB 1; Length 516;
Best Local Similarity 71.5%; Pred. No. 1,1e-15;
Matches 108; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

OY 2 tgcacctgggacacttcgaagagcagcgtcaagcaaaagggaataaccagtatttca 61
| | | | |
.333 TCACCGTGGCCAGATTCAAGGAGCTGTAAACCAAGAAGGAGGACTACAGATCTACTTTA 392
| | | | |

OY 62 agaaagcgagtgtaagaatttcctctcgaggacaglttttgagagatctggagcagaga 121
| | | | |
Db 393 AGAAGTGATGAGTAGCAGATTGACCTGTGGTGTGTATTTGAGAAAGTAAGTACGGAGATGAGG 452
| | | | |

OY 122 cagtgctcccatgttagaaggcagagatcct 152
| | | | |
Db 453 CCGTCCTGCCTGCTTTTGAGAAAAGATCAT 483
| | | | |

RESULT 15
AA259709

LOCUS AA259709 526 bp mRNA EST 18-MAR-1997

DEFINITION v336f09.t1 Soares mouse JMEI2.5 Mus musculus cDNA clone

IMAGE:733481 5', mRNA sequence.

ACCSSION AA259709

VERSION AA259709.1 GI:1896194

KEYWORDS EST.

SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Euteleostomi;
Mammalia; Eutheria; Rodentia; Scleroptera; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 526)

AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K.K., Stepien,M., Tan,F., Underwood,K., Moore,B.,
Theisinger,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.

TITLE The WashU-HMI Mouse EST Project

JOURNAL Unpublished (1996)

COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel.: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
NCBI:450529
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 485.
Location/Qualifiers
1..526
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"

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/clone_lib="Soares mouse 3NME12 5"
/sex="unknown"
/tissue_type="fetus"
/dev_stage="12.5dpc total fetus"
/lab_host="DH10B"
/note="Organ: whole fetus; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
15', TGTACCAATCTGAAGTGGAGCGCGCCCTTATTTTATTTTATTTT
3', on total mouse RNA [provided by Minoru Ko, Wayne
State Univ.]; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      111 a      116 c      172 g      127 t
ORIGIN

```

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Query Match      53.7%; Score 82.2; DB 4; Length 526;
Best Local Similarity 71.5%; Pred. No. 1,1e-15;
Matches 108; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY      2      tgacctgggcaactcaagaagcagctcagcaaaaaaggaattacaggtatttca 61
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DB      112      TCACCTGGGCGCAGTCAAGAGAGCTCTAACCAAGAGGAGAGTACATCTT 171

QY      62      aagaagcgagtgacgaatttcgtcgcgagcagttttgagagatctggagcagaga 121
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DB      172      ACAAAAGTGATGATGCTTGAAGTGGTGTATTGAGGAGTACGAGATGAGG 231

QY      122      cagtgtcccccatgtacgaagcagatcct 152
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DB      232      CCGTCTTGCCCTGCTTTGAAGAAAGATCAT 262

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